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GenCore version 5.1.6
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OM protein - protein search, using sw model

February 10, 2004, 10:48:45; Search time 10.3976 Seconds (without alignments) 1331.870 Million cell updates/sec Run on:

US-10-067-385-8_COPY_630_773 Title:

748 1 HRVTVTIQNGKEMSSTIVSE.....ATVLDKNNISSKSTTNNPNK 144 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	serine proteinase,	metalloproteinase	hypothetical prote	claustrin - chicke	hypothetical prote		д	hypothetical prote					hypothetical prote	_	DNA topoisomerase					hypothetical prote		hypothetical prote	ORF MSV230 hypothe	probable transcrip	rhoptry protein -	hypothetical prote			Ω.
SUMMARIES	ΩI	F95074	A97942	T18467	JC5497	B71609	T18283	G81339	T25911	S46817	T14188	T47835	137271	T37189	A90570	T10466	T18427	T28771	B72291	D86432	T32879	T20410	A84152	T28391	S41552	T28676	B81594	C72074	E86549	867610
	DB	7	~	~	~	~	~	~	7	N	~	~	~	~										~	~	7	~	~	~	04
	Length	2140	2144	558	1038	665	325	312	211	1345	988	644	348	535	622	1397	3724	210	219	540	253	385	614	670	1332	2401	508	508	508	700
**	Match	100.0	99.6	14.7	14.5	13.9	13.8	13.4	13.2	13.0	13.0	12.8	12.7	12.7	12.7	12.7	12.6	12.6	12.4	12.4				~1	Н	-	12	12.0	12.0	12.0
	Score	748	745	110	108.5	104	103.5	100	66	97.5	97	95.5	95	95	95	95	94.5	94	92.5	92.5	91	91	90.5	90.5	90.5	90.5	89.5	89.5	89.5	89.5
	No.	1	~	m	4	S.	9	7	60	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

merilloproteinase (EC 3.4.21.-) A [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C;Accession: A97942
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E
R;Hoskins, J.A.; Alborn Jr., W.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Hile: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234

RESULT 2

ankyrin related pr	unknown protein F2	conserved hypothet	hypothetical prote	hypothetical prote	hypothetical prote	protein T04A8.13 [hypothetical prote	hypothetical prote	hypothetical prote	IgA-specific metal	hypothetical prote	hypothetical prote	microtubule-associ	probable chloroqui	hypothetical prote
T19006	E96795	E89883	T39009	T33068	A71683	G88436	T24435	T23451	96196	A41859	T18477	F71621	QRMSP1	T09079	T49989
7	~	N	~	N	~	7	7	7	7	~	~	7	Н	~	~
1016	528	645	1888	301	371	762	791	276	1280	1702	2523	635	2464	2708	792
12.0	11.9	11.9	11.9	11.8	11.8	11.8	11.8	11.8	11.8	11.7	11.7	11.6	11.6	11.6	11.6
89.5	89	83	83	88.5	88.5	88.5	88.5	88	88	87.5	87.5	87	87	87	86.5
							37								

ALIGNMENTS

RESULT 1 F95074 Serine prot C;Species: C;Date: 03- C;Accession R;Tettelin, on, J.D.; U nson, T.; H Science 293 A;Authors: A;Title: Co A;Reference A;Accession A;Reference A;Accession A;Reference A;Accession A;Ac	RESULT 1 F95.074 Everine proteinase, subtilase family [imported] - Streptococcus pneumoniae (strain TIGR4) C.Species: Streptococcus pneumoniae C.Species: Streptococcus pneumoniae C.Species: Streptococcus pneumoniae C.Species: Old #sequence_revision 03-Aug-2001 C.Species: Old #sequence_revision 03-Aug-2001 C.Species: Old #sequence_revision 03-Aug-2001 C.Species: Old #sequence_revision 03-Aug-2001 C.Jougham, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, On, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, Old #stathors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A.Futle: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A.Facession: P95074 A.Facession: P95074 A.Facession: Ppellminary A.Facession: Ppellminary A.Facession: Porelminary A.Facession: Porelminary A.Facession: Paces Genome Sequence of A.Facession: Residues: L-2140 ckUR> A.Facession: A.Facession: Residues: L-2140 ckUR> A.Facession: A.Facessio
Query Beet Beet Oy Oy Oy Oy Db	Query Match 100.0%; Score 748; DB 2; Length 2140; Best Local Similarity 100.0%; Pred. No. 6.3e-49; 0; Gaps 0; Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 1 HRVTVIIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSK 60

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Page

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Molecule type:
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                                                                                                                                                                                                                                            1967 HRVTVTIONGKEMSSTIVSEEDFILPVYKGELEKGYQPDGWEISGFEGKKDAGYVINLSK 2026
            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2144 «KUR»
A;Cross-references: GB:AE007317; PIDN:AAK99365.1; PID:g15458138; GSPDB:GN00174
C;Genetics:
A;Gene: prtA
C;Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                               DTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDST 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FKKI--EEKKEE------ENKPTFDVSK-KKDNPQVNHSQLNE------SHRK 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NiAlternate names: keratan sulfate proteoglycan
Cispecies: Gallus gallus (chicken)
Cibate: 07-Jul-1997 #sequence_revision 12-Sep-1997 #text_change 21-Jul-2000
CiAccession: JC5497; PC4334; S37561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2002
                                                                                                                                                                                                                            HRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSK
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C;Species: Plasmodium falciparum
                                                                                                                                                                                        0;
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                                                                                                                                                    Length 2144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rilawson, D.; Bowman, S.; Barrell, B.
submitted to the EMBL Data Library, November 1998
A;Reference number: Z18937
A;Accession: T18467
A;Accession: T18467
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-558 claw>
A;Coros-references: EMBL:AL008970; NID:e1407852; PIDN:CAA15610.1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 558
                                                                                                                                                                                          Indels
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                                                                                                                                                       Score 745; DB 2; Le
Pred. No. 1.1e-48;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 14.7%; Score 110; DB 2; Best Local Similarity 29.3%; Pred. No. 0.5; Matches 54; Conservative 23; Mismatches 47,
                                                                                                                                                                                                                                                                                                                                                                                       2087 KDVTATVLDKNNISSKSTTNNPNK 2110
                                                                                                                                                                                                                                                                                                                                                                   KDVTATVLDKNNISSKSTTNNPNK 144
                                                                                                                                                       Query Match
Best Local Similarity 99.3%;
Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 3
A;Introns: 84/1; 160/1
A;Note: C0465c
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A; Accession: A97942
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J. Neŭrobiol. 25, 1-22, 1994
A;Title: Claustrin, an antiadhesive neural keratan sulfate proteoglycan, is structurally,
A;Reference number: JC5497; MUID:94157526; PMID:7906711
                                                                                                                                                                                                                                                                                                                             A, Experimental source: brain
C; Comment: This procein inhibits neural cell adhesion and neurite outgrowth in the nervo
C, Reywords: chondroitin sulfate proteoglycan; glycoprotein; keratan sulfate
F; 267-270/Region: cell attachment (R-G-D) motif
F; 112, 213, 490/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 152, 249, 440, 793, 820/Binding site: chondroitin sulfate (Ser) (covalent) #status predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE001410; GB:AE001362; NID:g3845245; PIDN:AAC71925.1; PID:g384524
A;Experimental source: clone 3D7
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cjaccession: B71609
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, I.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A;Reference number: A71600; MUID:99021743; PMID:9804551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein PPB0680w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C, Species: Dictyostelium discoideum
C, Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                           A;Accession: JC5497
A;Molecule type: mRNA
A;Residues: 1-1038 <BUR1>
A;Cross-references: EMBL:X67778; NID:g406318; PIDN:CAA47988.1; PID:g406319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQRE----EHSQKSDSTKDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein G5 - slime mold (Dictyostelium discoideum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 RKEDLQR-EEHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.5%; Score 108.5; D
28.6%; Pred. No. 1.3;
tive 25; Mismatches
                                                                                                                                                                                                                               A,Accession: PC4334
A,Molecule type: protein
A,Residues: 79-83;299-412;485-502 <BUR2>
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nes 34; Conserv
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Best Local Similarity
Matches 42: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-665 <GAR>
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m

ä

Gaps

102 128

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A;Residues: 1-1345 <FAV>
A;Cross-references: EMBL:U10556; NID:g500825; PIDN:AAB68895.1; PID:g500838; MIPS:YHR080c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 KKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLD--KNNISSKSTTN---NP 142
                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:U88309; PIDN:AAB42334.1; GSPDB:GN00019; CESP:T23B3.5 A;Experimental source: strain Bristol N2; clone T23B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein YHR080c - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 19-Apr-2002
                                                C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Appoinctical protein T28D5.30 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 28-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47 EGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNH----SQLNES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 KGELEKGYQFDGWEISGFEGKK-DAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 HRKEDLOREEHSOKSDSTKDVTATVLDKNNISSKSTTNNPNK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Description: The sequence of S. cerevisiae cosmid 9205. A; Reference number: $46795
                                                                                      C;Accession: T25911
R;Maggi, L.; Le, T.
Bubmitted to the EMBL Data Library, February 1997
A;Description: The sequence of C. elegans cosmid T23B3.
A;Reference number: Z20109
A;Accession: T25911
                       hypothetical protein T23B3.5 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
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                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
13.2%; Score 99; DB 3
Best Local Similarity 29.4%; Pred. No. 1.2;
Matches 30; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 12;
18; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Favello, T. submitted to the EMBL Data Library, June 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position: 8R .
C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: SGD:S0001122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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hes 33; Conserv
                                                                                                                                                                                                                                                                                                A; Residues: 1-211 <MAG>
                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 1
A;Introns: 30/2; 200/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
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R; Favello, T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable membrane protein Cj0692c [imported] - Campylobacter jejuni (strain NCTC 11168)
C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #text_change 03-Jun-2002
C;Accession: G8139
R;Parkhill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
C:W.; Qual, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S; Barrel
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Reterence number: A81250; MUID:20150912; PMID:10688204
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-312 < PAR>
A;Cross-references: GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CAB72966.1; PID:g696814
A;Experimental source: serottype O2, strain NCTC 11168
C;Genetics:
A;Gene: Cj0692c
C;Accession: T18283
R;Rieben Jr., W.K.; Gonzales, C.M.; Gonzales, S.T.; Filkington, K.J.; Kiyosawa, H.; Hugh Genetics 148, 1117-1125, 1998
A;Title: Dictyostelium discoideum nuclear plasmid Ddp5 is a chimera related to the Ddp1 A;Reference number: Z14684; MUID:98198836; PMID:9539429
A;Accession: T18283
A;Accession: T18283
A;Accession: T18283
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-325 <RIE>
A;Cross-references: EMBL:U00796; NID:g2702254; PID:g2702258; PIDN:AAC18634.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 NHIKDSGYYATNEEIEIFLESCTLCKEITAQTKRNSYKKRNIINKLPEEEEEEEEEEEE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 INL---SKDTFIKPVFKKIEEKKEEENKPT---FDVSKKKDNP----QVNHSQLNESHRK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --IEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKE-----DLQREEHSQKSDSTK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70
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                                                                                                                                                                                                                                                                                                                                                                                                                                          1 HRVTVTIQNGKEMSSTIVSEEDFILPVYK-GEL--EKGYQFDGWEISGFEGK-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDLOREEHSQKSDSTKDV--TATVLDKNNISSK--STTNNPN 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 ---KDAGYV-----INLSKDTFIKPV-----FKK----
                                                                                                                                                                                                                                                                                                                                         ch 13.8%; Score 103.5; DB 2; Similarity 23.8%; Pred. No. 0.86; 43; Conservative 25; Mismatches 50;
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Best Local Similarity
Matches 43; Conserv
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bovine and human sperm heads: the

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C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 21-Jul-2000 C;Accession: 137271; S52774 R;Hess, H.; Heid, H.; Zimbelmann, R.; Franke, W.W. Exp. Cell Res. 218, 174-182, 1995 A;Title: The protein complexity of the cytoskeleton of bovine and human sper A;Reference number: 137271; MUID:95255491; PMID:7737358
                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-348 <HES>
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                                                        R.Bevon, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancre submitted to the Protein Sequence Database, August 1999
A.Reference number: 217931
A.Accession: T148
A.Accession: T148
A.Accession: T188
A.
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T47835
R;Nyakatura, G; Fartmann, B; Dauner, D; Sterr, W; Holland, R.; Weichselgartner, M; Rinyakatura, G; Fartmann, B; Dauner, D; Sterr, W; Holland, R.; Weichselgartner, M; A;Reference number: Z24475
A;Accession: T47835
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Introns: 162/3; 201/3; 416/3; 438/3; 460/3; 482/3; 504/3; 519/3; 534/3; 559/3; 579/3; C;Superfamily: Arabidopsis thaliana hypothetical protein T21C14.40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 IKPVFKKIEEKKE------EENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   566 ------KKENDHQKKSDGNVKKENSKVKPRELRSŚTGKKKVEVENINNSKSSSKRKQ 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               442 VEPVGDDVRSSGDMSPNPSAANNVREGPATFDIMESEDNPGRDNVAPMEDHIRSEVQLSP 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           383 NGRQRNSNVQSSVDEILSYYTDKVPSGVGLNVSERDIVELVEDDVRSAGGLSPNVQRDN- 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 NGKEMSSTIVSEEDFILPVYKGELEKGY-----QFDGWEISGFEGKKDAGYVINLSKDTF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 QNGKEMSSTIVSEE----DPILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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12.8%; Score 95.5; DB 2;
Best Local Similarity 23.4%; Pred. No. 7.5;
Matches 34; Conservative 22; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | | | | | : : : | | : HVL---GAKDVTDVSDPTD 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 HSQKSDSTKDVT--ATVLDKNNISSKSTTNNPNK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
13.0%; Score 97; DB 2
Best Local Similarity 22.1%; Pred. No. 9.4;
Matches 34; Conservative 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 TKDVTATVLDKNNISSKSTTNNPNK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TKETAEVATGKRGRESGKDDKQPRK 640
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cylicin II - human C;Species: Homo sapiens (man)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85
                                                                                                                                                                                                                                                                                                                 86 SK--KKDNPQVNHSQLN-----ESHRKEDLQREEHSQKSDSTKD---VTATVLDKNNI 133
                                                                                                                                                                                                                                                                                                                                                     257 SKDAKKDAKEIKKGKKDKKKPSSTDSDSKDDVKKE---SKKDATKDAKKVAKKDTEKESA 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 PVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTK---- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:U49945; PIDN:AAC47924.1; GSPDB:GN00029; CESP:C02H7.1 A;Experimental source: strain Bristol N2; clone C02H7 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein CO2H7.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 18-Feb-2000 C;Accession: T37189  
%;Leimbac, D.; Minx, M. submitted to the EMBL Data Library, February 1996 A;Description: The sequence of C. elegans cosmid CO2H7. A;Reference number: Z20523 AA;Reference number: Z20523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lipoprotein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Accession: A90570
                                                                                                                                                                                                                        205 ESEGEKG----GTEKDSKKGKKDS----KKGKDSAIELQAVKADEKKDEDGKKDANKGDE
                                                                                                                                                                                        29 KGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTF---DV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 TIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIK
A; Cross-references: EMBL: Z46788; NID: 9758586; PIDN: CAA86752.1; PID: 9758587
                                                                                                                         56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 535;
                                                                                                                         39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: X
A;Introns: 47/3; 100/3; 149/3; 304/2; 347/3; 458/3
                                                           Query Match 12.7%; Score 95; DB 2
Best Local Similarity 30.9%; Pred. No. 4.1;
Matches 38; Conservative 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 95; DB;
Pred. No. 6.7;
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12.7%; Score 95; DB
Best Local Similarity 23.5%; Pred. No. 6.7;
Matches 35; Conservative 29; Mismatches
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submitted to the EMBL Data Library, August 1997
A;Reference number: Z18935
A;Accession: T18427
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                     32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                       A; Introns: 307/1; 1545/2
                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 32; Conserv
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Matches 28; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position:
                                                                                                                                                                                                                                                A; Note: C0335c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                    Aritle: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm Aritle: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm A; Reference number: A99512; MUID:21267165; PMID:11353084
A; Accession: A90570
A; Ascession: A90570
A; Residual avores: DRA
A; Residuale type: DNA
A; Residuale 1: DAA
A; Cross-references: GB:AL445566; PID:G14089879; PIDN:CAC13638.1; GSPDB:GN00153
A; Experimental source: strain UAB CTIP
A; Genetic so
A; Genetic so
A; Genetic code: SGC3
    F.; Moszer, I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: TopoII
A;Map position: 14
C;Superfamily: eukaryotic type II DNA topoisomerase; phage T4 DNA topoisomerase (ATP-hyd
C;Keywords: ATP; DNA binding; isomerase; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) II - malaria parasite (Plasmodium falc
                                                                                                                                                                                                                                                                                                                                                          5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 VFKKIEE------KKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENKPTFDVSKKKD----NPQVNHSQLNES--HRKEDLQREEHSQKSDSTKDVTATVLDKN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 16
T18427
Thypothetical protein C0335c - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Species: D5-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Plasmodium falciparum
Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                              18 VSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 NGKEMSSTIVSEEDFIL--PVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKP
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, Nucleic Acids Res. 29, 2145-2153, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.7%; Score 95; DB 2; Length 1397; 23.8%; Pred. No. 20; tive 36; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                              12.7%; Score 95; DB 2; Length 622; 25.4%; Pred. No. 7.9;
                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                          50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Plasmodium faiciparum.
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #teb
C;Accession: T10466
R;Cheeman, S.J.
submitted to the EMBL Data Library, September 1995
A;Reference number: Z17031
A;Accession: T10466
A;Eatus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1397 <CHE>
A;Censa-references: EMBL:X79345; NID:g994807
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 ---KSDSTKDVTATVLDKNNISSKSTTNNPN 143
                                                                                                                                                                                                                                                                                                                                                       26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 132 -NISSKSTTNNPNK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 SNDSKEKNDENTNK 201
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Best Local Similarity 25.4
Matches 34; Conservative
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Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                               85
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C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: B72291
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-210 <NEL>
A;Cross-references: EMBL:AF000299; PIDN:AAC47980.1; GSPDB:GN00022; CESP:E03H12.5
A;Experimental source: strain Bristol N2; clone E03H12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DIFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNH-SQLNESHRKEDLQREEHSQKSDS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 EGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKE 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
A;Residues: 1-3724 <LAW>
A;Cross-references: EMBL: 298547; NID:e1325376; PID:e1325379; PIDN: CAB11104.1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C'Species: Caenorhabditis elegans
C'Date: 29-0ct-1999 #sequence_revision 29-0ct-1999 #text_change 29-0ct-1999
C'Accession: T28771
R'Nelson, J.; Wohldmann, P.; Sansone, J.
submitted to the EMBL Data Library, June 1997
A'Description: The sequence of C. elegans cosmid E03H12.
                                                                                                                                                                                                                                                                                                                                                         1 HRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSK
                                                                                                                                                                                                                                                                                                                                                                                                                        1046 HKIEQDIQDIHSIQTNICDENN-IEQINEENSKKGVRISGTDM---ENKND----
                                                                                                                                                                                                                                                                                           33;
                                                                                                                                                                                                                         Length 3724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 210;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein - Thermotoga maritima (strain MSB8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein E03H12.5 - Caenorhabditis elegans
                                                                                                                                                                                                                         DB 2;
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28.6%; Pred. No. 2.8;
:ive 18; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                   12.6%; Score 94.5; DE
22.1%; Pred. No. 64;
iive 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 TKDVTATVLDKNNISSKSTTNNPNK 144
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Best Local Similarity 29.99
Matches 38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEKVEEK 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Gene: CESP: E02A10.2
                                                                                                                                                                                                                                                                                                                                                              A; Gene: CESP:C17F3.3
                                                                                                                                                                                           A; Accession: T32879
                                                                                                                                                                                                                                                                                                                                                                                       A, Map position: 1
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                                                              A,Accession: B72291
A,Status: preliminary
A,Molecule type: DNA
A,Molecule type: DNA
A,Essiduse: 1-219 <ARN>
A,Cross-references: GB:AE001771; GB:AE000512; NID:g4981678; PIDN:AAD36218.1; PID:g498168
C,Genetics: A,Gene: TM1142
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Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A; Raoney, T.; Rowley, D.; Sakano, H.
A; Atthors: Salzberg, S.L.; Sowley, D.; Sakano, H.
A; Atthors: Salzberg, S.L.; Sowley, D.; Sakano, H.
A; Atther Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
A; Scatus: DNA
A; Dreliminary
                              sed
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A;Reference number: A72200; MUID:99287316; PMID:10360571
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                                                                                                                                                                                                                                                                                                                                                                                                                     89 GEESVSYRDLFAGFGVRGTPTFFFFRGKEGLGYLPGYVDKDNFIK-ILKYVAQELKED-- 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 K---IEEKKEEENKPIFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTAT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S ESSPMKEKKEEVVKPEAEVEKKKE--BAAEEKVEEEKKSEAVVTEEAPKAETVEAVTEE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 PTFDVSKKKDNPQVNHSQLNESHRKED----LQREEHSQKSDS------TKD 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 GVEKSASFKEESDFFADLKESEKK-----ALSDLKSKLEEAIVDN----TLLKTKKK 94
                                                                                                                                                                                                                                                                                                                                                                                         30 GELEKGYQ--FDGWEISG-----FEGKKDAGYVIN-LSKDTFIKPVFKKIEEKKEEENK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE005172; NID:g4587525; PIDN:AAD25756.1; GSPDB:GN00141 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 GKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C;Accession: D86432
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                          33;
                                                                                                                                                                                                                                                                                          Length 219;
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                                                                                                                                                                                                                                                                                                                                          35;
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                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein T518.14 - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                        ch 12.4%; Score 92.5; DB 1. Similarity 28.1%; Pred. No. 3.8; 36; Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.4%; Score 92.5; DB
llarity 24.8%; Pred. No. 10;
Conservative 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VLDKNNISS 135
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153 IIPKEEVTT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203 VAKTLQEK 210
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Best Local Similarity
Matches 32; Conserva'
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Best Local Similarity
Matches 36; Conserv
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A;Residues: 1-540 <STO>
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RESULT 20 T32879

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-253 cGAT>
A;Residues: 1-253 cGAT>
A;Cross-references: EMBL:AF043692; PIDN:AAB97531.1; GSPDB:GN00019; CESP:C17F3.3
A;Experimental source: strain Bristol N2; clone C17F3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Molecule type: DNA
A,Residues: 1-385 «WIL»
A,Cross-references: EMBL:281053; PIDN:CAB02877.1; GSPDB:GN00023; CESP:E02A10.2
A,Experimental source: clone E02A10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 PVFKKIEEKKE---EENKPTFDVSKK------KDNPQVNHSQLNESHR---- 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 IXPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDV 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 TVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTF 63
hypothetical protein C17F3.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Bate: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T32879
R;Gattung, S; Scheet, P.
Submitted to the EMBL Data Library, January 1998
A;Description: The sequence of C. elegans cosmid C17F3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C.Accession: T20410
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hypothetical protein BH4017 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 ---KEDLOREEHSQKSDSTKDVTATVLDKNNISSK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 DEKKEDEKKESKEKSKDEEKKKDEVKDKKEDEKK 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R)Thomas, K. submitted to the EMBL Data Library, October 1996 A;Reference number: 219271 A;Reference number: 219271 A;Recession: T20410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 5
A;Introns: 32/1; 72/1; 85/1; 122/1; 133/1; 220/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 91;
Pred. No. 5
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32.6%;
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A;Residues: 1-1332 <STE>
A;Residues: 1-1332 <STE>
A;Cross-references: EMBL:Z35950; NID:g536341; PIDN:CAA85026.1; PID:g536342; MIPS:YBR081c
R;Andre, B.; Cziepluch, C.; Hein, C.; Jauniaux, J.C.; Urrestarazu, A.; Vissers, S.
submitted to the Protein Sequence Database, August 1994
A;Reference number: S45893
A;Accession: S45948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-835 <AND>
A;Cross-references: EMBL:Z35950; MIPS:YBR081c
A;Cross-references: EMBL:Z35950; MIPS:YBR081c
A;Haynes, S.R.; Dollard, C.; Winston, F.; Beck, S.; Trowsdale, J.; Dawid, I.B.
Nucleic Acids Res. 20, 2603, 1992
A;Title: The bromodomain: a conserved sequence found in human, Drosophila and yeast prot A;Reference number: $40800; MUID:92285152; PMID:1350857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Title: Sequence analysis of a 31 kb DNA fragment from the right arm of Saccharomyces c A,Reference number: S45462; MUID:95076715; PMID:7985423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-1332 <VAW>
A;Cross-references: EMBL:X76294; NID:g974203; PIDN:CAA53940.1; PID:e264674; PID:g558360
A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 463-523 «HAX»
A;Cross-tences: BMBL:M87651; NID:g172683; PIDN:AAA35087.1; PID:g172684
R;van der Aart, Q.J.M.; Barthe, C.; Doignon, F.; Aigle, M.; Crouzet, M.; Steensma, H.Y.
Yeast 10, 959-964, 1994
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                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-1332 <GAN>
A;Cross-references: EMBL:L22537; NID:g349189; PIDN:AAC37424.1; PID:g349190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-1332 <GAW>
A;Cross-references: EMBL:L22537; NID:g349189; PIDN:AAC37424.1; PID:g349190
A;Cross-references: EMBL:L22537; NID:g349189; PIDN:AAC37424.1; PID:g349190
B;Van der Aart, O.J.M.
submitted to the EMBL Data Library, August 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 VTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFI
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            C, Accession: S41552; S45946; S45948; S40800; S45478; S54985; S59716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-624, LRGKRKI', 633-1332 <VAN>
A;Cross-references: EMBL:X76294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                               R;Steensma, H.Y.; van der Aart, Q.J.M.
aubmitted to the Protein Sequence Database, August 1994
A;Reference number: $45932
A;Accession: $45946
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                                    RiGansheroff, L.; Dollard, C.; Tan, P.; Winston, F. Bubnitted to the BMBL Data Library, July 1993 A; Reference number: 841552 A; Accession: 841552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.1%; Score 90.5; Di
ilarity 24.5%; Pred. No. 41;
Conservative 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: SGD:S0000285; MIPS: YBR081c
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A;Accession: S59716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S45478
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C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: A84152
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Status: preliminary
A;Residues: preliminary
A;Residues: 1-614 <870>
A;Cross-references: GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BAB07736.1; GSPDB:GNOG A;Cross-references: strain C-125
C;Genetics:
A;Gene: BH4017
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C;Species: Malanoplus sanguinipes entomopoxvirus
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T281-200 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T283-552, 1999
A;Yitol: 73, 533-552, 1999
A;Yitol: T28391
A;Reference number: Z20484; MUID:99102612; PMID:9847359
A;Accession: T28391
A;Reference number: Z20484; MUID:99102612; PMID:9847359
A;Accession: T28391
A;Residues: 1-670 <AFO>
A;Residues: 1-670 <AFO>
A;Cession: T28301
A;Roserences: EMBL:AF063866; NID:g4049647; PIDN:AAC97713.1; PID:g4049753
A;Note: MSV230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 YVINLSKDTFIKPVFKKIEEKK--EEENKPTFDVSKKK----DNPQVNHSQLNESHRKED 107
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probable transcription factor SPT7 - yeast (Saccharomyces cerevisiae)
N.Alternate names: protein YBR0739; protein YBR081C
C;Species: Saccharomyces cerevisiae
C;Species: 28-Jan-1994 #sequence_revision 09-Sep-1994 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 23
T28391
ORP MSV230 hypothetical protein - Melanoplus sanguinipes entomopoxvirus
C;Species: Melanoplus sanguinipes entomopoxvirus
C;Species: Melanoplus sanguinipes entomopoxvirus
C;Date: 21-7an-2000 #sequence_revision 21-7an-2000 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.1%; Score 90.5; D
26.1%; Pred. No. 17;
tive 26; Mismatches
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Best Local Similarity 22.54
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 26.1
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hypothetical protein - Chlamydophila pneumoniae (strain CWL029)
Cispecies: Chlamydophila pneumoniae, Chlamydia pneumoniae
Cispecies: Chlamydophila pneumoniae, Chlamydia pneumoniae
Cipate: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
CiAccession: C72074
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J., Astrie Genet. 21, 385-389, 199
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-508 <ARN>
A;Cross-references: GB:AE001632; GB:AE001363; NID:g4376755; PIDN:AAD18613.1; PID:g437675
A;Experimental source: strain CWL029
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C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Accession: E86549
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is Nucleic Acids Ree. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 VKGVFKKTPQARPEVSSPRLPSHVQHGQRLPGLEGFRDRIQKRSENPEADLGKWKRSYSD 151
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A;Cross-references: GB:BA000008; NID:g8978843; PIDN:BAA98679.1; GSPDB:GN00142
A;Experimental source: strain J138
                                                                       Gaps
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                                                                       33; Indels
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                                                                                                                                                                                                                                                                                                                                                          152 GDLDRVGHDSNEDSTEDSRS---EGGEPSSKSSS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 EDLOREEHSOKSDSTKDVTATVLDKNNISSKSTT 139
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                                                                                                                                                                                                                                                                                                          106 EDLOREEHSQKSDSTKDVTATVLDKNNISSKSTT
                                   Pred. No. 16; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 89.5; D
; Pred. No. 16;
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 IKPVFKKIEEKKEEENKPTFD----
24.5%; Pic. 17;
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                                                                                                                                                       64 IKPVFKKIEEKKEEENKPTFD-
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Best Local Similarity 24.5%;
Matches 23; Conservative 1'
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Best Local Similarity 24.5%
Matches 23; Conservative
                                                                               23; Conservative
                                   Best Local Similarity
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A;Status: preliminary
A;Molecule type: DNA
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                                                                               Matches
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R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39. A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: B81594
A;Scatus: preliminary
A;Molecule type: DNA
A;Residues: 1-508 < REA>
A;Residues: 1-508 < REA>
A;Cross-references: GB:AE002189; GB:AE002161; NID:g7189205; PIDN:AAF38139.1; PID:g718920C;Genetics:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rhoptry protein - Plasmodium yoelii (fragment)
C;Species: Plasmodium yoelii.
C;Species: Dasmodium yoelii.
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 01-Dec-2000
C;Accession: T28676, A45521
R;Sinha, K.A.; Keen, J.K.; Ogun, S.A.; Holder, A.A.
Mol. Bicchem. Parasitol. 76, 329-332, 1996
A;Aitle: Comparison of two members of a multigene family coding for high-molecular mass A;Reference number: Z20507; MulD:97077455; PMID:8920022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: DNA
A;Residues: 1-2401 <SIN>
A;Residues: 1-2401 <SIN>
A;Residues: BBBL: U36927; NID:g1041784; PID:g1041785; PIDN:AAB41263.1
R;Keen, J.; Holder, A.; Playfair, J.; Lockyer, M.; Lewis, A.
Mol. Biochem Parasitol. 42, 241-246, 1990
A;Title: Identification of the gene for a Plasmodium yoelii rhoptry protein. Multiple (A;Reference number: A45521; MUID:91101660; PMID:2270106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          924 TSKNHEEKISDIRKNSLKIIQDFSEESYINDI-KKELEKNVLESONNNTDINOYLSKIEN 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 GYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREE 112
                                                                                                                               | :| | : | | : | | | : | | | | : | | | | : | | | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
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;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35;
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                                                                                                                                                                                                                                   104 RKEDLOR-EEHSOKSDSTKDVTATVLD-KNNISSKSTTN 140
                                                                                                                                                                                                                                                                                  1 (| | | 1172
1036 CQSKIKSTIDDNYVSECIKNITNLKTYIVNEKNNINT 1072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 90.5; 1
Pred. No. 79;
                                                                                   K---PVFKKIEEKKEEENKPTFD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 27.4%;
Matches 43; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DMA
A;Residues: 2260-2401 <KEE>
A;Cross-references: GB:M34281
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                                                                                   65
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Length 508;

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12.0%; Score 89.5;

Query Match

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Length 1016;

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C;Accession: E96795
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Cin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
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C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
                                                                                                                                                    -----LTFTGADVLGVADKECIDYLVELA-DTV- 302
                                                                                                                                                                                                                                                                    74 KKEEENKPIFDVSKKK--DNPQVNHSQLNESHRKEDLQREEH-----SQKSDSTKD- 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: E89883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: GB:AE005173; NID:g6143888; PIDN:AAF04434.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown protein F28016.8 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 KPVFKKIEEKKEEE----NKPTFDVSKKKDNPQVNHSQ-LNESHRKEDLQ-REEHSQK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 ELEKGYOFDGW------EISGFEGKKDAG----YVINLSKDTFIKPVFKKIEE
                                                                                                                   5 VTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFI
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                                                         38;
   DB 2;
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19;
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                                                                                                                                                                                                                                                                                                                                                   -----SDSTKDVTAT-VLDKNNISS 135
12.0%; Score 89.5; Di
21.6%; Pred. No. 36;
:ive 33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.9%; Score 89; DB 24.3%; Pred. No. 19; Live 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    317 MEEDVVTETVKTETSEDMKLLSQN 340
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                                                            Conservative
                                                                                                                                                       : ::|| |:|
265 ILLENGAELSD-----
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Best Local Similarity
Matches 35; Conserv
                              Best_Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Residues: 1-528 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                             303
      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 31
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                                                                                                                            probable membrane protein YDL074c - yeast (Saccharomyces cerevisiae)
NyAlternate names: hypothetical protein D2483
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Bate: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
C;Accession: S67610
R;Wambutt, R.; Wedler, H.; Wedler, E.; Scharfe, M.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67608
A;Accession: S67610
A;Molecule type: DNA
A;Residues: 1-700 cWAM'
A;Residues: 1-700 cWAM'
A;Residues: 1-700 cWAM'
A;Residues: S0000232
A;Genetics: SGD:S000232
A;Genetics: A;Genetics: SGD:S000232
A;Gross-references: SGD:S000232
A;Gross-references: SGD:S000233
A;Map position: 4L
C;Keywords: transmembrane protein
F;69-85/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89
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A;Introns: 27/3; 94/3; 279/3; 352/2; 462/2; 523/3; 569/2; 657/2; 718/3; 766/3; 833/3;
C;Keywords: phosphoric monoester hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
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R; Matthews, P.
Bubmitted to the EMBL Data Library, January 1995
A; Reference number: Z19510
A; Accession: T22086
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1016
A; Cross-references: EMBL: Z47809; PIDN: CAA87782.1; GSPDB: GN00020; CESP: C06C3.1
A; Experimental source: clone F42A8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
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A;Molecule type: DM.
A;Residues: 1-1016 <WIL>
A;Cross-references: EMBL:236719; PIDN:CAABS318.1; GSPDB:GN00020; CESP:C06C3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---DAGYVINL-SKDTF---IKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.0%; Score 89.5; DB 2; Length 700; 23.5%; Pred. No. 24; ive 29; Mismatches 47; Indels 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 NGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ankyrin related protein C06C3.1 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contains: myosin-light-chain-phosphatase (EC 3.1.3.53)
Species: Caenorhabditis elegans
      GDLDRVGHDSNEDSTEDSRS---EGGEPSSKSSS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                481 TKADQKYFAAMRSKDSILIEIKTLSKSLSKSNEL----
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R,Berks, M.
By Berks, M.
A,Reference number: Z19058
A,Accession: T19006
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 RKEDLQREEHSQKSDSTKDVTATVLDKNVISSK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :: || : : ||:| | ::| || |:| KOLDLSONNERRLIDSSKTETLKIIDLNNTSTK 566
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Matches 36; Conservative
      152
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A,Gene: CESP:C35E7.9
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A;Reference number: 221815
A;Recession: T39009
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1.1888 <GEN>
A;Cross-references: EMBL:298531; PIDN:CABI1064.1; GSPDB:GN00066; SPDB:SPAC6B12.02c
A;Experimental source: strain 972h-; cosmid c6B12
C;Genetics:
A;Gene: SPDB:SPAC6B12.02c
A;Wap position: 1
C;Superfamily: Schizosaccharomyces hypothetical protein SPAC6B12.02c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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                                                  A;Cross-references: GB:BA000018; PID:g13700929; PIDN:BAB42225.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
                                                                                                                                                                                                                                                                                          355 SVENNESMMDTFVKH-----PIKTGMLNGKKYMVMETTNDDYWKDFMVEGQRVRTISKDA 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 470 NSAKKBATPATPSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKP 529
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                                                                                                                                                                                                                                                                                                                                                                                                                                            NKPTFDV----SKKKDNPQVNHSQLNESHRKEDLQ----REEHSQKSDSTKDVT-ATVL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        390 SSSLTSENPFQLNVAANAVSTIPVYRTTKTKMKKN-RFKYVEVEKLPDLILESYGKKAPK 448
                                                                                                                                                                                                                                                                 20
                                                                                                                                                                                                                                                                                                                                                      ----DAGYVINL-SKDTFIKPVFKKIEEKKEEE 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein SPAC6B12.02c - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein C35E7.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T; McDonald, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Species: Schizosaccharomyces pombe
Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                        Gaps
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R;Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood,
submitted to the EMBL Data Library, August 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30;
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                                                                                                                                                                        DB 2; Length 645; 24;
                                                                                                                                                                                                                    63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 SQKSDS-TKDVTATVLDKN-----NISSKSTTNN 141
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                                                                                                                                                                                                                                                               6 TIQNGKEMSSTIVSEEDFILPVYKGELE-KGYQF-
                                                                                                                                                                        Query Match
11.9%; Score 89; DB 2
Best Local Similarity 21.9%; Pred. No. 24;
Matches 43; Conservative 26; Mismatches
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Matches 37; Conservative
                    Molecule type: DNA
Residues: 1-645 <KUR>
A;Status: preliminary
                                                                                                                               A;Gene: SA0976
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A;Residues: 11371 cAND>
A;Cross-references: GB:AJ235271; GB:AJ235269; NID:g3868717; PIDN:CAA14739.1; PID:g386083
A;Experimental source: strain Madrid E
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R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology. A;Reference number: A75000; MUID:99069613; PMID:9851916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:AF067216; PIDN:AAC17524.1; GSPDB:GN00019; CESP:C35E7.9 A;Experimental source: strain Bristol N2; clone C35E7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        235 QMDEEREELPKLAEILPQY-----AQANIDKHAKLYAKQYQTKIENDPNYKELEKLQ 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 KIEEKKEE----ENKPTFDVSKKKDNPQVN---HSQLNESHRKEDLQREEHSQKSDSTK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 GITIAGWILAGCGGKKKKDGKSSTASAAAPKADSKMKPPVENVKSKKSEKKEEPKKEEEP 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Wolecule type: DNA
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C;Species: Caenorhabditis elegans
C;Date: 10-May_2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 KEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKK-DAGYVINLSKDTFIKPVFK
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                Length 301;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                35 GYQFDGWEISGFEGKK-----DAGYVINLSKDTFIKPVFKKI-
submitted to the EMBL Data Library, May 1998
A;Description: The sequence of C. elegans cosmid C35E7.
A;Reference number: Z21278
A;Accession: T33068
                                                                                                                                                                                                                                                                                                                                                                                                              38;
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                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                             ; Score 88.5; DI
; Pred. No. 11;
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.8%; Score 88.5; Dilarity 23.1%; Pred. No. 14; Conservative 33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVTATVLDKNNISSKSTT----NNPN 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E---IVSKIEYSKKSKTNDIIINNPN 309
                                                                                                                                                                                                                                                                                                                                                                11.8%; 24.8%;
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 24.8*
Matches 27; Conservative
                                                                                                                                                                                                                                                                                     A; Map position: 1
A;Introns: 30/3; 193/1; 236/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                A; Residues: 1-301 <GRA>
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A;Accession: T23451
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                     A; Introns: 81/3; 102/3; 169/1; 211/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.8%; 23.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
           A; Reference number: Z19743
                                                                                                                      A; Residues: 1-276 <WIL>
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                              A;Gene: CESP:K08E3.2
A;Map position: 3
                                                                                         A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Simi
Matches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position:
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                                                                                                                                                                                                          C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 40
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A; Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_eleA;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: G88436
A;Accession: G88436
A;Status: prelimity
A;Nolecule type: DNA
A;Residues: 1-762 <STO>
A;Coss=references: GB:chr_III; PIDN:CAA84732.1; PID:g3879347; GSPDB:GN00021; CESP:T04A8
A;Genetics:
A;Genet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T23451
R;McMurray, A.
submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 SGKQIMKPGY--DKKEGLGMDQKEIVGDDKKDKEARKRERKLQDEFAE--LKKDBEKDKE
                                                                                                                                                                                                                                                                                                                                                                                                                             SEEDFILPVYKGELEKGYQPDGWEISGFEGK-KDAGYVINLSKDTFIKPVFKKIEEKKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 SEEDFILPVYKGELEKGYQFDGWEISGFEGK-KDAGYVINLSKDTFIKPVFKKIEEKKEE
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11.8%; Score 88.5; DB 2; Length 791;
Best Local Similarity 25.2%; Pred. No. 32;
Matches 32; Conservative 25; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                               Length 762;
                                                                                                                                                                                                                                                                                                               ch 11.8%; Score 88.5; DB 2; Length 7. Similarity 25.2%; Pred. No. 31; 32; Conservative 25; Mismatches 65; Indels
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Best Local Similarity
Matches 32; Conserv
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Hypothetical protein F28016.18 [imported] - Arabidopsis thaliana Cypothetical protein F28016.18 [imported] - Arabidopsis thaliana (mouse-ear cress)
CjSpecies: Arabidopsis thaliana (mouse-ear cress)
CjSpecies: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
CjAccession: G36796
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Juu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, E.; Kim, C.A.; Li, T.H.; Lin, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Reference and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IGA-specific metalloendopeptidase (EC 3.4.24.13) type 1 precursor - Haemophilus influenz C;Species: Haemophilus influenzae A;Variety: strain HK715
                                                                                                                                                                                                                                                                                                                                                 ë,
                                                                                                                                                                                                                                                                                                                                                                                                                      58 LSKDTFIXPVFKKIEBKKEEE--NKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                F-----KKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKS 117
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A;Cross-references: EMBL:Z81568; PIDN:CAB04590.1; GSPDB:GN00021; CESP:K08E3.2 A;Experimental source: clone K08E3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1280 <STO>
A;Cross-references: GB:AE005173; NID:g6143896; PIDN:AAF04442.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 QNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPV
                                                                                                                                                                                                                                                                                                                                                 22;
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                                                                                                                                                                                                                                                                        Length 276;
                                                                                                                                                                                                                                                                                                                                                 29;
                                                                                                                                                                                                                                                                        DB 2;
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; Pred. No. 61;
24; Mismatches
                                                                                                                                                                                                                                                                                                                                             10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 KSDSTKDVTATVLDKNNISSKSTTNNPNK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 KK-----TAEEKENNEKKDENKNKNK 128
                                                                                                                                                                                                                                                                    ch 11.8%; Score 88; 1 Similarity 31.5%; Pred. No. 38; Conservative 10; Mişmatcl
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C,Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Dec-2000

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Cyaccession: A41859

R; Poulsen, K.; Keinholdt, J.; Kilian, M.

J. Bacteriol. 174, 2913-2921, 1992

A;Title: A comparative genetic study of serologically distinct Haemophilus influenzae ty A;Reference number: A41859; MUID:92234949; PMID:1373717

A;Accession: A41859

A;Reference number: A41859; MUID:92234949; PMID:1373717

A;Accession: A41859

A;Reference number: A41859; MUID:9148906; PIDN:AA24966.1; PID:9148907

A;Residues: 1-1702 PMOU>

A;Residues: Brain HK715

A;Residues: Carain HK715

A;Roberimental source: strain HK715

A;Roberimental source: strain HK715

A;Roberimental source: strain HK715

A;Roberimental source: metalloendopeptidase
C;Superfamily: IgA-specific metalloendopeptidase
C;Superfamily: IgA-specific metalloendopeptidase
C;Reywords: hydrolase; metalloroteinase

Query Match

Query Match

Airica Matches
A; Conservative
A; Mismatches
A; DB 2; Length 1702;
Best Local Similarity
A; Score 87.5; DB 2; Length 1702;
Best Local Similarity
A; ScinkskDrPIKRVPKKIEEKKEEENKPTFDVSKKKONPQVNHSQLNESHRKEDLQREEHS-
BD 1296 INTGSATAITETAEKSDKPQTETAASTEDASQHKANTVADNSVANNSESSEPKSRRRSI 1355

Qy
A 115 --QKSDSTKDVTAITVLDKNNISSKSTTNNPNK 1387

Db 1356 SQPQETSAEETTAASTEDASKENPN 1387
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Search completed: February 10, 2004, 10:58:33 Job time: 12.3976 secs

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February 10, 2004, 10:48:44; Search time 32.7596 Seconds (without alignments) 697.707 Million cell updates/sec
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748
1 HRVTVTIQNGKEMSSTIVSE.....ATVLDKNNISSKSTTNNPNK 144
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                          - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		di			SUMMARIES	
Result No.	Score	Query Match	Query e Match Length DB I	DB	ΙD	Description
٦.	748	100.0	773	22	AAB48343	S. pneumoniae Sp13
7	748	100.0		21	AAY81710	Streptococcus pneu
m	748	100.0		24	ABU01020	S. pneumoniae type
4	615	82.2		13	AAW55096	Streptococcus pneu
Ŋ	615	82.2	117	23	ABP54590	S. pneumoniae SP04
9	110	14.7			AAG81779	S. epidermidis ope
7	110			23	ABP39023	Staphylococcus epi
80	106.5			21	AAG47777	Arabidopsis thalia
6	104			21	AAB18278	Plasmodium falcipa

	Plasmodium falcipa Staphylococcus epi Drosophila melanog Plasmodium falcipa Human ORFX ORF2661 Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Human cell cycle r Human colon cancer Shrimp white spot S. aureus SdrD pro Pathogen specific Staphylococcus aur Staphylococcus aur Staphylococcus aur Human sodium chann Human sodium chann Human sodium chann S. aureus trigger Staphylococcus hae S. aureus trigger Staphylococcus hae S. aureus trigger Staphylococcus hae S. aureus trigger	NMENTS ccal; otitis media; nasopharyngeal; immune response; immunotherapy;	Sp130 polypeptides, for treating and
ABB61977 AAK216636 AAK250967 AAK35091 ABH319106 ABH56888 AABF6888 AABF6888 AABF73992 AAM739318 AAM79318	AAB18176 ABB40312 ABB40312 ABB181769 AAB42897 AAG37133 AAX4364 AAG37132 AAX08642 AAG3733 AAX08642 AAG3733 AAX08134 AAG3734 AAG3199 AAX08215 AAX08215 AAX08215 AAX08215	ALIG moco on;	or
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2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		71 P Z 2 2 4 4 7	
101 101 6 4 4 5 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	1 43 AB48343 sta AB48343; 0-APR-2001 . pneumonia mmunogenic; ronchial; l ntibacteria treptococcu 0200076540- 1-DEC-2000; 9-JUN-2000; 0-JUN-1999; MEDI-) MEDI ARDI-) MEDI PI; 2001-11	ccines
	: ସର୍ଷ୍ଟିସ୍ଟିକ୍ଟିକ୍ଟି : : : :	RESULT A A B B B B B B B B B B B B B B B B B	

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This sequence represents a Streptococcus pneumoniae protein of the invention. The proteins (or their homologues, derivatives and/or fragments) are useful as immunogens or antigens. Immunomogenic or antigenic compositions comprising the proteins are useful as vaccines and also in diagnostic assays. The sequences are useful for the detection or diagnostic assays. The sequences are useful for the detection or compositions in the treatment or prophylaxis of S. pneumoniae (or medical compositions in the treatment or prophylaxis of S. pneumoniae (or infection. As the sequences can be used to treat S. pneumoniae infection, the elderly, and in patients with predisposing conditions cuch as asplenia, heart, lung and kidney disease, diabetes, alcoholism, or with immunosuppressive disorders, especially AIDS. They can also be used to treat pneumococcal septicaemia, othic sinusitis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1943 HRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSK 2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDST
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         Claim 2; Page 41-42; 76pp; English
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(GENO-) INST GENOMIC RES.
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N-PSDB; ABX06302.
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                                                                                                                                                                                                                                                                                                                       from S. pneumoniae. Vaccines comprising the polypeptides are useful for the treatment and prevention of pneumococal infections, particularly infections caused by Streptococcus, such as citis media, nasopharyngeal, bronchial, lung or blood infections. The antigens are used as immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             630 HRVTVIIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSK 689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   agents to stimulate an immune response. The antisera and antibodies may also be used in diagnosing and treating pneumococcal infections. Recombinant polypeptides serve as a mechanism for stimulating production of antibodies for use in passive immunotherapy, diagnostic reagents, and as reagents in other processes such as affinity chromatography. The present sequence represents the S. pneumoniae Sp130 polypeptide.
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                                                                                                                                                                                                                                                                         Sp128 and Sp130 are useful for
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preventing pneumococcal infections, particularly infections caused by Streptococcus, e.g. otitis media, nasopharyngeal, bronchial, lung or blood infections -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 773;
                                                                                                                                                                                                                                                                              The invention relates to novel immunogenic polypeptides,
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Pred. No. 1.7e-67;
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                                                                                                                                                                                       Claim 8; Page 51-54; 54pp; English.
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100.0%;
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N-PSDB; AAZ91806.
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Best Local Similarity
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9

Gaps

; 0

Indels

DB 21; Length 2120;

Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis

Kunsch CA;

Johnson LS,

Hromockyj A,

Choi GH,

WPI; 1998-272224/24. N-PSDB; AAV27357.

(HUMA-) HUMAN GENOME SCI INC

97WO-US19422.

30-OCT-1997;

96US-0029960.

31-OCT-1996;

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The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS56454. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the nucleic acid cited above or fragments between nucleotides 8-100 of a sequence not defined in the specification, for amplifying a target sequence contained within a Streptococcus nucleic acid sequence, where the first primer is substantially complementary to the target sequence and the second primer is substantially complementary to the target compolement of the target sequence, and where the parts of the primers complement of the target sequence, and where the parts of the primers with the protein, and determining whether the test compound binds to the protein and a Streptococcus pneumoniae bacterium, where one or more genes encoding the proteins has been rendered inactive. The proteins, nucleic acid molecules, antibody and compositions are useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, particularly S. pneumoniae, such as pneumonia, or ear infection. They are also useful in developing vaccines, diagnostics and antibiotics. The methods are useful for the parts of the 2469 proteins expressed by the identified coding regions from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1963 HRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSK 2022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2023 DTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDST 2082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDST 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae, antigen; vaccine, infection; diagnosis; detection; pneumonia; otitis media; meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 748; DB 24; Length 2140;
100.0%; Pred. No. 7.1e-67;
tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae SP0043 protein.
                                         Claim 1; SEQ ID No 1180; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2083 KDVTATVLDKNNISSKSTTNNPNK 2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KDVTATVLDKNNISSKSTTNNPNK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW55096 standard; Protein; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pneumoniae
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2140 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genomic sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW55096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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The present sequence represents a protein from Streptococcus pneumoniae.

The nucleic acid sequence encoding the Streptococcus pneumoniae protein
can be useful in vaccines for inducing protective antibodies against
Streptococcus pneumoniae, for treatment or prevention of infection e.g.
care used to detect Streptococcus infection (by usual hybridisation or
amplification methods), also for isolating Streptococcus genes or their
callelic variants. The protein can be used similarly to detect specific
allelic variants and instance and the protein are used to
monitoring infections. Antibodies which bind the protein are used to
detect corresponding antigens, to purify the protein and for passive
immunisation (optionally coupled to a toxin). Vaccines are administered,
city. by injection, orally or through the skin, typically at 0.01-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 YKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 KKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 KKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 YKGELEKGYOPDGWEISGFECKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSK
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0
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82.2%; Score 615; DB 19; Length 117;
Best Local Similarity 100.0%; Pred. No. 5e-55;
Matches 117; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S. pneumoniae SP043 protein sequence SEQ ID NO:68
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                                                                                                                                                                                                                                                        Claim 11; Page 62; 118pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-SEP-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHOI/) CHOI G H.
(KUNS/) KUNSCH C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2002061545-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-OCT-1997;
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X#X#X#X#X#X####X###X
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WO9818930-A2

07-MAY-1998

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13-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 YKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSK 60
                                                                                                                                                                                                                                             ABQ84792 to ABQ84904 represents nucleic acids which encode the Streptococcus pneumoniae antigens given in ABP54557 to ABP54669. The S. pneumoniae antigens have antibocrerial activity and can be used in vaccines. The S. pneumoniae antigens can also be used to prevent or attenuate a Streptococcal infection in an animal. The polynuclectides encoding the S. pneumoniae antigens can be used to detect trreptococcus nucleic acids. ABQ84905 to ABQ85130 represent primers used in the cloning of S. pneumoniae ORFS (Open reading frames) which are used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKDNPOVNHSOLNESHRKEDLOREEHSOKSDSTKDVTATVLDKNNISSKSTTNNPNK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 YKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIFEKKEEENKPTFDVSK
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                New Streptococcus pneumoniae antigens, useful for detecting
Streptococcus and for preventing or attenuating disease caused by

    epidermidis open reading frame protein sequence SEQ ID NO:652.

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                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 82.2%; Score 615; DB 23; Length 117; Best Local Similarity 100.0%; Pred. No. 5e-55; Matches 117; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 epidermidis SR1 strain; infection; diagnosis;
                                                                                 B,
                                                                                  Dougherty
                                                                               Barash SC, Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ä.
                                                                                                                                                                                                                      Claim 11; Page 29; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG81779 standard; Protein; 746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus epidermidion vaccination; endocarditis
                                                                                                                                                                                          Streptococcus infection
BARASH S C.
DILLON P J.
DOUGHERTY B.
FANNON M R.
                                                                                 Kunsch CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-316495/33.
N-PSDB; AAH52629.
                                                                                                                       WPI; 2002-479261/51,
N-PSDB; ABQ84825.
                                                      ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                       117 AA;
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                                                                                             Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG81779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88
                                                                                                                                                                                                                                                                                                                                                                                         Sequence
 (BARA/)
(DILL/)
(DOUG/)
(FANN/)
(ROSE/)
                                                                                  E,
                                                                                 Choi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
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ANH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.

(II) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the pelypeptides. The polypeptides (II) fand/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55091 represent specifically claimed S. epidermidis genomic DNA polymucleotide sequences from the present invention. AAH55091 to the examplification of the containing primers which are used in the example of the containing the containing the containing the cused in the example of the containing the contain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            655 TKGNGFVTNQSISKGQIIK------NKDKIEVSLSAEDTDDDQEKTDEDSSDN 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus epidermidis, open reading frame; ORF; bacterial infection; antibacterial; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4465 to 4472,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.7%; Score 110; DB 22; Length 746; 27.0%; Pred. No. 0.027; ive 22; Mismatches 52; Indels 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 HRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNN 141
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                                                                                                                                                                                              Claim 18; Page 208; 2188pp; English
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990S-0144085
990S-0144331
990S-01443331
                    99US-0130891
99US-0131449
                                                                                                          05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
 23-APR-1999;
23-APR-1999;
28-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 -NDD-E0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      628 ITICNGKOIKQOSVKSGTKVLPHSKVMLMTDGELTMP-DMTGWTKEDVLAFEDLTKIKVS 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 KKDAGYVIN--LSKOTFIKPVFKKIEEKKEEENKPTFDVS----KKKDNPQVNHSQLNES 102
                                                                                                                                          ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis lifection.

Source or inhibit S. epidermidis infection.

NB. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             687 TKGNGFVTNQSISKGQIIK------NKDKIEVSLSAEDTDDDQEKTDEDSSDN 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 VTIQNGKEMSSTIVSEEDFILPVYK-----GELEKGYQFDGW---EISGFE-----G 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                     Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           23; Length 778;
                                                                                                                                                                                                                                                                                                                                                                                                                                              52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana protein fragment SEQ ID NO: 60255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 HRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNN 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
14.7%; Score 110; DB 23
Best Local Similarity 27.0%; Pred. No. 0.028;
Matches 43; Conservative 22; Mismatches 5
                                                                                                              Disclosure; SEQ ID 3868; 267pp; English.
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99US-0123180.
99US-0123748.
99US-0125788.
99US-012624.
99US-0126785.
99US-0128714.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana.
WPI; 2002-381255/41.
N-PSDB; ABN91568.
                                                                                                                                                                                                                                                                                                                                                                     778 AA;
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05-MAR-1999;
09-MAR-1999;
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PR 20.7UL-1999 9918-0144642

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PR 21.7UL-1999 9918-0145086

PR 22.7UL-1999 9918-0145088

PR 22.7UL-1999 9918-0145088

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PR 22.7UL-1999 9918-014508

PR 22.7UL-1999 9918-0145128

PR 22.7UL-1999 9918-0145214

PR 22.7UL-1999 9918-014724

PR 22.7UL-1999 9918-0145214

PR 22.7UL-1999 9918-0145214

PR 22.7UL-1999 9918-014724

PR 23.7UL-1999 9918-014724

PR 24.7EL-1999 9918-014772

PR 25.7EL-1999 9918-014772

PR 26.7UL-1999 9918-014772

PR 27.7UL-1999 9918-014772

PR 27.7UL-
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1 HRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYOFDGWEISGFE------GKKDA 52
                                                                                                                                                                                                                                                                                                                                     53 GYVINLSKOTFIKPVFKKIEEKKEEENKPTFDVSKKKDN--------PQ 93
                                                                                                                                                                                                                                                                                                                                                                                 94 VNHSQLNE-----SHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 144
                                                                                                                                                                                                                                                                                                                                                                                             206 ENRDQVRQTESAEKSHRKENVTKSEKPRDQEGVKKTEAKDKDRNKEKKEEKTESINK 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum, chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide.
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum chromosome 2 related protein SEQ ID NO:135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proteins encoded by chromosome 2 of the human malarial parasite,
                                                                                                                                                                                                                                                                        45;
                                                                                                                                                                                                                                                Query Match 14.2%; Score 106.5; DB 21; Length 484; Best Local Similarity 20.3%; Pred. No. 0.033; Matches 36; Conservative 31; Mismatches 65; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gardner M, Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB18278 standard; Protein; 665 AA
                                        99US-0160767.
99US-0160768.
99US-0160770.
                                                                        99US-0160814.
99US-0160815.
99US-0160980.
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99US-0161993.
99US-0162142.
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99US-0161361
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99US-0159637
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                                                                                                         99US-01
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(CARU/) CARUCCI D.
(GARD/) GARDNER M.
(VENT/) VENTER J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200025728-A2.
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                  18-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
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26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
29-0CT-1999;
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                                                                                                                                         25-OCT-1999;
25-OCT-1999;
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AAB18278
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Sequence
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                                                         The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (1) inclocide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).

(I) and (II) are useful for the development of vaccines against P. falciparum infection. (I) and polyclonal antisera or a monoclonal antisera by the capture of the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum can aid the identification of drugs to treat or prevent P. falciparum C. P. falciparum Sequencing of the Plasmodium chromosome 2 and the subsequent identification of proceins encoded by it will help to expand complexity of the parasite biology, a process hampered by the complexity of the parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito contract of insecticides have led to a resurgence of malaria in many contracts.
                                                                                                                                                                                                                                                                                        parts of the world, and there is a pressing need for vaccines and new thuge. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 LSKDTFIKPVFKKIEEKKE-----EENKPTFD----VSKKKDNPQVNHSQLNESH 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 HRVT-VTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEI--SGFEGKKDAGYVIN 57
Plasmodium falciparum, useful as antimalarial vaccines and in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                             26;
                                                                                                                                                                                                                                                                                                                                                                                  ch 13.9%; Score 104; DB 21; Length 665; Similarity 25.9%; Pred. No. 0.093; 42; Conservative 29; Mismatches 35; Indels 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RKEDLOR-EEHSOKSDSTKDVTATVLDKNNISSKSTTNNPNK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster polypeptide SEQ ID NO 12723
                                      Disclosure; Page 321-322; 577pp; English.
             diagnosis of P.falciparum infection -
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                          665 AA;
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pharmaceutical
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticidaes, therapeutics and pharmaceutical furgs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL018176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDLDTPLSESRFSK--VFDGWVDEHRDEHDGHDVQEPSGEALDDHDEHDDHEDEDEE 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVFKKIEEKKEEENKPT-----FDVSKKKDNPQVNHSQL/NESHRKEDLQREEHSQKSDS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 EDFILPVYKGELEKGYQFDGW-----EISGFEGKKDAGYVI-----NLSKDTFIK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.6%; Score 101.5; DB 22; Length 564; ilarity 24.5%; Pred. No. 0.13; Conservative 29; Mismatches 51; Indels 25;
                                                                                                                                                                                                                                      Disclosure, SEQ ID NO 12723; 21pp + Sequence Listing; English.
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23-AUG-2000; 2000US-0649167.
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2001-656860/75.
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nes 34; Conserv
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                                N-PSDB; ABL06080
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Nilsson M;

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Frykberg L,
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                                                                                                                                                                                                                                             Sequence
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                  Guss B,
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AAY35091
ID AAY35
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                                                                           The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, and for thromosome and gene mapping, and in recombinant production of (II). The controlled of the combinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human confinent amino acid sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 LSKDTFIKPVFKKIEBKKEBENKPTFDVSKKKONPQVNHSQLNESHRKEDLQRE----E 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "Mature von Willebrand factor binding protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 13; Gaps
diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus lugdunensis von Willebrand factor binding protein
                                                                                                                                                                                                                                                                                                                                                                                                         Length 2519;
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 12.4%; Score 92.5; DB 22; Best Local Similarity 31.0%; Pred. No. 8.8; Matches 22; Conservative 19; Mismatches 17;
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                                                       Claim 20; SEQ ID No 46995; 103pp; English.
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/label= Signal_peptide
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741 KEEKKEPKKEV 751
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SKDTFIKPVFKKIEE-----KKEEENKPTFDVSKKKDNPQVNHSQLNESHRKE--DLQ 109
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                                                                                                                                                                                                                                                                                                                                                          The present invention relates to von Willebrand factor binding protein polypeptide (vWb) from Staphylococci. The vWb and immunogens of vwb are useful in vaccines to combat infections caused by Staphylococci. The invention is also useful for detection of staphylococcal infection and purifying von Willebrand factor from a complex solution. The present sequence is Staphylococcus lugdunensis vWbl protein.
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                                                                                                                                                                           von Willebrand factor binding protein from Staphylococci, useful determining and treating staphylococcal infection
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12.2%; Score 91; DB 23; Length 2060;
Best Local Similarity 25.0%; Pred. No. 9.5;
Matches 36; Conservative 24; Mismatches 48; Indels 3
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Ahlen J,
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Jacobsson K,
                                                                                                                                                                                                                                                                                             Claim 3; Page 35-41; 53pp; English.
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                                                                    WPI; 2002-304928/34.
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at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : | | | | | : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : : : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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                            C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharymgitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used infununogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
   frames in the complete genome (see AAX91990) of Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                              Length 511;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           12.0%; Score 89.5; 24.5%; Pred. No. 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 IKPVFKKIEEKKEEENKPTFD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                  511 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ABL02807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200171042-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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88888888888888888
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                                                                                                                                    646 NGKOKLNASKETKTSEKDFKEVIEVSKKE-EKNDNQESKELENQDGKLPKDQDYLDVKPP 704
                                                                                                                                                                        -----INLSKDTFIKPVFK----KIEEKKEEENKPTFDVSKKKDNPQVNHSQLN 100
                                                                                                                                                                                                                                                                 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel method for identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, tumour, allergen, a tissue or host prone to auto-immunity, where the antigens are used in a vaccine, comprises providing antibody preparation from a plasma pool of a type of animal, or individual sera with antibodies against the specific pathogen, tumour, allergen, tissue or host prone to auto-immunity. The hyperimmune serum-reactive antigens comprising any of the 62 sequences of 53-2261 amino acids fully defined in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibacterial, virucide, fungicide, protozoacide, cytostatic, anti-HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pathogen specific antigen related staphylococcal protein SEQ ID No 414.
                                                                                                                                                                                                 705 MESKEYSEPLAVKLGEDVSKSPSNESSDTKISEVKGEE--PRANGELPKTGEQVKQPEKS
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen; auto-immunity; vaccine; staphylococcal infection; antibody; cancer; autoimmune disease; HIV; hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying, isolating and producing hyperimmune serum-reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zauner W;
Hafner M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antigens from a pathogen, for preparing vaccine or medicament for treating or preventing e.g. staphylococcal infections, comprises providing antibody preparation
                                                                 61;
                                  Length 1408;
                                                                 Indels
                                                                                                   9 NGKE----MSSTIVSEEDF--ILPVYKGELEKGYQFDGWEISGFEGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Henics T,
Weichhart T,
                                  22;
                                                                 62;
                                  8
                              Quéry Match
12.0%; Score 89.5; Di
Best Local Similarity 24.7%; Pred. No. 8;
Matches 48; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klade C,
Dryla A, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 7; Page 220; 252pp; English
                                                                                                                                                                                                                                           ESHRK-EDLOREEHSOKSDSTKDVT-
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Etz H, D
                                                                                                                                                                                                                                                                                                                                                                                                                                      ABJ19106 standard; Protein; 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JAN-2001; 2001AT-0000130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JAN-2002; 2002WO-EP00546
                                                                                                                                                                                                                                                                                                                NNISSKSTTNNPNK 144
                                                                                                                                                                                                                                                                                                                                               SNDVSVIKPSEPDE 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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Minh DB, Vytvytska O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-075410/07.
1408 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200259148-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tempelmaier B;
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 Seguence
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specification, or their hyperimmune fragments are useful for the manufacture of a pharmaceutical preparation, particularly a vaccine against taphylococcal infections or colonisation against S. auceus or S. epidermidis. The preparation of antibodies is useful for the manufacture of a medicament for treating or preventing staphylococcal infections or colonisation against S. aureus or S. epidermidis. The antibody preparations may also be used for diagnostic and imaging purposes. Other conditions that can be treated include cancer, autoimmune diseases or infections caused by viral (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This sequence represents a staphylococcal protein relating to the method for identifying and producing pathogen specific antigens of the invention.
             888888888888888888888
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645 AA; Sequence

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355 SVENNESMADIFVKH----PIKTGMLNGKKYMVMETTNDDYWKDFMVEGQRVRIISKDA 409
                                                                                                                                                                                 NKPTFDV----SKKKDNPQVNHSQLNESHRKEDLQ----REEHSQKSDSTKDVT-ATVL 128
                                                                                                                           78
                                                                                                                                                                                                   -----DAGYVINL-SKDTFIKPVFKKIEEKKEEE
                                                                                                                                                       410 KONTTRIIIFPYVEGKTLYDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQQD
                                            Gaps
                                          64;
                                                                     TIQNGKEMSSTIVSEEDFILPVYKGELE-KGYQF-----DGWEISGFEGKK-
             Length 645;
                                          63; Indels
              DB 24;
                                          26; Mismatches
             11.9%; Score 89; 21.9%; Pred. No.
                                                                                                                                                                                                                                           129 DKNNISSKSTTNNPNK 144
                                                                                                                                                                                                                                                                     530 TKGEVESSSTT--PTK 543
Query Match
Best Local Similarity 21.3.
Best Local 43; Conservative
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Staphylococcus epidermidis KrkN protein SEQ ID NO:10.
  ABP56879 standard; Protein; 654 AA.
             (first entry)
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Staphylococcus aureus, Staphylococcus epidermidis, MSCRAMM, antibody, microbial surface component recognising adhesive matrix molecule; surface protein, infection, antibacterial, antiinflammatory; vaccine; immunosuppressive, antiarthritic; gene therapy; pneumonia; endocarditis; septic arthritis; biomaterial related infection.

Staphylococcus epidermidis

WO2002102829-A2

27-DEC-2002

17-JUN-2002; 2002WO-US19220 15-JUN-2001; 2001US-298098P (INHI-) INHIBITEX INC. (QUEE-) QUEEN ELIZABETH COLLEGE DUBLIN. (QUEE-) QUEEN ELIZA (UYPA-) UNIV PAVIA. Hall A, Hutchins JT, Patti JM, Speziale 1 Foster TJ, Roche F, Patel P, Syribeys P,

Domanski P;

WPI; 2003-167481/16. N-PSDB; ABZ22903 New isolated antibody that binds to a staphylococcal surface protein,

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The present invention describes an isolated antibody (I) that binds to a staphylococcal surface protein selected from any of the 12 sequences of 354-2281 amino acids given in ABPS6875 to ABPS6886. Also described:

(I) an isolated antisera (II) comprising (I); (2) a diagnostic kit (III)

(M) an infection of Staphylococcus aureus by adding (I) to a sample cuspected of being infected with the infection, and determining if antibodies have bound to the sample; (4) a pharmaceutical composition (IV) for treating or preventing an infection, and a vehicle, carrier or excipient; (5) treating (M2) or preventing an infection of S. aureus by administering (I) to a human or animal patient; (6) producing (M3) an immunological response by administering an infection of S. aureus by administering (I) to a human or animal patient; (6) producing (M3) an immunological response by administering an infection of S. aureus or animal an immunogenic amount of the isolated surface protein; (7) and isolated active fragment (V) from the A domain of the DsgA protein; and isolated active fragment (V) from the A domain of the DsgA protein; and comprising the surface protein in an amount effective to elicit an immuno response, and a vehicle, carrier or excipient. (I) has antinflammatory, antibacterial, immunosuppressive and antiarthritic activities, and can be useful for treating or preventing anewal sifection in a human or aliminal such as pneumonnia, septic arthritis, endecaditis or biomaterial animan animan animal animan and animan and animan and animan and animan and animan and animal animan animan animal animan animan animal animan animal animan animal an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         419 KNNTRIIFPYVEGKTLYDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQQD 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NKPTFDV----SKKKDNPQVNHSQLNESHRKEDLQ----REEHSQKSDSTKDVT-ATVL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            364 SVENNESMADTFVKH-----PIKTGMLNGKKYMVMETTNDDYWKDFMVEGORVRTISKDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------DAGYVINL-SKDTFIKPVFKKIEEKKEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 TIONGKEMSSTIVSEEDFILPVYKGELE-KGYQF-----DGWEISGFEGKK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
userul for treating or preventing Staphylococcus aureus infections, such as pneumonia, septic arthritis, endocarditis or biomaterial related infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            related infections. The present sequence represents Staphylococcus epidermidis K-RN protein, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 89; DB 24; Length 654; Pred. No. 3.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63;
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21.9%; Pred. No. 5.r.
-ive 26; Mismatches
                                                                                                                                                  Claim 1; Page 29-30; 122pp; English.
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ABB64828 standard; Protein; 281 AA. 539 TKGEVESSSTT--PTK 552 26-MAR-2002 ABB64828; RESULT 17 ABB64828 셤

DKNNISSKSTINNPNK 144

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Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical. Drosophila melanogaster polypeptide SEQ'ID NO 21276.

Drosophila melanogaster.

WO200171042-A2

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PE CORP NY.
                                                                     N-PSDB; AAH62788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Candida albicans
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                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                         Query Match
(PENY-)
                    (SINO-)
                                       Xu X,
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ABP73992
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                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical furugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                  KDTFIKPVFKKIEE-KKEEENKPTFDVSKKKDNPQVNHSQLNE----SHRKEDLQREEH 113
                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shrimp white spot Bacilliform virus; WSBV; diagnosis; viral infection; antiviral agent; gene expression; antisense construct; transgenic viral resistant shrimp.
                                                                                                                                                                                                                                                                                                                                                                          -----NTS
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                      23;
                                                                                                                                                                 Disclosure; SEQ ID NO 21276; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                 11.8%; Score 88.5; DB 22; Length 281; 22.1%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                          9 NGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVI
                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shrimp white spot Bacilliform virus (WSBV) protein 99
                                                                                                                                                                                                                                                                                                                                                     52;
                                                                                                                                                                                                                                                                                                                                                      34; Mismatches
                                                                     Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG85008 standard, Protein, 1141 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 SQKSDSTKDVTATVLDKNNI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 IREYDLDQDNHINFEESNNM 268
                                                                     Li PWD,
23-MAR-2001; 2001WO-US09231
                   23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-NOV-2000; 2000WO-US28888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99CN-0124717
                                                                                                                                                                                                                                                                                                                                                      31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          White spot syndrome virus.
                                                                     Venter JC, Adams M,
                                                                                                                                                                                                                                                          (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                          2001-656860/75
                                                 (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                              281 AA;
                                                                                                    N-PSDB; ABL08931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200138351-A2
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                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                      189
                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG85008
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The invention provides the primary nucleotide sequence of the WSBV genome (AAH62689), predicted transcript sequences (AAH62689-AAH62839) and encoded proteins (AAG84910-AAG85051) and oligonucleotide sequences (AAH62840-63160) suitable for use as primars or probes. The nucleic acid molecules and proteins of the invention are useful for diagnosis and monitoring viral infection, in screens for antiviral agents and for monitoring viral gene expression or activity during a treatment regimen. The nucleic acid molecules are also useful as antisense constructs to control viral gene expression in infected cells and tissues and to create transgenic viral resistant shrimp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 EKKEEENKPTFDVSKKKUNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNN 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 STIVSEEDFILPVYKGELEKGYQFDGWEISGFEG--KKDAGYVINLSKDTFIKPVFKKIE 72
                                                                                                                                                                                                                                      virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S
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signal transduction; DNA replication; cell division; growth;
proliferation; Candida albicans; fungicide; antifungal.
                                                                                                                                                                                                                                Primary nucleotide sequence of the shrimp white spot Bacilliform (WSBV), useful for producing viral polypeptides that can be used screen for agents that are useful for treating WSBV infection -
                                                                                     Kodira C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1141;
                                                                                     Υ,
                                                                                         Shen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Candida albicans essential protein SEQ ID NO 7829.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43;
   C A
OCEANOGRAPHY STATE OCEANI
                                                                                     Ye Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.8%; Score 88.5; 23.3%; Pred. No. 7.5
                                                                                     Σ
                                                                                         He
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP73992 standard; Protein; 225 AA.
                                                                                                                                                                                                                                                                                                                                                          Claim 1; Figure 3; 626pp; English
                                                                                     Yang F, He J, . Pham L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-DEC-2000; 2000US-259128P.
20-FEB-2001; 2001US-0792024.
22-AUG-2001; 2001US-314050P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-DEC-2001; 2001WO-US49486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ELIT-) ELITRA PHARM INC.
                           SINOGENOMAX CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 ISSKSTTNN 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     718 SSSSSSSS 726
                                                                                                                                                WPI; 2001-355877/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1141 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sest Local Similarity
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The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying cone allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by comprising modifying cher allele by promoter; so that expression of the second allele by regulated by the promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles modified are useful for identifying a gene that contributes to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent, an antifungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of a mammalian activity of a gene product, preferably enzymatic activity, carbon catabolism, biosynthetic, transporter, transcriptional, compound catabolism, biosynthetic, transporter, transcriptional, compound inhibit growth or proliferation and cell division activity. The method is useful for identifying a compound having the ability to inhibit growth or proliferation of C. albicans cells and for treating infection by C. albicans. The present sequence is that of an essential Candida albicans protein used in the method of the invention. Note: The sequence data for this patent is not represented in the printed the Euronean Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YDDDDDEFEGFESSNGAAKELNLSESQAIKEWKQRRDLEIEEREKLNSKKKEEIIEKAKS 139
                                                                                                    targets
allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 YOFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKK----IEEKKEEENKPTFDVSKKK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detection; diagnosis; antisense therapy; gene therapy.
                                                                                              Constructing strains for identifying gene products as effective for therapeutic intervention, by inactivating in the strain one of a gene and placing other allele of the gene under conditional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -- DNPQVNHSQLNESHRKEDLQREEH--SQKSDSTKDVTATVLDKNN 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 44; SEQ ID NO 7829; 167pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23; Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43; Indels
Ohlsen KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.8%; Score 88; DB 23 28.0%; Pred. No. 0.89; ive 22; Mismatches
  Bussey H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human protein sequence SEQ ID NO:15383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB94584 standard; Protein; 258 AA.
Boone C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUL-2000; 2000EP-0116126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
  Jiang B,
                                     2002-566694/60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 AA;
                                                          N-PSDB; ABZ32542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP1074617-A2
                                                                                                                                                             expression
  Roemer T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S:
Matches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB94584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB94584
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the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense thereapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNas. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNas. The primers allow obtaining of the full-length cDNas the primers allow obtaining of the full-length cDNas are assily without any specialised methods. AH03166 to AH13628 and AH13633 to AH13642 represent human cDNA sequences, AAB92446 to
                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the polynucleotide which comprises a 3'-end sequence of polynucleotide which comprises a 3'-end sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB95893 represent human amino acid sequences, and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV; hyperimmune; erum-reactive; antigen; pathogen; tumour; allergen; auto-immunity; vaccine; staphylococcal infection; antibody; cancer; auto-immune disease; HIV; hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 SKKKDNPQ-----VNHSQLNESHRKEDLQREEHSQKSDSTKDVTATV--LDKNNISSK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pathogen specific antigen related staphylococcal protein SEQ ID No 142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 YKGELEKGYQFDGWEISGFEGKKDAGY--VINLSKDTFIKPVFKKIEEKKEEENKPTFDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 WEGEDEDUVEDNWEDDEDEKKEEAEVKPEVKISEK---KKIAEKIKEKERQQKKRQEEI
                                                                                                                                                                                                                                                                              Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                          Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.8%; Score 88; DB 22; Length 258; 26.3%; Pred. No. 1.1;
                                                                                                                                                                          Saito K,
Otsuki'
                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; SEQ ID 15383; 2537pp + CD ROM; English.
                                                                                                                                                                          nikawa T, Hayashi K, S
Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABJ18979 standard; Protein; 645 AA.
                                                                                                                                                                        Ota T, Isogai T, Nishikawa
Ishii S, Sugiyama T, Wakama
                  27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
                                                                                    09-JUN-2000; 2000JP-0241899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31; Conservative
                                                                                                                                 (HELI-) HELIX RES INST
                                                                                                                                                                                                                                          WPI; 2001-318749/34.
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ABJ18979
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cell proliferation; cell differentiation; gene therapy;

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Human; cytokine; cell proliferation; cell differentiation; gene the vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                            03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0566075.
20-UUN-2000; 2000US-0598075.
19-JJJ-2000; 2000US-062325.
01-SEP-2000; 2000US-0654936.
15-SEP-2000; 2000US-0654936.
20-CT-2000; 2000US-063325.
30-NOV-2000; 2000US-0728422.
                                                          Human protein SEQ ID NO 2964.
                                                                                                                                                                                                                                                                  05-FEB-2001; 2001WO-US04098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-476283/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAK52451
                                                                                                                                                                                                     WO200157190-A2.
                                                                                                                                                                        Homo sapiens.
                               06-NOV-2001
                                                                                                                                                                                                                                   09-AUG-2001,
AAM79318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rang YT,
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셤
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                                                                                                                                                                                                                                                                                                                                                                                                      The structure of a large and a large a large of animal, or individual sera with antibodies a gainst the specific pathogen, tumour, allergen, tissue or host prone to the 62 sequences of 53-2261 amino acids fully defined in the specification, or their hyperimume fragments are useful for the manufacture of a pharmaceutical preparation, particularly a vaccine against staphylococcal infections or colonisation against S. aureus or S. epidermidis. The preparation of antibodies is useful for the manufacture of a medicament for treating or preventing staphylococcal infections or colonisation against S. aureus or S. epidermidis. The manufacture of a medicament for treating or preventing staphylococcal infections or colonisation against S. aureus or S. epidermidis. The manufacture of a medicament for treating or preventing staphylococcal infections or conditions that can be treated include cancer, autoimmune diseases or protozoan pathogens. This sequence represents a staphylococcal protein relating to the method for identifying and producing pathogen specific antigens of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         355 SVENNESMMDTFVKH-----PIKTGMLNGKKYMVMETTNDDYWKDFMVEGORVRTISKDA 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NKPTFDV----SKKKDNPQVNHSQLNESHRKEDLQ----REEHSQKSDSTKDVT-ATVL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----SKDTFIKPVFKKIEEKKEEE 78
                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel method for identifying, isolating and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              410 KNNTRTIIFPYVEGKTLYDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 TIQNGKEMSSTIVSEEDFILPVYKGELE-KGYQF-----DGWEISGFEGKK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                 Identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, for preparing vaccine or medicament for treating or preventing e.g. staphylococcal infections, comprises providing antibody preparation
                                                                                                                                                                                       Zauner W;
Hafner M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.8%; Score 88; DB 24; Length 645; 21.9%; Pred. No. 3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63; Indels
                                                                                                                                                                                   Von Ahsen U, Klade C, Henics T,
O, Etz H, Dryla A, Weichhart T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26; Mismatches
                                                                                                                                                        (CIST-) CISTEM BIOTECHNOLOGIES GMBH,
                                                                                                                                                                                                                                                                                                                                                               Claim 21; Page 168; 252pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DKNNISSKSTTNNPNK 144
                                                                                         21-JAN-2002; 2002WO-EP00546
                                                                                                                         26-JAN-2001; 2001AT-0000130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 21.5.
Best Local Similarity 21.5.
An 43; Conservative
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                                                                                                                                                                                Meinke A, Nagy E, Von
Minh DB, Vytvytska O,
Tempelmaier B;
                                                                                                                                                                                                                                                WPI; 2003-075410/07.
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 Staphylococcus sp
                                                            01-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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Cao Y,

A C, Wang 7

u P, Xu (Chen R,

Zhou

', Asundi V, Zhou Zhang J, Ren F, ', Goodrich R;

Liu C, Drmanac RT, Wang D, Wang J, Zh Yang Y, Wejhrman T,

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encoded polypeptides (AAM/8323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hammunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 -KKDNPQVNHSQLNESHRKED-----LQREEHSQKSDSTKDVTATVLDKNNISSKST 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87
                                                                                                                                                                                                                                                                                                                                                                       treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 GELEKGYQFDGWEISG--FEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSK
                                                              The invention relates to polynucleotides (AAK51456-AAK53435) and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22; Length 817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.8%; Score 88; DB 22
27.3%; Pred. No. 5.3;
:ive 21; Mismatches
Claim 20; Page 215; 6221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 27.3% nes 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              817 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139 T 139
                                                                                                                                                                                                                                                                                                                                                                                                          inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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AAM79318 standard; Protein; 817 AA.

RESULT 22 AAM79318

315 T 315

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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymerledes are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                           Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ma Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inflammation.

Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drmanac RT, Asundi V, Zhou P, Xu C, Ca
Wang J, Zhang J, Ren F, Chen R, Wang
Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; Page 215; 6221pp; English.
                               AAM79319 standard; Protein; 817 AA.
                                                                                                                              Human protein SEQ ID NO 2965.
                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUL 2000; 2000US-0620325.
01-SEP-2000; 2000US-0654936.
15-SEP-2000; 2000US-0654936.
20-OCT-2000; 2000US-0693325.
30-NOV-2000; 2000US-0728422.
                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0560875.
2000US-0598075.
                                                                                                                                                                                                                                                                                                                                                  05-FEB-2001; 2001WO-US04098
                                                                                                                                                                                                                                                                                                                                                                                   03-FEB-2000; 2000US-0496914
                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-476283/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu C, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         817 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAK52452
                                                                                                                                                                                                                                                                                  WO200157190-A2.
                                                                                                                                                                                                                                                                                                                                                                                                     27-APR-2000;
20-JUN-2000;
                                                                                                                                                                                                                                                   Homo sapiens,
                                                                                                06-NOV-2001
                                                                                                                                                                                                                                                                                                                   09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang YT,
Zhao QA,
                                                               AAM79319;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xue AJ,
RESULT 23
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The invention relates to human nucleic acids (AAIS7798-AAI61369) and
the encoded polypeptides (AAM18642-AAM42213) with nootropic,
the encoded polypeptides (AAM18642-AAM42213) with nootropic,
immunosuppressant and cytostatic activity. The polymucleotides are useful
immunosuppressant and cytostatic activity. The polymucleotides are useful
in gene therapy. A composition contealing a polypeptide or polymucleotide
of the invention may be used to treat diseases of the peripheral nervous
system, such as peripheral nervous injuries, peripheral nervous as
localised neuropathies and central nervous system diseases, such as
alerral sclerosis, and Shy-Drager Syndrome. Other uses include the
cutilisation of the activities such as: Immune system suppression,
cutilisation of the activity, chemotactic/chemokinetic activity, haemostatic
and thrombolytic activity, cancer diagnosis and therapy, drug screening,
and thrombolytic activity, arthritis and inflammation, leukaemias and
c.N.S. disorders.

Note: The sequence data for this patent did not form part of the printed
- KKDNPQVNHSQLNESHRKED-----LQREEHSQKSDSTKDVTATVLDKNNISSKST 138
                 Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Allzhaimer's; parkinson's disease; Humington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ren F, W. Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen R, Ma Y, C
Xu C, Xue AJ,
, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; SEQ ID NO 3095; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen R,
                                                                                                                                                                                      AAM39950 standard; Protein; 607 AA
                                                                                                                                                                                                                                                                                          Human polypeptide SEQ ID NO 3095.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu C, Asundi V, Ch.
Wang Z, Wehrman T, Xi
Zhou P, Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-APR-2000; 2000US-0552317.
09-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-0620312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0662191.
19-OCT-2000; 2000US-0693036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0488725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0727344
                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAIS9106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200153312-A1.
                                                                   T 139
                                                                                                   315 T 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-NOV-2000;
                                                                                                                                                                                                                                                          22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                 leukaemia.
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Wang J, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang J, V
Zhao QA,
 88
                                                                   139
                                                                                                                                                                                                                        AAM39950;
                                                                                                                                                      RESULT 24
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55; Indels 12; Gaps

DB 22; Length 817;

Query Match
11.8%; Score 88; DB 3
Best Local Similarity 27.3%; Pred. No. 5.3;
Matches 33; Conservative 21; Mismatches

196 GQEKKQESFKSWEASGKHQEVSKPAVSLEQRKQDTSKLRSTLPEEGXKQEISKSKPSPSQ 255

30 GELEKGYQFDGWEISG--PECKKDAGYVINLSKDTFIKPVFKKIBEKKEBENKPTFDVSK 87

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635 AA;

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Sequence
                                                 Query Match
                                                                                                  Aatches
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ABP
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Also described are: (1) nuclectide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).

(I) and (II) are useful for the development of vaccines against

P. falciparum infection. (1) and polyclonal antisers or a monoclonal entitle of immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of fargs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in P. falciparum. Sequencing of the Plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand cour understanding of parasite biology, a process hampered by the complexity of the parasitic lifecyle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mogguito vaccine and drug development.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not
                                                                                                                                                                                                     59 SKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSD 118
                                                                                                                                                                                                                                  The present invention describes proteins and their fragments (I) encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       resistance to insecticides have led to a resurgence of malaria in many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide.
                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum chromosome 2 related protein SEQ ID NO:33.
                                                                                                                                                    ö
                                                                                                     Length 607;
                                                                                                  11.6%; Score 87; DB 22; Length 60
33.3%; Pred. No. 4.5;
ive 12; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             specifically mentioned within the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 85-86; 577pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gardner M,
                                                                                                                                                                                                                                                                                                                                                                              AAB18176 standard; Protein; 635 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US26796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0107131
                                                                                                                            Best Local Similarity 33.3
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hoffman S, Carucci D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-365347/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GARD/) GARDNER M. (VENT/) VENTER J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HOFF/) HOFFMAN S.
(CARU/) CARUCCI D.
(GARD/) GARDNER M.
                                                    607 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200025728-A2
specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAY-2000.
                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                AAB18176;
                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                             RESULT 25
AAB18176
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7;
                                                                                                                                                                                                                         92 PQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLD------KNNISSKS 137
                                                                                                                                                                                                                                                            epidermidis; open reading frame; ORF; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis lifection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N.B. The sequence data for this patent did not form part of the printer specification, but was obtained in electronic format directly from the USPTO web site.
                                                                                                                                               202 LQKKYNIQDDEEEDNETIRSDSKLRDIYSDSQSKDIMMSSSPNKEEES-----MSSDNHN
                                                                                                               32 LEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5157
                                                    24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20;
11.6%; Score 87; DB 21; Length 635; 23.8%; Pred. No. 4.8; tive 20; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 11.6%; Score 87; DB 23; Length 902; Best Local Similarity 25.3%; Pred. No. 7.8; Matches 85; Indels Matches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID 5157; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP40312 standard; Protein; 902 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENO-) GENOME THERAPEUTICS CORP.
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97US-064964P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibacterial; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                       Conservative
                          Similarity
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                                                                                                                                                                                                                                                                                                                                        138 TTNNPN 143
                                                                                                                                                                                                                                                                                                                                                                                                312 NNNNSN 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ABN92857.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-AUG-1997;
     Ma.
Local St..
30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP40312;
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the present invention describes process and the process of the human malarial parasite, plasmodium falciparum.

Also described are: (1) nucleotide sequences (11) encoding (1); and (2) vaccines against P. falciparum infection comprising (1) or (11).

(1) and (11) are useful for the development of vaccines against P. falciparum infection. (1) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (1), are useful in the detection of infection with P. falciparum. Furthermore, (1) (sepecially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in P. falciparum. Sequencing of the Plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand cur understanding of parasitic biology, a process hampered by the complexity of the parasitic lifeoyle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              resistance to insecticides have led to a resurgence of malaxia in many parts of the world, and there is a pressing need for vaccines and new furgs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the specification.
 Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 malarial parasite, vaccines and in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes proteins and their fragments (I)
                                                                                                                                                                                                                                                                    Plasmodium falciparum chromosome 2 related protein SEQ ID NO:29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                   137
                                                                       104 RKEDLQREEHSQ-----KSDSTKDVTATVLDKNNISSKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.6%; Score 86.5; DB 21; 23.8%; Pred. No. 36; ive 27; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   roteins encoded by chromosome 2 of the human lasmodium falciparum, useful as antimalarial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 75-82; 577pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis of P.falciparum infection
                                                                                                                                                                     AAB18172 standard; Protein; 2485 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gardner M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US26796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0107131
                                                                                                                                                                                                                                     07-NOV-2000 (first entry)
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Matches 36; Conservative
:| :|||:
343 TGGKGKKEGA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carucci D,
                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-365347/31.
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CARUCCI D.
GARDNER M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2485 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VENTER J C
                                                                                                                                                                                                                                                                                                                                                                                    WO200025728-A2
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                                                                                   390
                                                                                                                                                                                                      AAB18172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARU/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GARD/)
                                                                                                                                       RESULT 28
                                                                                                                                                    AAB18172
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                       ----KPTFDVSKKKDNPQVNHSQLNESHRKEDLQREE 112
                                                                                        44 SGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEBNKPTFDVSKKKDNPQVNHSQLNESH 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43
      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL36511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
     TVTIQNGKEMS-STIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGY-VINLSKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --IVSEEDFILPVYKGELEKGYQFDGWEI
                                                                                                                                                                                                                                                                                                                                                                                    developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47;
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                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster polypeptide SEQ ID NO 3099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.6%; Score 86.5; DB 22; 21.7%; Pred. No. 13; ive 28; Mismatches 51;
                                                                                                                                       141
                                                                                                                                                         | :: | : | :: | :: | 867 VESPENDERIDIRODFMDRVNEDIESASDN 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li PWD, Myers EW;
                                                                                                                                       113 -HSQKSDSTKDVTATVLDKNNISSKSTTNN
                                                                                                                                                                                                                                                        ABB58769 standard; Protein; 1183 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                      TFIKPVFKKIEEKKEEEN-
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                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 35; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                       pharmaceutical
                                                                                                                                                                                                                                                                                                                         26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                        Drosophila;
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                                                                      62
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                                                                                  KK----EEENKPTFDVSKKKDNPQVN----HSQLNESHRKEDLQ------REEH---- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; open reading frame; ORPX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosupressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; antianteant; antianteant; antianteant; antifungal; antichnematic; antithyroid; antianteant; gene therapy; cancer; proliferative disorder; hypoterension; neurodegenerative disorder; proliferative disorder; hypoterension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; alleryy; aplastic anaemia; nocturnal heemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
ELEKGYOFDGW------EISGFE-----GKKDAGYVINLSKDTFIKPVFKKIEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                         ENERGDEKDGYEEMNGGDKNEEMNGGDKNEEMNVGDKNGG--IN---
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human ORFX ORF2661 polypeptide sequence SEQ ID NO:5322.
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                                                                                                                                                                     114 ---SQKSDSTKDVTATVLDKNNISSKSTTNN 141
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                                                                                                                                                                                                                                                                                                                     AAB42897 standard; Protein; 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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N-PSDB; AAC77106
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51 DAG----YVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNH-----SQLNE 101
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         the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, allergies, aplastic anaemia, burns, wounds, bone and cartiage damage, nocturnal haemoglobinuria, antinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                        88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
 The sequences can be used for determining
                                                                                                                                                                                                                                                                                                               9 NGKEMSSTIVSE--EDFILPVYKGELEKGYQF-----DGWE-----ISGFEGKK
                                                                                                                                                                                                                                                                 42;
                                                                                                                                                                                                                                    21; Length 209;
                                                                                                                                                                                                                               11.5%; Score 86; DB 21; Length 209
Similarity 29.1%; Pred. No. 1.3;
14: Conservative 13; Mismatches 52; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG37134 standard; Protein; 408 AA
antithyroid; and antianaemic.
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99US-0123180.
99US-0125788.
99US-012678.
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99US-0128784.
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99US-0130077
99US-0130049.
99US-0130510.
99US-0131449.
99US-0132407.
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                                                                                                                                                                                                                                                                 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana.
                                                                                                                                                                                                         Sequence 209 AA;
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25-MAR-1999;
29-MAR-1999;
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04-MAY-1999;
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PR 05-WAY-1999 9905-0112465.

PR 11-WAY-1999 9905-0112465.

PR 11-WAY-1999 9905-0114256.

PR 11-WAY-1999 9905-0114256.

PR 11-WAY-1999 9905-0114256.

PR 11-WAY-1999 9905-0114259.

PR 11-WAY-1999 9905-0114459.

PR 11-
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US-01450897 US-01450897 US-0145185 US-0145185 US-0145218 US-0145218 US-0145213 US-0145213 US-0145213 US-0145318 US-0145318 US-0145318 US-0145318 US-0145318 US-0145318 US-0145318 US-0145318 US-0145318 US-0145318 US-0145318	9908-01-9908-0	US-0151080 US-0151303 US-0151303 US-0151933 US-0153050 US-0153050 US-0153050 US-0154018 US-0154039 US-0155458	905-0158369 905-0158369 905-0159293 905-0159295 905-0159330 905-0159330 905-0159631 905-0159631 905-0159631 905-0159631
2.7UL - 1999 2.7UL - 1999 3.7UL - 1999 3.7UL - 1999 4.7UL - 1999 7.7UL - 1999 7.7UL - 1999 8.7UL	04+AuG-1999) 05-AuG-1999) 05-AuG-1999) 06-AuG-1999) 09-AuG-1999) 10-AuG-1999) 11-AuG-1999) 11-AuG-1999) 12-AuG-1999) 13-AuG-1999) 13-AuG-1999) 13-AuG-1999) 13-AuG-1999) 25-AuG-1999) 25-AuG-1999) 25-AuG-1999) 25-AuG-1999)	7-AUG-1999 11-SEP-1999 10-SEP-	8-0CT-1999 3-0CT-1999 3-0CT-1999 3-0CT-1999 4-0CT-1999 4-0CT-1999 4-0CT-1999 1-0CT-1999
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990S-0132485.
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990S-01342186.
990S-0134218.
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990S-0144332.
99US-0132484
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                                                                                                                                                                                                                                                                        59 SKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSD 118
                                                                                                                                                                                                                                                                                    261 NKETYLQ-AMEEYKRTKEEE-----ALSQKKE-----EBELLKLHKQEALQMLKKKEKTD 309
                                                                                                                                                                                                                            1 HRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGY--VINL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                         55; Indels 30; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana protein fragment SEQ ID NO: 45609.
                                                                                                                                                                                                                                                                                                                                  119 STKDVTATVLDKNNISSKSTTNN--PNK 144
                                                                                                                                                                                                                                                                                                                                                                                            AAG37133 standard; Protein; 456 AA
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990S-0123180.
990S-0125788.
990S-0125788.
990S-0126785.
990S-0126785.
990S-0128234.
990S-013824.
990S-0130891.
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990S-0130891.
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99US-0160815.
99US-0160980.
99US-0160981.
99US-0161404.
99US-0161406.
99US-01611359.
99US-0161359.
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PR 11-AUG-1999 9905-01477204

PR 11-AUG-1999 9905-01477204

PR 11-AUG-1999 9905-0149722

PR 23-AUG-1999 9905-0149722

PR 24-AUG-1999
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59 SKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSD 118
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                    99US-0160770.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Potential phosphorylation site'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "Potential glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Potential glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "Potential glycosylation site"
                                                                                                                                                                                                                                                                                                                                           55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Potential glycosylation
                                                                                                                                                                                                                                                                                                             DB 21;
                                                                                                                                                                                                                                                                                                           11.5%; Score 86; DB
llarity 23.6%; Pred. No. 4;
Conservative 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               378 N-----LIKKEKATKKKNENVDPNK 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STKDVTATVLDKNNISSKSTTNN--PNK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cell cycle regulation protein-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY44364 standard; protein; 757
99US-0160767.
99US-0160768.
99US-0160770.
                                                             99US-0160815.
99US-0160980.
99US-0160981.
                                                                                                              99US-0160989.
99US-0161404.
99US-0161405.
                                                                                                                                                                                                                             99US-0161920.
99US-0161992.
99US-0161993.
99US-0162142.
                                                  99US-0160814
                                                                                                                                                               99US-0161406
99US-0161359
                                                                                                                                                                                             99US-0161360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note=
                                                                                                                                                                                                                                                                                                                          Local Similarity
es 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
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                                                                                                                                                                                                                 26-OCT-1999
                                                                                                                                                                                                                              28-OCT-1999
                                                                                                                                                                                                                                               28-OCT-1999
                                                                                                                                                                                                  26-OCT-1999
                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                           59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY44364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119
                                                                                                                                                                25-OCT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 33.
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English.

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AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB5234 to AAB54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular; neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polymucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polymucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, immune strength and cardiovascular disorders, reproductive disorders, immune diseases, and cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 DAG----YVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNH-----SQLNE 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         470 KGGRGSHRAKNKSKETFLGSV------KETFDAMKNSTKEFVRHHKEKIKQAKE 517
                                                                                                         ed gene sequences, referred to as colon cancer the treatment, prevention, and diagnosis of colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 NGKEMSSTIVSE--EDFILPVYKGELEKGYQF-----DGWE-----ISGFEGKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.5%; Score 86; DB 21; Length 758; llarity 29.1%; Pred. No. 7.7; Conservative 13; Mismatches 52; Indels
                                                                                                                                                                                              Claim 11; Page 1408-1411; 2104pp;
                                                                                                                                  antigens, useful for the treatmes
disorders such as colon cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-NOV-2000; 2000WO-US28888.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99CN-0124717.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  White spot syndrome virus
                                                                                                           cancer associated
Rosen CA, Ruben SM;
                                           2000-587534/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
es 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          758 AA;
                                                              N-PSDB; AAC98076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200138351-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG85023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                           Colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                               The present sequence is cell cycle regulation protein-5 (CECRP-5). Blast analytical method was used to identify this protein. CECRPs are activacrs of cell proliferation or inhibitors of cellular processes that modulate proliferation. They are used to treat or prevent cell proliferative diseases like cancers, atherosclerosis, cirrhosis, hepatitis, psoriasis, immune system disorders (e.g. acquired immune deficiency syndrome, allergy, asthma, Crohn's disease, rheumatoid arthritis). Antibodies are raided socreen for specific binding agents. The corresponding nucleic acid is used in gene therapy, chromosomal mapping and isolation of related sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      469 KGGRGSHRAKNKSKETFLGSV------KETFDAMKNSTKEFVRHHKEKIKQAKE 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cytostatic; cardioactive; neuroprotective; vulnerary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder.
                                                                                                                                                                          Novel regulatory proteins, for diagnosis, treatment and prevention of cell proliferative and immune system diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 NGKEMSSTIVSE--EDFILPVYKGELEKGYQF-----DGWE-----ISGFEGKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DAG----YVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNH-----SQLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42; Gaps
                                           Baughn MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.5%; Score 86; DB 21; Length 757; 29.1%; Pred. No. 7.7; ive 13; Mismatches 52; Indels '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human colon cancer antigen protein sequence SEQ ID NO:859.
                                           Corley NC, Guegler KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHRKEDLOREEHSOKSD--STKDVTATVLDK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A-VKENLKKFSDSVKSTFRHFKDTTKNIFDE 546
                                                                                                                                                                                                                                            Claim 1; Page 70-71; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB53319 standard; Protein; 758 AA
                                           Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-MAR-2000; 2000WO-US05883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 29.1 tes 44; Conservative
(INCY-) INCYTE PHARM INC.
                                                                                                           2000-105887/09
                                           Lal P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    757 AA;
                                                                                                         WPI; 2000-105887/
N-PSDB; AAZ29484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200055351-A1
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                                                              Patterson C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-SEP-2000
                                           Bandman O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Matches
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Gaps

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Shrimp white spot Bacilliform virus; WSBV; diagnosis; viral infection; antiviral agent; gene expression; antisense construct; transgenic viral resistant shrimp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shrimp white spot Bacilliform virus (WSBV) protein 114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PENY-) PE CORP NY.
(THIR-) THIRD INST OCEANOGRAPHY STATE OCEANI C A.
SHRKEDLQREEHSQKSD--STKDVTATVLDK 130
                                            : ||:|:: | || || : |:
518 A-VKENLKKFSDSVKSTFRHFKDTTKNIFDE 547
                                                                                                                                                                                                                                                                              AAG85023 standard; Protein; 922 AA
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FORFAS T/A BIORESEARCH IRELAND.
UNIV TEXAS A & M.
PATTI J M.
                                                  JOSEFSSON E.
EIDHIN D N.
HOOK M A O.
                                        FOSTER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-MAR-2003
                                                                                                                              Perkins SE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                       (FOST/)
(JOSE/)
(EIDH/)
(HOOK/)
                                                                                        (PERK/)
                                                                                                                 Eidhin
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                                                                                                                                                                The invention provides the primary nucleotide sequence of the WSBV genome (AAH62689), predicted transcript sequences (AAH62689-AAH62839) and encoded proteins (AAG8940-AAG85051) and oligonucleotide sequences (AAH62840-63160) suitable for use as primers or probes. The nucleic acid molecules and proteins of the invention are useful for diagnosis and monitoring viral infection, in screens for antiviral agents and for monitoring viral gene expression or activity during a treatment regimen. The nucleic acid molecules are also useful as antisense constructs to control viral gene expression in infected cells and tissues and to create
                                                                                                                                                                                                                                                                                                                                                                                                            310 VIESMRNGCCCFKNDKWLAKRESNLKSLNNTVFGEEDDEKSAYAYSDSEDEDEDENEEEV 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                    310 DYDYNNETIESSVG-----NVIKNLIRKTIGLSDVEEEKEEGEQSEEEEEDSDDDD 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fibrinogen-binding protein, alpha chain; beta chain; ClfB; SdrC; SdrD; SdrE; fibrinogen, medical device; competitive inhibitor; pharmaceutical; tractment; infection; septicemia; osteomyelitis; mastitis; endocarditis; extracellular matrix; vascular graft; vascular stent; vaccine; intravenous catheter; artificial heart valve; cardiac assist device;
                                                                                                                                                                                                                                                                                                                                                                                      3 VTVTIQNG-----KGELEK 34
                                                                                                                                                                                                                                                                                                                                                                                                                                       35 GYQFDGWEISGFEGKKDAGYVINLSKDTFIKPV-FKKIEEKKEEENKPTFDVSKKKDNPQ 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      422 DASSVCSSSSSSSSTVVAAAAEEEEEEDEEDKD-TATVVEDEDDKESVISSSSEDS 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 VNHSQLNESHRKEDL-----QREEHSQKSDSTKDVTATVL----DKNNISSKSTTNN 141
                                                                                         Primary nucleotide sequence of the shrimp white spot Bacilliform virus (WSBV), useful for producing viral polypeptides that can be used to screen for agents that are useful for treating WSBV infection -
                              Kodira C;
                                                                                                                                                                                                                                                                                                                                                             48;
                                                                                                                                                                                                                                                                                                                                Match 11.5%; Score 86; DB 22; Length 922; Local Similarity 21.9%; Pred. No. 10; les 39; Conservative 28; Mismatches 63; Indels
                           Shen Y,
                             Ye Y,
                             Σ
                              He
                                                                                                                                                                                                                                                                                   transgenic viral resistant shrimp.
                                                                                                                                           Claim 1; Figure 3; 626pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY08642 standard; Protein; 1315
                             Pham L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0098427.
97US-0066815.
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   (SINO-) SINOGENOMAX CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S. aureus SdrD protein.
                              Yang F, He J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (updated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus.
                                                    WPI; 2001-355877/37.
N-PSDB; AAH62803.
                                                                                                                                                                                                                                                                                                            922 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibacterial
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09-AUG-1999
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                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                     Query Match
                              Κu Χ,
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(INHI-) INHIBITEX INC.

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Thus invention describes move staphylococus and least The proteins that bind both the alpha and beted fibrinogen chains. The proteins (and their encoding nucleic acids are CIEB, SdrC, SdrD and SdrE). Staphylococus aureus is thought to utilize fibrinogen to adhere to medical devices, binding proteins that bind both the alpha and beta fibrinogen chains (CIEB, SdrC, SdrD and SdrE) can therefore be used as competitive inhibit cors to blook this binding. Antibodies against CIEB, SdrC, SdrD and SdrE inhibit CIEB, SdrC, SdrD and SdrE mediated binding. The proteins of the invention can be used in a pharmaceutical composition. The proteins of the invention can be used in a pharmaceutical composition. The proteins of the stratechlular matrix. The proteins or their fragments osteomyelitis, mastitis or endocarditis or to inhibit the binding of Staureus to the extracellular matrix. The proteins or their fragments may be used to coat a medical device to reduce the Staureus infection of an indwalling medical device, especially where the medical device is selected from the group consisting of vascular grafts, vascular stents, intravenous catheters, artificial heart valves, and cardiac assist cenconing gene may be used as a vaccine. The DS (aspartate serine) repeat region or a gene encoding it may be used as an identifying probe for the invention have antibacterial activity. The proteins of the invention have antibacterial activity.

The proteins of the invention have antibacterial activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes novel Staphylococcus aureus fibrinogen-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pathogen specific antigen related staphylococcal protein SEQ ID No 124.
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                                                                                                                                                                                                                                                                                                      Staphylococcus aureus fibrinogen-binding proteins for treating septicemia, osteomyelitis, mastitis or endocarditis
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                                                                    Patti JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65; Indels
                                                                    Hook MAO, Josefsson E,
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                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; Fig 8; 143pp; English.
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Matches 36; Conservative
                                                                        Foster TJ,
                                                                                                                                                                                     WPI; 1999-357844/30.
PERKINS S E
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New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                            Staphylococcus aureus cellular proliferation protein #678.
                                                                                                                                                Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                  2000US-206848P.
2000US-207727P.
2000US-242578P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-NOV-2000; 2000US-253625P.
22-DEC-2000; 2000US-257931P.
16-FEB-2001; 2001US-269308P.
                                                                                                                                                                                                                                                                                                                                        21-MAR-2001; 2001WO-US09180.
                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                 Staphylococcus aureus
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                                                                     14-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                   21-MAR-2000;
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                              AAU34402;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel method for identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, tumour, allergen, a tissue or host prone to auto-immunity, where the antigens are used in a vaccine, comprises providing antibody preparation from a plasma pool of a type of animal, or individual sera with antibodies against the specific pathogen, tumour, allergen, tissue or host prone to auto-immunity. The hyperimmune serum-reactive antigens comprising any of the 62 sequences of 53-2261 amino acids fully defined in the more pecification, or their hyperimmune fragments are useful for the manufacture of a pharmaceutical preparation, particularly a vaccine against staphylococcal infections or colonisation against S. aureus or S. epidermidis. The preparation of antibodies is useful for the manufacture of a medicament for treating or preventing staphylococcal infections or colonisation against S. aureus or S. epidermidis. The antibody conditions may also be used for diagnostic and imaging purposes. Other conditions that can be treated include cancer, autoimmune diseases or infections caused by viral (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This sequence represents a staphylococcal protein relating to the method for identifying and producing pathogen specific antigens of the invention.
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hyperimmune; serum-reactive; antigen; protozoacide; cytostatic; anti-HIV; auto-immunity; vaccine; staphylococcal infection; antibody; cancer; autoimmune disease; HIV; hepatitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, for preparing vaccine or medicament for trating or preventing e.g. staphylococcal infections; comprises providing antibody preparation
                                                                                                                                                                                                                                                                                                                                                                Zauner W;
Hafner M;
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                                                                                                                                                                                                                                                                                                                                                           Von Ahsen U, Klade C, Henics T,
O, Etz H, Dryla A, Weichhart T,
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                                                                                                                                                                                                                                     21-JAN-2002; 2002WO-EP00546.
                                                                                                                                                                                                                                                                            26-JAN-2001; 2001AT-0000130
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Best Local Similarity 24.2
Matches 36; Conservative
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Vytvytska O,
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                                                                                                              Staphylococcus sp
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                                                                                                                                                                                                                                                                                                                                                              Meinke A,
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Carr GJ;

Wall D, Trawick JD,

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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are genes themselves and the encoded proteins. The prokaryotes used are communiae, Pseudomonas aeruginosa and Enterococcus facealis. The invention is also useful for the identification of potential new targets invention is also useful for the identification of potential new targets or identify proteins used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery comported in proliferation in the proteins are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Contact the printed specification, but was obtained in electronic form part for the print while processed or contact of the printed specification, but was obtained in electronic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences.
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AAU34402 standard; Protein; 1349 AA

RESULT 38 AAU34402

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VTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGF--EGKKDAGYVINLSK 60
                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are bacherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonsa aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the express choteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense mucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             οŧ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             essential prokaryotic cellular proliferation protein.
Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic
format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.5%; Score 86; DB 22; Length 1349; ilarity 24.2%; Pred. No. 17; Conservative 22; Mismatches 65; Indels 20
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                                                                                                                                                                       Staphylococcus aureus cellular proliferation protein #1714.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                 Antisense, prokaryotic cellular proliferation protein, antibiotic, antibacterial, drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Seg ID No 13137; 511pp; English.
  121 KD-----VTATVLDKNNISSKSTINNPN 143
                 ftp.wipo.int/pub/published_pct_sequences.
                                                                                           AAU37544 standard; Protein; 1349 AA
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27-NOV-2000; 2000US-253625P.
22-DEC-2000; 2000US-257931P.
16-FEB-2001; 2001US-26930BP.
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2000US-207727P.
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                                                                                                                                               (first entry)
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Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                         Staphylococcus aureus
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N-PSDB; AAS55403.
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Best Local Similarity
Matches 36; Conserv
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26-MAY-2000;
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Gaps

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DTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDST 120
                                                                                                         invention also provides the SCNBA encoding gene sequence and an antibody against the sodium channel. The SCNBA protein alpha subunit and its encoding cDNA can be used in the elucidation of the physiological mechanisms of excitatory cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37 QFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 SQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPN 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human sodium channel 8A (SCN8A) protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sodium channel 8A; SCN8A; human; excitatory cell
                                                                                                                                                                               KD-----VTATVLDKNNISSKSTINNPN 143
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                                                                                                                                                                                                          (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 5-12; 14pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                      AAB23563 standard; Protein; 1980 AA
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N-PSDB; AAA93791.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                      819 VTVTLKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JP2000201684-A.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

February 10, 2004, 10:48:44; Search time 6.69436 Seconds (without alignments) 1011.574 Million cell updates/sec Run on:

US-10-067-385-8_COPY_630_773
748
1 HRVIVTIQNGKEMSSTIVSE.....ATVLDKNNISSKSTINNPNK 144 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 segs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% . Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. Score 1 97.5	Mate 13	i Fe	B		ρ ιι
92.5 92.5 90.5	12222			TOP2 PLAFK MAPB HUMAN SPT7 YEAST	plasm bomo sacch
87.5 87.5 87 87 86.5	нннн	1888 1702 893 2464 1006		YDT2_SCHPO IGA2_HAEIN GYRAZ_STAEP MAPB_MOUSE RAT1_YEAST	O14207 schizosacch P45384 haemophilus P54112 staphylococ P14873 mus musculu Q02792 saccharomyc
88 88 8. 7. 7. 8. 4. 6. 7. 7. 8. 4. 6. 7. 7. 8. 4. 6. 7. 7. 4. 6. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7.				GLNA_PYRKO TIG_STAAM DPOM_ASCIM IF2_STAEP IGAO_HAEIN YFK8_YEAST	pyroc staph ascob staph haemo
83 68 83 68 82 83 83 83 68 82 5 5 88 88 88 88 88 88 88 88 88 88 88 88		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		MUZEL HUMAN 1F31 HUMAN 1F31 HUMAN TONB HAEIN LIP STAEP ADSV HUMAN GLNA PYRAB DNLI CAEEL ARS2 DROME ARS2 DROME ARSY YEAST YME4 YEAST YKT5 YEAST GLNA PYRWO GLNA PYRWO	Q116695 homo sapien Q15695 homo sapien Q75822 homo sapien P42872 haemophilus Q02510 staphylococ Q94613 homo sapien Q27474 caenorhabdi Q27474 caenorhabdi Q9997 drosophila P15205 rattus norv P49957 saccharomyc P36046 saccharomyc Q5907 pyrococcus P36087 pyrococcus
31 82 32 82 33 81.5	0.01	914 949 572		PBPA BACSU IF2 HELPJ LMD1 HUMAN	P39793 bacillus su Q9zm46 helicobacte P29536 homo sapien

P32892 saccharomyc P08750 bacillus su P25644 saccharomyc P2588 saccharomyc P2588 saccharomyc O09847 caenorhabdi Q9zh79 pasteurella P75280 mycoplasma O60841 homo sapien P36188 homo sapien P36188 homo sapien P36188 homo sapien	
DRS1_YEAST DACA_BACSU PAT1_YEAST YCG1_YEAST YAE6_SCHPO UN89_CABEL TONB PASMU YP06_MYCPN IF2P_HUMAN IF2P_HUMAN CENC_HUMAN CENC_HUMAN CENC_HUMAN	
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81.5 81 81 81 81 81 80.5 80.5 79.5	
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## ALIGNMENTS

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STANDARD;
                                                                                                      Eukaryota; Alveo
NCBI_TaxID=5839;
                                 01-FEB-1995
01-FEB-1995
30-MAY-2000
             PLAFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACT SITE
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SK--KKDNPQVNHSQLN-----ESHRKEDLQREEHSQKSDSTKD---VTATVLDKNNI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           257 SKDAKKDAKEIKKGKKDKKKPSSTDSDSKDDVKKE---SKKDATKDAKKVAKKDTEKESA 313
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUB=Testis;
MEDLINE=9525591; PubMed=7737358;
Hess H., Heid H., Zimbelmann R., Franke W.W.;
Hess H., Heid H., Zimbelmann R., Franke W.W.;
"The protein complexity of the cytoskeleton of bovine and human sperm heads: the identification and characterization of cylicin II.";
Exp. Cell Res. 218:174-182 (1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 KGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIBEKKEBENKPTF---DV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                             BE INVOLVED IN SPERMATID DIFFERENTIATION.
-!- SUBCELLULAR LOCATION: CALYX; SPERM HEAD CYTOSKELETAL STRUCTURE.
-!- TISSUE SPECIFICITY: Testis.
                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rioskeleton; Structural protein; Repeat; Sperm; Spermatogenesis.

25 347 31 X 3 AA REPEATS OF K-K-X.

MAIN 157 240 3 X APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM; 604035; -.
GO; GO:0005200; F:structural constituent of cytoskeleton; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.7%; Score 95; DB 1; Length 348; llarity 30.9%; Pred. No. 2.1; Conservative 20; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39079 MW; D86766599C1809E7 CRC64;
                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
08-EFB-2003 (Rel. 41, Last annotation update)
Cylicin II (Multiple-band polypeptide II).
                                                                                                                  348 AA
                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z46788; CAA86752.1; -.
                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genew; HGNC:2583; CYLC2.
 | : ||::
1150 SHDKHRPFHSKVE-
                                                                                                                                                                                               Homo sapiens (Human)
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213 2
348 AA;
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Matches 38; Conserv
                                                          QK 1203
                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  314 DSK 316
                                   143 NK 144
                                                                                                                                                                                    CYLC2 OR CYL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM; 604035;
                                                                                                                CYL2 HUMAN
Q14093;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ridley R.G., Kilbey B.J.;
"The gene encoding topoisomerase II from Plasmodium falciparum.";
Nucleic Acids Res. 22:2547-2551(1994)
-!- FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY TRANSIENT
BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPOISOMERASE II
MAKES DOUBLE-STRAND BREAKS.
-!- CATALYNIC ACTIVITY: APP-dependent breakage, passage and rejoining
of double-stranded DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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|:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: 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ISOMERASE; TOPOISOMERASE II; 1.
ISOMERASE; TOPOISOMERASE; DNA-Dinding; Nuclear protein.
NP BIND 144 149 ATP (POTENTIAL).
ACT SITE 830 830 DNA CLEAVAGE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Nuclear.
-!- MISCELLANEOUS: EUKARYOTIC TOPOISOMERASE I AND II CAN RELAX BOTH
NEGATIVE AND POSITIVE SUPERCOLLS, WHEREAS PROKARYOTIC ENZYMES
RELAX ONLY NEGATIVE SUPERCOLLS.
-!- SIMILARITY: Belongs to the type II topoisomerase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=94316496; PubMed=8041616;
Cheesman S., McAleese S., Goman M., Johnson D., Horrocks P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum (isolate Kl / Thailand).
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53; Indels
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308 316 POLY-ASN.
1089 1093 POLY-LYS.
127 1234 POLY-LYS.
1398 AA; -161029 MW; BAAD7BEE88FESBE9 CRC64;
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                                                                                                                 FEB-1995 (Rel. 31, Created)
(Rel. 31, Last sequence update)
MAY-2000 (Rel. 39, Last annotation update)
topoisomerase II (RC 5.99.1.3).
PRT; 1398 AA
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Pred. No. 9.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ffan; PRO0204; DNA gyraseB; 1.
Pfam; PRO0521; DNA topoisolv; 1.
Pfam; PRO0515; HATPASE c; 1.
PRINTS; PRO0615; CCAATSUBUNTA.
PRINTS; PRO0018; TPIZFAMILY.
PRODOM; PRO00742; DNA topoisolV; 1.
SWART; SMO043; TOP2C; 1.
SWART; SMO043; TOP2C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003594; ATPbind ATPase.
InterPro; IPR003957; CBFA HVFB topis.
InterPro; IPR001241; DNA topoisoII.
InterPro; IPR002205; DNA_topoisoIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X79345; -; NOT_ANNOTATED_CDS.
HSSP; P06786; 1BGW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.7%;
23.8%;
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Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 VFKKIEE---
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SEQUENCE
DOMAIN
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1190 DIEKVEEAIEFQRNVELSNREESNK--FKVARKQ-----GPSSMKKKKKKKKLSSDEESE 1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Fetal brain;

MEDLINE=95104835; PubMed=7806212;

MEDLINE=95104835; PubMed=7806212;

MEDLINE=95104835; PubMed=7806212;

"Cloning of human microtuble-associated protein 1B and the identification of a related gene on chromosome 15.";

Genomics 22:273-280(1994).

-! FUNCTION: THE FUNCTION OF BRAIN MAPS IS ESSENTIALLY UNKNOWN.

PHOSPHORYLATED MAPIB MAY PLAY A ROLE IN THE CYTOSKELETAL CHANGES THAT ACCOMPANY NEURITE EXTENSION. POSSIBLY MAPIB BINDS TO AT LEAST TWO TUBULIN SUBUNITS IN THE POLYMER, AND THIS BRIDGING OF SUBUNITS MIGHT BE INVOLVED IN NUCLEATING MICROTUBULE POLYMERIZATION AND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: 3 DIFFERENT LIGHT CHAINS, LC1, LC2 AND LC3, CAN ASSOCIATE WITH MAP1A AND MAP1B PROTEINS.

DOWAIN: Has a highly basic region with many copies of the sequence KKEE and KKEI/V, repeated but not at fixed intervals, which is responsible for the binding of MAP1B to microtubules.

PTM: LC1 is coexpressed with MAP1B. It is a polypeptide generated from MAP1B by proteclytic processing. It is free to associate with both MAP1B and MAP1B. It interacts with the amino-terminal region of MAP1B (By similarity).
                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last amnotation update)
Microtubule-associated protein 1B (MAP 1B) [Contains: MAP1 light chain
                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 157129; -.
GO; GO:0005875; C:microtubule associated complex; TAS.
InterPro; IRR000102; MAPIB neuraxin.
Pfam; PF00414; MAPIB neuraxin; 10.
PROSITE; PS00230; MAPIB NEURAXIN; 6.
Microtubules; Repeat; Phosphorylation.
Microtubules; Repeat; Phosphorylation.
                                        2468 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAP1B 1.
MAP1B 2.
MAP1B 4.
MAP1B 4.
MAP1B 5.
MAP1B 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAP1B 8.
MAP1B 9.
MAP1B 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STABILIZING MICROTUBULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L06237; AAA18904.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew; HGNC:6836; MAP1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1997
                                                                                                                                                                            HUMAN
MAPB HUMAN
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                                                                                                                                                                                                                                                                                                                                       MAP1B.
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MAPB_HU
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                                                                                                                                                                                                                                                              58 LSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLORE----E 112
                                                                                                                                                                                                                                                                                                                               638 VKKETKVKP-----EDKKEEKEKPKKEVAKKEDKTPI----KKEEKPKKEEVKKEVKKEIK 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIRAIN=52000;
MEDLINE=5952904; PubMed=7713415;
Gansheroff L.J., Dollard C., Tan P., Winston F.;
Ansheroff L.J. and C., Tan P., Winston F.;
"The Saccharomyces cerevisiae SPT7 gene encodes a very acidic protein important for transcription in vivo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The bromodomain: a conserved sequence found in human, Drosophila and
                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          yeast proteins.";
Nucleic Acids Res. 20:2603-2603(1992).
-!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR OF TY ELEMENTS AND POSSIBLY
589 790 LYS-RICH (HIGHLY BASIC, CONTAINS MANY KKEE AND KKEI/V REPEATS). 2468 AA; 270618 MW; 540839CBDF09D461 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95076715; PubMed=7985423;
van der Aart Q.J.M., Barthe C., Doignon F., Aigle M., Crouzet M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Andre B., Cziepluch C., Hein C., Jauniaux J.C., Urrestarazu A.,
Vissers S.,
                                                                                                                                                               ; Pred. No. 26;
19; Mismatches 17; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Sequence analysis of a 31 kb DNA fragment from the right arm Saccharomyces cerevisiae chromosome II.";
                                                                                                                                 DB 1; Length 2468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 463-523 FROM N.A.
BEDLINE-92285152; PubMed=1350857;
Haynes S.R., Dollard C., Winston F., Beck S., Trowsdale J.,
Dawid I.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Transcriptional activator SPT7.
9PT7 OR YBR081C OR YBR0739.
                                                                                                                                 Score 92.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: Contains 1 bromodomain.
                                                                                                                                 12.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-835 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics 139:523-536(1995).
                                                                                                                      Query Match
Best Local Similarity 31.08
Marches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     :| : |:|
690 KEEKKEPKKEV 700
                                                                                                                                                                                                                                                                                                                                                                                                   113 HSQKSDSTKDV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Keast 10:959-964(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Steensma H.Y.;
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P35177;
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K---PVFKKIEEKKEEENKPTFD-----VSKKKD------NPQVNHSQLNESH 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wood V., Gwilliam R., Rajandram M.A., Lyne M., Lyne R., Stewart A.,

Brooks K., Brown D., Hayles J., Baker S., Basham D., Bowman S.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

A Holroyd S., Hornsby T., Howarth S., McConnald S., Jagels K.,

James K., Jones L., Jones M., Leather S., McConnald S., McLean J.,

Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

A James K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,

Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

Retton J., Simmonds M., Squares R., Squares S., Stevens K.,

A Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

Berzym K., Langer I., Wadbut R., Pohl T.M.,

Berzym K., Langer I., Wadbutt R., Purnelle B.,

Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 VTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                       Transcription regulation; Nuclear protein; Activator; Bromodomain. DOMAIN 458 528 BROMODOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  37;
                                                                                                                                                                                                                                                                                                                                                                                                           12.1%; Score 90.5; DB 1; Length 1332; 24.5%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                   1332 AA; 152616 MW; 083B63624669244F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 RKEDLQR-EEHSQKSDSTKDVTATVLD-KNNISSKSTTN 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               655 KNEEQDMVEESSKTEDSSKDADAAKKDTEDGLQDKTAEN 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                    26; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Hypothetical protein (6B12.02c in chromosome
SPACGB12.02C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                        PRINTS; PROGSO3; BROMODOMAIN.
SMART; SMO2297; BROMO; 1.
PROSTIE; PSO0633; BROMODOMAIN 1; 1.
PROSITE; PSS0014; BROMODOMAIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                            SGD, SC000285; SPT7.
GG, GG:0000124; C:SAGA complex; II
InterPro; IPR001487; Bromodomain.
Pfam; PF00419; bromodomain, 1.
                                   EMBL; X76294; CAAS3940.1;
EMBL; Z35950; CAA85026.1;
EMBL; M87651; AAA35087.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                 PIR; S41552; S41552.
HSSP; Q92831; 1B91.
                                                                                                                    HSSP; Q92831; 1B91.
TRANSFAC; T04835; -
                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 39; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4896;
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014207;
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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YDT2_SCHPO
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 YVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEH 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :: :: | | | | :: :: | | | 449 FLRVFARSSSHIP--KMIRRKRQMDSKKYFSFDKESDRQVIDQVLSDWYSGKHELVQQSH 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 SSTIVSEEDF-----GKKDAG 53
Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; "The genome sequence of Schizosaccharomyces pombe."; Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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01-NOV-1995 (Rel. 32, Last sequence update)
828-FEB-2003 (Rel. 41, Last annotation update)
Immunoglobulin Al protease precursor (EC 3.4.21.72) (IGAl protease).
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Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 POLY-LEU.
217432 MW; 8AD3BBCE32397C29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 SQKSDS-TKDVTATVLDKN-----NISSKSTTNN 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    507 SYKKPSDSKSVGGNIFSVNSKKHSVNINAKTAANN 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 89; DB 1;
Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1702 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z98531; CAB11064.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T39009; T39009.
OB_SPombe; SPAC6B12.02c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similary,
hes 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      935
1053
1356
1665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haemophilus influenzae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1662
1888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical
TRANSMEM 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995
01-NOV-1995
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IGA2 HAEIN
P45384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GeneDB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGAZ_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
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[2]
SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAPB MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P14873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAPB_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
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                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation he Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1296 INTGSATAITETAEKSDKPQTETAASTEDASQHKANTVADNSVANNSESSEPKSRRRSI 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 INLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHS- 114
                              SUBCELLULAR LOCATION: Secreted.

DOMAIN: THE SIGNAL PEPTIDE GUIDES THE PRECURSOR TO THE PERIPLASMIC SPACE, AND THE CARBOXY-TERMINAL HELPER DOMAIN ASSOCIATES WITH THE OUTER MEMBRANE TO FORM A PORE FOR EXCRETION OF THE PROTEASE DOMAIN. THE HELPER DOMAIN IS THEN RELEASED BY AUTOPROTEOLYSIS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X 8 AA TANDEM REPEATS OF A-K-V-E-K-E-E-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                InterPro; IPR005415; Autotransport.
InterPro; IPR005546; Autotransporter.
InterPro; IPR000510; IgA_S6.
InterPro; IPR0004999; Perfactin.
Pfam; PP03797; Autotransporter; 1.
Pfam; PF03295; IGA1; 1.
Pfam; PR03212; Perractin; 1.
Pfam; PR00921; IGASERPTASE.
TIGRFAMS; TIGR01414; autotrans_barl; 1.
Hydrolase; Serine protease; Iransmembrane; Zymogen; Repeat; Signal.
CATALYTIC ACTIVITY: Cleavage of immunoglobulin A molecules at certain Pro-|-Xaa bonds in the hinge region. No small molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Chen Z., Wen Y.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.7%; Score 87.5; DB 1; Length 1702; 27.2%; Pred. No. 42; ive 14; Mismatches 50; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                         IMMUNOGLOBULIN AL PROTEASE.
HELPER PEPTIDE (POTENTIAL).
PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1702 AA; 186539 MW; 860F70D2667807A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1282;
                                                                                                        SIMILARITY).
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 -- QKSDSTKDVTATVLDKNNISSKSTTNNPNK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA gyrase subunit A (EC 5.99.1.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              893 AA
                                                                                                                                                                                                                    or send an email to license@igb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                             EMBL; M87489; AAA24966.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                            1702
288
1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1116
                                                                                                                                                                                                                                                           A41859; A41859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                        MEROPS; S06.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GYRA OR SE0005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GYRA STAEP
P54112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT SITE
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
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d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112
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                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS RESPONSIBLE FOR DNA BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HYDROLYSIS. THE ENZYME FORMS AN A282 TETRAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 TFIKPVFKKIEEKKEEEN------KPTFDVSKKKDNPQVNHSQLNESHRKEDLQREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     802 QEVSTVAKVNEEDDNEENADEAQQSTTTETADVEEVVD----DQTPGNAIHTEGDAEMES
                                                                                                                                                                     Antimicrob. Agents Chemother. 35:2151-2154(1991).

-!- FUNCTION: DNA GYRASE NEGATIVELY SUPERCOLLIS. CLOSED CIRCULAR DOUBLE. STRANDED DNA. IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES THE INTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED DNA RINGS, INCLUDING CATERANDES AND KNOTTED RINGS.
-!- CATALYTIC ATP-dependent breakage, passage and rejoining of double-stranded DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 TVTIQNGKEMS-STIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGY-VINLSKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                    Sreedharan S., Peterson L.R., Fisher L.M.; Ciprofloxacin resistance in coagulase-positive and -negative staphylococci: role of mutations at serine 84 in the DNA gyrase A protein of Staphylococcus aureus and Staphylococcus epidermidis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 123 DNA CLEAVAGE (BY SIMILARITY).
84 84 S->F: RESISTANT TO CIPROFLOXACIN.
893 AA, 100113 MW; 2A6A7CD345A526CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
Microtubule-associated protein 1B (MAP 1B) (MAPI.2) (MAPI(X))
MAPIB OR MTAPIB OR MTAP5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00434; TOP4c; 1.
TIGRFAMS; TIGR01063; gyrA; 1.
Topoisomerase; Isomerase; DNA-binding; Antibiotic resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.6%; Score 87; DB 1; Length 893; 25.3%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65; Indels
OF SER-84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 25.3%; Pred. No. -...
Matches 38; Conservative 27; Mismatches
AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 -HSQKSDSTKDVTATVLDKNNISSKSTTNN 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VESPENDDRIDIRODFMDRVNEDIESASDN 887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP, P09097; 1AB4.
InterPro; IPR02205; DNA topoisolV.
PFdm; PF01989; DNA gyraseA C; 6.
ProDom; PD000742; DNA_topolsolV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE016744; AAO03602.1; -. EMBL; S72603; AAB20672.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A49832; A49832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
ACT SITE 123
MUTAGEN 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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Created)

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01-OCT-1993
01-OCT-1993
15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                        activity
                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the burpopan Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     989
                                                                                                                                                                                                                            SUBGINIT: 3 DIFFRENT LIGHT CHAINS, LCI, LC2 AND LC3, CAN ASSOCIATE WITH MAPLA AND MAPLE PROTEINS.

MOMAIN: Has a highly basic region with many copies of the sequence KKEE and KKEI/V, repeated but not at fixed intervals, which is responsible for the binding of MAPLE to microtubules.

PRIM: LCI SCORENERSEED WITH MAPLE. IT IS APLYPEPTIDE GENERATED PROM MAPLE BY PROTEGULYIC PROCESSING. IT IS FREE TO ASSOCIATE WITH BOTH MAPLE AND MAPLE. IT INTERACTS WITH THE AMINO-TERMINAL REGION
                                                                                                            J. Cell Biol. 109;3367-3376(1989).

-!- FUNCTION: THE FUNCTION OF BRAIN MAPS IS ESSENTIALLY UNKNOWN.

-PHOSPHORYLATED MAPLE MAY PLAY A ROLE IN THE CYTOSKELETAL CHANGES

THAT ACCOMPANY NEURITE EXTENSION. POSSIBLY MAPIB BINDS TO AT LEAST

TWO TUBLILIS SUBUNITS IN THE POLYMER, AND THIS BRIDGING OF SUBUNITS

MIGHT BELINVOLVED IN NUCLEATING MICROTUBULE POLYMERIZATION AND IN

STABILIZING MICROTUBULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20; Gaps
                                           Noble M., Lewis S.A., Cowan N.J.; "The microtubule-associated protein "The microtubule binding domain of microtubule-associated protein MAP1B contains a repeated sequence motif unrelated to that of MAP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYS-RICH (HIGHLY BASIC, CONTAINS MANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 2464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKEE AND KKEI/V REPEATS).
2464 AA; 270408 MW; FBD3DD99CFDBDA87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----EHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     687 KKEERKELKKEVKKETPLKDAKKEVKKEEKKEVKKEEKEPKK 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Microtubules, Repeat, Phosphorylation.
CHAIN? 2464 MAP1 LIGHT CHAIN LCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; S07549; QRMSP1.
MGD; MGI:1306778; Mtaplb.
GO; GO:0016358; P:dendrite morphogenesis; IMP.
GO; GO:0001578; P:microtubule bundling; IMP.
IMCePro; IPR00102; MAPIB neuraxin.
Pfam; PF00414; MAPIB_neuraxin; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.6%; Score 87;
28.4%; Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAPIB 2.
MAPIB 3.
MAPIB 3.
MAPIB 4.
MAPIB 6.
MAPIB 6.
MAPIB 6.
MAPIB 9.
MAPIB 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00230; MAPIB_NEURAXIN; 7
            STRAIN-Swiss Webster; TISSUE-Brain;
MEDLINE-90094539; PubMed-2480963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X51396; CAA35761.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: TO MAPIA.
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1907
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2060
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Matches 29; Conserv
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PRT; 1006 AA.

STANDARD;

RESULT 10 RATI_YEAST ID _RATI_YEAST

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                                                                                                                                                                                                                                          MEDLINE=92331925; PubMed=1628825; Ambbry D.C., Goldstein A.L., Cole C.N.; Amberg D.C., doldstein A.L., Cole C.N.; Isolation and characterization of RATI: an essential gene of Saccharomyces cerevisiae required for the efficient nucleocytoplasmic trafficking of mRNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [5]
SEQUENCE FROM N.A.
BODOTIN-Fukuhara M., Daignan-Fornier B., Dang D.V.,
Valens M.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May function in the processing and/or trafficking of
-nuclear mRNA. May be involved in general transcription as well.
Possesses 5'->3' exoribonuclease activity degrading poly(A) to
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93109318; PubMed=8417335; Sefana M., Stevens A., Stevens A., McCammon M., Douglas M.G.; McCammon M., Ban essential yeast gene with homology to the exonuclease-encoding XRN1/KEM1 gene also encodes a protein with exoribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Structure of the yeast TAP1 protein: dependence of transcription activation on the DNA context of the target gene."; Mol. Cell. Biol. 13:3434-3444(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93268292; PubMed=8497260;
Aldrich T.L., di Segni G., McConaughy B.L., Keen N.J., Whelen S.,
                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                      exoribonuclease)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0005634; C:nucleus; IDA.
GO; GO:0004534; F:5'-3' exoribonuclease activity; IDA.
GO; GO:0006355; P:35S primary transcript processing; IMP.
GO; GO:0006396; P:RNA processing; IMP.
InterPro; IPRO46359; Put_53exo.
Pfam; PF03159; XRN_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unseld M.; to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                              [2] SEQUENCE FROM N.A., AND EXORIBONUCLEASE ACTIVITY
                                 01-OCT-1993 (Rel. 27, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ribonucleic acid trafficking protein 1 (5'-3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M95626; AAA34960.1; -.
EMBL; L066011; AAAA6950.1; -.
EMBL; 211746; -; NOT ANNOTATED CDS.
EMBL; Z74956; CAA99240.1; -.
PIR; S20126; S20126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . Cell. Biol. 13:341-350(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mainly 5'-AMP.
COFACTOR: Requires magnesium.
                                                                                            (EC 3.1.11.-) (P116).
RAT1 OR HKE1 OR TAP1 OR YOR048C
                                                                                                                                                                                                                                                                                                                                         Genes Dev. 6:1173-1189(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; S61567; AAB26818.1; -.
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SEQUENCE FROM N.A.
Landt O., Hiesel R., Ur
Submitted (JUL-1996) t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                         NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                       œ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415 MSKGQDRHPTVATEQ---LQMYDTQGNLAKG----SWNLTTSD------MVRLKKELML 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 ----KPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQ------LNESHRK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 IQNGKEMSSTIVSEEDFILPVY--KGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFI 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae; Thermococcus.
                                                         POLY-ASN.

CONTAINS 2 X SRYD, 2 X NNNY, AND 2 X YSGN REPEATS.
Y->H: IN ALLELE TAP1-1; ACTIVATES TRANSCRIPTION OF THE PROMOTER-DEFECTIVE YEAST SUP4 TRNA(TYR) ALLELE SUP4A53T61.
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97316461; PubMed=9172372;
Adul Rahman R.N.Z., Jongsareejit B., Fujiwara S., Imanaka T.;
Adul Rahman R.N.Z., Jongsareejit B., Fujiwara S., Imanaka T.;
"Characterization of recombinant glutamine synthetase from the
hyperthermophilic archaeon Pyrococcus sp. strain KOD1.";
Appl. Environ. Microbiol. 63:2472-2476 (1997).
-1- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase) (GS)
                                                                                                                                                                                                                                                                                                                                                                                       47; Indels 49;
                                                                                                                                                                                                                                                                                                                    11.6%; Score 86.5; DB 1; Length 1006; 19.0%; Pred. No. 29; tive 40; Mismatches 47; Indels 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 EDLQREEH-----SQKSDSTKDVTATVLDK-----NNISSKSTT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- SUBCELLUTAR LOCATION: Cytoplasmic (Potential).
   Nuclease; Exonuclease; Repeat
                                                                                                                                                                                                                                                     1006 AA; 115933 MW; 5DDD5B0245F3E12A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                443 AA
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InterPro; 1PR001691; GLN synth.
InterPro; 1PR001691; GLNA.
InterPro; 1PR001637; GLNA adenyltn.
Pfan, PP00150; gln-synt, 1.
ProDom, PD001057; Gln-synt, N; 1.
ProDom, PD001057; Gln-synt, C; 1.
TIGRRAMS; TIGRR0653; GLNA, 1.
PROSITE; PS00180; GLNA, 1; 1.
PROSITE; PS00181; GLNA, ATP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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   Hydrolase;
                                                                                                                                                                                                                                                                                                                                                  Local Similarity 19.0
les 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pyrococcus kodakaraensis.
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                                                               797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=69014;
Nuclear protein;
                                                               793
955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L-glutamine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=KOD1;
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                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                          MUTAGEN
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                                    DOMAIN
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                                                                                          DOMAIN
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                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=M150, ATCC 700699, and N315;
MEDLINE=21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Kuroda M., Ohta T., Aoki K.-I., Nagai Y., Lian J.-O., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lancet 359:1819-1827(2002).
-!- FUNCTION: Involved in protein export. Acts as a chaperone by maintaining the newly synthesized protein in an open conformation (By similarity).
-!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. TIG SUBFAMILY.
                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                              -----NPQVNHSQLNESHRKEDLQREEHSQKSD---STKDVTATVLD 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=MW2;
MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
Yamamoto K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-
                                                                                                              72;
AMP (UNDER CONDITIONS OF ABUNDANT
                                                                         DB 1; Length 443;
                   GLUTAMINE) (BY SIMILARITY).
443 AA; 50259 MW; 9426DCCFEEF18168 CRC64;
                                                                                                                46; Indels
                                                                                                                                                    28 YKGELEKGYOFDGWEISGFEGKKDAGYVINLSKDTFI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2005 ......
Trigger factor (TF).
Trigger factor (TF).
TIG OR SAV1675 OR SA1499 OR MW1619.
Staphylococcus aureus (strain N315), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus (strain MW2),
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=158878, 158879, 196620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                         Query Match 11.5%; Score 86; DB 1
Best Local Similarity 17.8%; Pred. No. 13;
Matches 31; Conservative 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             433 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
   362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acquired MRSA.";
   362
                                                                                                                                                                                                                                                                                                                                                                                                                                         TIG STAAM
Q99TI6;
                                                                                                                                                                                                                                                                                                          16
                                       SEQUENCE
   BINDING
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Complete proteome
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  EMBL; X15982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  5-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Translation
                                                                                                                                                                                                                                                                                                                                                                                                                                      15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                              IF2 STAEP
Q8CST4;
                                                                                                                                               Query Match
                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
IF2_STAEP
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                                                                                                                                                                                                                           13;
                                                                                                                                                                                                                                                                                                                      EKKE------BE---NKPTFDVS----KKKDNPQVNHSQLNE-----SHRKE 106
                                                                                                                                                                                                                                                                                                                                                                                 211 EEKDVVVTFPEEYHAEBLAGKEATFKTKVNEIKFKEVPELTDEIANELDAEANTVDEYKE 270
                                                                                                                                                                                                                                                                                                      35 -----KBYQFDGWEISG--FEGKKDAGYVINLSKDTFIKPVFK-----KIE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        extrachromosomal DNA of the ascomycete Ascobolus immersus.";
Mol. Gen. Genet. 218:523-530(1989).
-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- MIŚCELLANEOUS: THIS DNA POLYMERASE REQUIRES A PROTEIN AS A PRIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY. STRONG, TO
DNA POLYMERASE OF OTHER FUNGAL AND PLANTS MITOCHONDRIAL PLASMIDS.
                                                                                                                                                                                                                             Gaps
          PIR; A89951; A89951.
HAMAP, MP 00303; -; 1.
HAMAP, MP 00303; -; 1.
HAMAP, MP 00303; -; 1.
HAMAP, PREGORDITO; FERP PPIABE.
INTERPO; IPR00115; Trig_fac.
PERM: TIGROVIIS; TKBP; 1.
TIGREAMS; TIGROVIIS; Itig; 1.
PROSITE; PS00451; FKBP PPIASE 1; FALSE NEG.
PROSITE; PS0059; FKBP PPIASE 2; FALSE NEG.
PROSITE; PS0059; FKBP PPIASE 2; CALSE NEG.
PROSITE; PS0059; FKBP PPIASE 2; PALSE NEG.
PROSITE; PS0059; FKBP PPIASE 3; PPIASE.
PROSITE; PS0059; FKBP PPIASE 3; PRAD-TVPP
DOMAIN 163 248 PPIASE.
                                                                                                                                                                                                                           83;
                                                                                                                                                                                                11.4%; Score 85.5; DB 1; Length 433; 22.9%; Pred. No. 14; Live 30; Mismatches 52; Indels 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Pezizomycotina; Pezizomycetes;
Pezizales; Ascobolaceae; Ascobolus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kempken F., Meinhardt F., Esser K.;
"In organello replication and viral affinity of linear,
                                                                                                                                                                      433 AA; 48609 MW; 8865D9AF6A1BC1E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             DLQREEHSQKSDSTKDVTATVLDKNNISSKSTTN 140
                                                                                                                                                                                                                                                                                                                                                                                                                            3 VTVT-IQNGKE--MSSTIVSEEDFILPVYKG-ELEK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
10-EG-1998 (Rel. 37, Last annotation update)
Probable DNA polymerase (EC 2.7.7.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90066356; PubMed=2573821;
EMBL; AP003134; BAB42766.1; -. EMBL; AP004827; BAB95484.1; -.
                                                                                                                                                                                                           Best Local Similarity 22.9%
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ascobolus immersus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=5191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA (N)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DPOM ASCIM
P22374;
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                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 LSKDTFIKPVFKKIE-----EKKEEENK-PTFDVSKKKDNPQVNHSQLNESHRKEDLQR 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                397 IKKDIVVKDINKKINFNGLDLPKTMDLSKWPNLKLNKDKTSGEIRMTIKNKNNQSYDI-- 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRUMMATCC 12228;
Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
Chen Z., Wen Y.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: One of the essential components for the initiation of
protein synthesis. Protects formylmethionyl-tRNA from spontaneous
hydrolysis and promotes its binding to the 30s ribosomal subunits.
Also involved in the hydrolysis of GTP during the formation of the
70s ribosomal complex (By similarity).
-:- SUBCELLULAR LOCATION: Cytoplasmic.
-:- SIMILARITY: BELONGS TO THE IF-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 TVTIQNGKEMSSTIVSEEDFILPVYKGELEK-----GYQFDGWEISGFEGKKDAGYVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29;
                                                                                                                                                                                                                                                                                                                                                                                       11.4%; Score 85.5; DB 1; Length 1202; 22.5%; Pred. No. 41;
                                                           Interpro; IPR006172; DNA_pol_B.
InterPro; IPR004868; DNA_pol_B_2.
InterPro; IPR004868; DNA_pol_B_2.
SWART; SW00486; PollBc; I.
PROSITE; PS00116; DNA_POLYMERASE B; 1.
PROSITE; PS00116; DNA_POLYMERASE B; 1.
DNA_binding; Plasmid; Mitochondrion.
SEQUENCE 1202 AA; 138279 MW; 51D41FCEBDBF2CDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 BEHSOKSDSTKDVTATVLDKNNI-----SSKSTTNNPN 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              455 IGHMIINDGENVITFNRAVDNSIIKIFTVTDSMGNTNDPN 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            initiation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus epidermidis.
Bacteria, Firmicutes; Bacillales; Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                720 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  initiation factor IF-2.
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TIGRFAMS; TIGR00231; small_GTP; 1.
PROSITE; PS01176; IF2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAMAP; MF_00100; -; 1.
Pfam; PF050009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF04760; IF2_N; 2.
ProDom; PD186100; IF2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE016747; AA004542.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-SEP-2003 (Rel. 42, Created)
CAA34106.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                        S05362; S05362.
                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                      71 IEEKKEEENKPTFDVSKKKD----NPQVNHSQLNESHRKEDLQREEHSQKSDSTK----D 122
                                                                                                                                                                                                                                           38 LEEEQIKALDKKFKASQAKDTNKQNTQNNHQKSNNKQNSNDKEKQQSKNNSKPTKKKEQN 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Secreted.

DOMAIN: THE SIGNAL PEPTIDE GUIDES THE PRECURSOR TO THE PERIPLASMIC
SPACE, AND THE CARBOXY-TERMINAL HELPER DOMAIN ASSOCIATES WITH THE
OUTER MEMBRANE TO FORM A PORE FOR EXCRETION OF THE PROTEASE
DOMAIN: THE HELPER DOMAIN IS THEN RELEASED BY AUTOPROTEOLYSIS (BY
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter J.C.;
"Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=Rd / KW20 / ATCC 51907;
STRAIN=Rd / KW20 / ATCC 51907;
STRAIN=Rd / KW20 / ATCC 51907;
Fleischmann R.D., Adama M.D., White O., Clayton R.A., Kirkness E.F., Fleischmann R.D., Adama M.D., White O., Clayton R.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-1., Glodek A., Kalley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Spriggs T., Gaudek D.M., Brandon R.C., Ghine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Immunoglobulin Al protease precursor (EC 3.4.21.72) (IGA1 protease).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- FUNCTION: VIRULENCE FACTOR; CLEAVES HOST IMMUNOGLOBULIN A PRODUCTION INTACT FC AND PAB FRACHENTE.
-1- CATALYTIC ACTIVITY: Cleavage of immunoglobulin A molecules at certain Pro-|-Xaa bonds in the hinge region. No small molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                        DB 1; Length 720;
                                                                                                                     ch 11.4%; Score 85; DB 1; Length 720
1 Similarity 28.0%; Pred. No. 26;
23; Conservative 15; Mismatches 36; Indels
G-DOMAIN.
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Serotype D;
Wright A., Fishman Y., Tai F., Plaut A.G.;
Submitted (MAY-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S6.
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1694 AA
                                                                                                                                                                                                                                                                                      123 VTATVLDKNNISSKSTTNNPNK 144
                                                                                                                                                                                                                                                                                                             98 NKGKQQNKNNKTNKNQKNNKNK 119
                                                                                  79343 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           substrates are known.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 269:496-512(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haemophilus influenzae
  225
231
277
277
331
720 AA;
                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEOUENCE FROM N.A.
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  DOMAIN
NP BIND
NP BIND
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SEQUENCE
                                                                                                                                                                  Matches
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1288 INTGSATAITETAEKSDKPQTETAASTEDASQHKANTVADNSVANNSESSDPKSRRRRSI 1347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sasanuma S.-I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical 88.7 kDa helicase in CDC26-SAP155 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-5286. / AB972;
MEDLINE-55400292; PubMed=7670463;
MUTAKANI Y.; Naitou M., Hagiwara H., Shibata T., Ozawa M.,
Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K.,
Yamazaki M., Tashiro H., Eki T.;
Analyasis of the nucleotide sequence of chromosome VI from
Saccharomyces cerevisiae. ",
Nat. Genet. 10:261-268(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 1694;
                                                                                                                                                                                                                         Hydrolase; Serine protease; Transmembrane; Zymogen; Signal;
                                                                                                                                                                                                                                                                IMMUNOGLOBULIN A1 PROTEASE.
HELPER PEFTIDE (POTENTIAL).
EN -> GV (IN REF. 1).
G -> A (IN REF. 1).
G -> E (IN REF. 1).
S -> T (IN REF. 1).
A -> D (IN REF. 1).
A -> G (IN REF. 1).
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MEDLINE=96287654; PubMed=8686381;
Eki T., Naitou M., Hagiwara H., Abe M., Ozawa M., Sasanum
Sasaanuma M., Teuchiya Y., Shibata T., Wtanabe K., Ono A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.3%; Score 84.5; DB 1; Length 1 26.1%; Pred. No. 70; Ative 15; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      1694 AA; 185539 MW; C52427013F93178C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : | : | | : | | : | | : | 1348 SQPQETSAEETTAASTDETTIADNSKRSKPNR 1379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 -- QKSDSTKDVTATVLDKNNISSKSTTNNPNK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                778 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                           Pfam: PF03197; Autoriansporter; 1.
Pfam: PF02195; IGA1; 1.
Pfam: PF03121; Pertactin; 1.
PRINTS; PR00921; IGASERPYASE.
TIGREPAMS; TIGR01414; autotrans_barl; 1.
                                                                                 Incerpro; IPR006315; Autotransport.
InterPro; IPR00546; Autotransporter.
InterPro; IPR000710; IgA S6.
InterPro; IPR004899; Perfactin.
          EMBL; X59800; -; NOT ANNOTATED_CDS.
EMBL; U32779; AAC22651.1; -.
PIR; H64106; H64106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                          1036
1074
1421
1545
                                                        MEROPS; S06.001; -.
TIGR; HI0990; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                       Complete proteome.
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Local S. 24;
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                                                                                                                                                                                                                                                                   CHAIN
PROPEP
ACT SITE
CONFLICT
CONFLICT
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YFK8_YEAST
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Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----EEHS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 DELSEMDTKTVSLKLKKLNEFVRQSQVYSSIIADTLLHRSNEVANANTKDNSNSDDEEHS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 MSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIE 72
                              ŏ
Yamazaki M.-A., Tashiro H., Hanaoka F., Murakami Y.;
"Fifteen open reading frames in a 30.8 kb region of the right arm
chromosome VI from Saccharomyces cerevisiae.";
Yeast 12:177-190(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Garbarino J.E., Gibbons I.R.; "Expression and genomic analysis of midasin, a novel and highly
                                                                                                                                                                                                                                                                                                                                                                                     SGD; S0001934; YFR038W.
InterPro; IPR001410; DEAD.
InterPro; IPR001650; Helicase_C.
InterPro; IPR001310; SNF2_N.
Pfam; PF00271; helicase_C; 1.
Pfam; PF00176; SNF2_N; 1.
SMART; SM00487; DEXDC; 1.
Hypothetical protein; Nuclear protein; DNA-binding; Helicase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 EKKEEENKPTFDVSKKKDNPQVNHSQLNES-----HRKEDLQR----
                                                                                             -!- SUBCELLULAR LOCATION: Nuclear (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match 11.2%; Score 84; DB 1; Length 778; Local Similarity 25.5%; Pred. No. 33; hes 37; Conservative 18; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             352 355 DEGH BOX.
778 AA; 88730 MW; 3E6C0857B5EABD84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conserved AAA protein distantly related to dynein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MDN1_HUMAN STANDARD; PRT; 5596 AA. Q9NUZ2. 015019; Created)
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Midasin (MIDAS-containing protein).
HOMO Sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1255-2356 AND 3550-5596 FROM N.A.
TISSUE-Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 QKSDSTKDVTATVLDKNNISSKSTT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 SKKRKTKKKSITDFFKKQKKNEDTT 200
                                                                                                                                                                                                                                                                                                                                           EMBL; D50617; BAA09277.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3MC Genomics 3:18-18(2002).
                                                                                                                                                                                                                                                                                                                                                                PIR; S56293; S56293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Testis;
PubMed=12102729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
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         SO THE REAL PROPERTY OF THE PR
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 VINLSKOTFIKPVFKKIEEKKEEENKPTFDVSKKKONPQVNHSQLNESHRKEDLQREEHS 114
                                                              Nagase T., Ishikawa K.I., Nakajima D., Ohira M., Seki N., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; Tranaka A., Kotani H., Nomura N., Ohara O.; The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro."; DNA Res 4.141-150(1997).

-I. FUNCTION: May function as a nuclear chaperone and be involved in the assembly/disassembly of macromolecular complexes in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 HRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKG-----YQFDGWEISGFEGKKDAGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.2%; Score 84; DB 1; Length 5596
23.2%; Pred. No. 2.7e+02;
tive 27; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5596 AA; 632802 MW; 586C62616A1F96D4 CRC64;
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EMBL; AL096678; CAB86660.1; -.
EMBL; AL096678; CAB86660.1; -.
EMBL; AB002293; BAA20716.1; -.
Genew; HGNC.18302; MDM.
GO; GO:0005634; C:nucleus; NAS.
GO; GO:0005754; F:chaperone activity; NAS.
GO; GO:0007574; F:chaperone activity; NAS.
GO; GO:000754; F:chaperone activity; NAS.
InterPro; IPR00393; AAA ATPase.
InterPro; IPR003035; VWF_A.
Ffam; PF00004; AAA; 1.
SWART; SM00382; AAA; 7.
SWART; SM00382; AAA; 7.
FROSTIF; PS50234; VWFA; 1.
PROSTIF; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                 (By similarity).
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ATP (POTENTIAL).
POLY-GLU.
                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Nuclear (By 8: SIMILARITY: Contains 1 VWFA domain.
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POLY-GLU.
POLY-GLU.
VWFA.
                                              MEDLINE=97349984; PubMed=9205841;
SEQUENCE OF 3550-5596 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29; Conservative
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1760
2073
3573
4791
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5583
2312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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1753
2066
3566
4784
5008
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5384
2287
                                                                                                                                                                                                                                                                               nucleus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 VN------HSQLNESHRKEDLQREEHSQKSDSTKDVTATVLD--KNNISSKSTTNNP 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 KDAGYVINLSKDTFIKPVFKKIEEKK-------EEENKPTFDVSKKKDNPQ 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-96212931; PubMed-8630064; Pearsall R.S., Shibata H., Brozowska A., Yoshino K., Okuda K., Pearsall R.S., Shibata H., Brozowska A., Yoshino K., Okuda K., Dejong P.J., Plass C., Chapman V.M., Hayashizaki Y., Held W.A.; Absence of imprinting in UZAFBPL, a human homologue of the imprinted mouse gene UZafbp-rs."; Diochem. Biochem. B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Isolation and mapping of human homologues of an imprinted mouse gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50102; RRW 11. PALSE NEG.
PROSITE; PS00030; RRW RNP 1; FALSE NEG.
Nuclear procein; RNA-binding; Ribonucleoprotein; Zinc-finger; Repeat.
DOMAIN 203 309 RNA-BINDING (RRM).
SEQUENCE 479 AA; 57643 MW; 96F326694BD4E7C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 29; Gaps
UZR1_HUMAN STANDARD; PRT; 479 AA.
015659; 013570;
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
related-protein in.
US small nuclear ribonucleoprotein auxiliary factor 35 kDa subunit related-protein 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain;
MEDLINE=96163878; PubMed=8586425;
Kitagawa K., Wang X., Hatada I., Yamaoka T., Nojima H.,
Inazawa J., Abe T., Mitsuya K., Oshimura M., Murata A., Monden M.,
                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 479;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; 601079; -.
GO; GO:0005634; C:nucleus; NAS.
GO; GO:0005723; F:RNA binding activity; NAS.
GLIGEPEO; IPRO00564; RNA rec mot.
InterPro; IPRO00571; Znf_CCCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00076; rrm; 1. – Pfam; PF00076; rrm; 1. – SMART; SM00360; RRM; 1. SMART; SM00356; ZnF_C3H1; 2.
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                                                                                                                                                                                                                                                     Homo sapiens (Human).
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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110 7131 (HOWAN STRUMARD) FRIT, 258 AA.

DT 30-MAY-2000 (Rel. 39) Creeded)

DT 30-MAY-2000 (Rel. 30) Creeded (Rel. 30) Creeded (Rel. 30) (Rel. 30) (Rel. 30) (Rel. 30) (Rel. 31) (Rel. 31)
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NCBI_TaxID=1282;
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Q02510;
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DOMAIN
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         39 WEGEDEDUVKDNWDDDDDEKKEEAEVKPEVKISEK---KKIAEKIKEKERQQKKRQEEI 95
                                                                                   .; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 SKKKDNPQ-----VNHSQLNESHRKEDLQREEHSQKSDSTKDVTATV--LDKNNISSK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: INTERACTS WITH OUTER MEMBRANE RECEPTOR PROTEINS THAT CARRY OUT HIGH-AFFINITY BINDING AND ENERGY DEPENDENT UPTAKE INTO THE PERIPLAAMIC SPACE OF SPECIFIC SUBSTRATES. IT COULD ACT TO TRANSDUCE ENERGY FROM THE CYTOPLASMIC MEMBRANE TO SPECIFIC ENERGY-REQUIRING PROCESSES IN THE OUTER MEMBRANE, RESULTING IN THE RELEASE INTO THE PERIPLASM OF LIGANDS BOUND BY THESE OUTER
                                                                                                                                                                                                                                                                                                                                                                                       12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A functional tonB gene is required for both utilization of heme and virulence expression by Haemophilus influenzae type b."; Infect. Immun. 62:2470-2477(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=RG KWGO N.A.

STRAIN=RG KWGO N.A.

MEDLINE=95350630; PubMed=7542800;

Pleistchmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F.

Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Witcrback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Wenter J.C.,
                                                                                   GO; GO:0005852; C:eukaryotic translation initiation factor 3 . GO; GO:0003743; F:translation initiation factor activity; TAS. GO; GO:0006446; P:regulation of translational initiation; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                           DB 1; Length 258; 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=NTHI TN106;
MEDLINE=94245357; PubWed=8188372;
Jarosik G.P., Sanders J.D., Cope L.D., Muller-Eberhard U.,
                                                                                                                                                                                                                                                                                                                                                                                     51; Indels
                                                                                                                                                                                                                                                                                                   83624235424445AA CRC64;
                                                                                                                                                                                                                                                         E -> G (IN REF. 1).
A -> T (IN REF. 2).
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01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                     30; Conservative 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270 AA
                                                                                                                                                   Initiation factor, Protein biosynthesis.
                                                                                                                                                                                                                                                                                                                                             11.1%; Score 83; 25.4%; Pred. No.
                                                                                                                                                                       POLY-ALA.
POLY-GLY.
POLY-ASP.
                                                                                                                                                                                                                                       POLY-LYS
                                                                                                                                                                                                                                                                                                   29062 MW;
    EMBL; BC002719; AAH02719.1;
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Science 269:496-512(1995)
                      HGNC:3270; EIF3S1.
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Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                        Genew; HGNC:
GK; 075822;
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                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                   SEQUENCE
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    SFTT FFT FFT SQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGREAMS, TIGRO1352; tonB Cterm; 1.

Transport; Protein transport; Inner membrane; Periplasmic;

Transmembrane; Signal-anchor; Repeat; Virulence; Complete proteome.

DOWAIN

1 7 CYTOPLASMIC (POTENTIAL).
REQUIRED FOR HEME UTILIZATION AND VIRULENCE.
                     SUBCELLULAR LOCATION: PERIPLASMIC. ANCHORED TO THE CYTOPLASMIC MEMBRANE VIA ITS N-TERMINAL SIGNAL-LIKE SEQUENCE, SPANS THE PERIPLASM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Lipase precursor (EC 3.1.1.3) (Glycerol ester hydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL-ANCHOR (POTENTIAL).
PERIPLASMIC (POTENTIAL).
4 X 2 AA TANDEM REPEATS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A -> V (IN STRAIN TN106).
E -> K (IN STRAIN TN106).
D -> N (IN STRAIN TN106).
MISSING (IN STRAIN TN106).
G -> E (IN STRAIN TN106).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G -> E (IN STRAIN TN106).

G -> E (IN STRAIN TN106).

E -> D (IN STRAIN TN106).

E -> D (IN STRAIN TN106).

K -> R (IN STRAIN TN106).
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLU/PRO-RICH.
GLU/LYS/PRO-RICH.
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STRAIN=9;
MEDILINE=9171870; PubMed=8436947;
Parrell A.M., Foster T.J., Holland K.T.;
                                                                                                     -!- SIMILARITY: BELONGS TO THE TONB FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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146 E
226 K
29193 MW;
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28-FEB-2003 (Rel. 41, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR01374; TONBPROTEIN.
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InterPro; IPR006260; TonB
Pfam; PF03544; TonB; 1.
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Best Local Similarity 32...
Best Local Similarity
Lac 26; Conservative
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NCBI_TaxID=9606;
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REPEAT
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                                                                                                                                                                                                                                                                        CONVERSION).
-!- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 TIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFE-GKKDAGYVINLSKDTFI
                                                                    STRAIN=ATCC 12228;
Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
Zhang Y., Ren S.,
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
-!-CATALYTIC ACTIVITY: Triacylglycerol + H(2)0 = diacylglycerol + a
fatty acid anion.
-!-SUBCELLULAR LOCATION: Secreted.
-!-MISCELLANEOUS: THE EXPRESSION OF STAPHYLOCOCCUS LIPASE IS
NEGATIVELY REGULATED BY BACTERIOPHAGE LYSOGENIZATION (LIPASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 11.1%; Score 83; DB 1; Length 688;
Best Local Similarity, 24.5%; Pred. No. 35;
Matches 35; Conservative 28; Mismatches 60; Indels 20; Gaps
"Molecular analysis and expression of the lipase of Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIPASE.
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
W -> L (IN REF. 1).
E -> G (IN REF. 1).
6C95DB3A78AF86F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADSV HUMAN STANDARD; PRT; 715 AA. 09Y6Ü3; Q8WU97; 16-OCT-2001 (Rel. 40, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 42, Last annotation update) Adseverin (Scinderin).
                                    Gen. Microbiol. 139:267-277(1993).
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190 SKTTDLL-----RATAQNQSK 205
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648 648 CHZ
96 96 W I
120 120 E -
688 AA; 77343 MW; 6
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O., Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C., Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.; An integrated analysis of the genome of the hyperthermophilic archaeon Pyrococcus abyssi.",
Mol. Microbiol. 47:1495-1512(2003).
-!- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pyrococcus abyssi.
Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
Loort-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase) (GS)
                                                                                                                                                                                                                                                                                   36;
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-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
                                                                                                                                                                                                       ch 11.1%; Score 83; DB 1; Length 715; l Similarity 23.1%; Pred. No. 36; 34; Conservative 30; Mismatches 47; Indels
                             POLYPHOSPHOINOSITIDE BINDING
SIMILARITY).
R -> H (IN REF. 2).
45FBE42CBCBFDDB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 439 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 INLSKDTFIK------PVFKK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (Sons send an email to license@isb-sib.ch).
SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 DNPQV--NHSQLNESHRKEDLQREEHS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      380 SSPOMAAQHNMVDDGSGKVEIWRVENN 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP, P06201; 1LGR.;
InterPro; PR001691; GLN synth.
InterPro; IPR004809; GlnA.
InterPro; IPR001637; GlnA_adenyltn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00120; gln-synt; I.
Pfam; PF03951; gln-synt; I.
Probom; PD01057; gln-synt_C; 1.
TIGRFAMs; TIGR00653; GlnA; I.
PROSITE; PS00180; GLNA_1; 1.
PROSITE; PS00181; GLNA_ATF; 1.
Ligase; Complete proteome.
BINDING 358 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AJ248288; CAB50513.1; -. PIR; C75009; C75009.
                                                                                                                                      80508 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLNA OR PYRAB16090 OR PAB1292.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=GES / Orsay;
PubMed=12622808;
                                                                                                     · 61
715 AA;
                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=29292;
                                       138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLNA PYRAB
Q9UY99;
                                                                                                         CONFLICT
                                                                                                                                         SEQUENCE
                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                     102 VLKRVIEKLAEMGIKAYIGPEPEFYLFKKNGSWELEIPDVGGYFDILTLDKAKDIKREIA 161
                                                                                                                                                                                            99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WormPep; C29A12.3; CE05328.

InterPro; IPR000977; DNA_ligase.
Pfam; PF04668; DNA_ligase_AC; 1.
Pfam; PF04675; DNA_ligase_AC; 1.
Pfam; PF04675; DNA_ligase_AC; 1.
TIGRFAMS; TIGR00574; dnl1; 1.
PROSITE; PS00033; DNA_LIGASE_AC; 1.
PROSITE; PS50160; DNA_LIGASE_AC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 IQNGKEMSSTIVSEEDFILPVYKGE-----LEKGYQFDGWEISGFEGKKDAGYVINL-
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA ligase (BC 6.5.1.1) (Polydeoxyribonucleotide synthase [ATP]).
LIG-1 OR C29A12.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29;
                                                                                                                                      69
                                                                                                                                                                                         -- KP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wilkinson J.;
Submitted (JUV-1996) to the EMBL/GenBank/DDBJ databases.
Submitted (JUV-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN SEALS DURING DNA.
RECOMBINATION AND DNA REPAIR NICKS IN DOUBLE-STRANDED DNA.
-!- CARALYTIC ACTIVITY: ATP + {deoxyribonucleotide} (N) + {deoxyribonucleotide} (M) + {deoxyribonucleotide} (M+M).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 847;
                                                                                 Length 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60; Indels
                                                                                                                                      Indels
GLUTAMINE) (BY SIMILARITY)
62CCFD3970A98AF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      363 363 AMP (BY SIMILARITY).
847 AA; 94501 MW; A32B7D279F91002F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            92 ------POVNHSQLNESHRKEDLQREEHSQKSDS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                             162 EYMPSFGLVPEVLHHEVGKAQHEIDFRYDEALKTADN 198
                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                         32 LEKGYOFDGWEISGFEGKKDAGYVINLSKDTFI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  847 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.0%; Score 82.5; Di
26.3%; Pred. No. 48;
tive 23; Mismatches
                                                                                                  17.8%; Pred. ...
rive 24; Mismatches
                                                                                                                                                                                                                                                                                                 67 VFKKIEEKKEEEN-----KPTFDVSKKKDN--
                                                                              11.0%; Score 82.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
28-FEB-2003 (Rel. 41, Last ann
                         49742 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z73970; CAA98242.1; -. PIR; T19544; T19544.
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                                                                                                                                      28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 40; Conserv
                            439 AA;
                                                                              Query Match
Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=6239;
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                              SEQUENCE
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RESULT 26
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Amanatides P.G., Scherer S.E., Li P.W., Hobkins R.A., Galle R.F.,
Googe R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
R. Googe R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
R. Googe R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
R. Gutcon G.G., Wortnam J.R., Yandell M.D., Zhang Q., Chen L.X.,
R. Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
R. Ballew R.M., Bard M. H.-J., Andrews-Pfannkoch C., Baldwin D.,
R. Beeson K.Y., Bence B.V., Berman B.P., Bhandari D., Bolbakov S.,
R. Burtis R.C., Busam D.A., Bullke C., Davenport L.B., Davies P.,
R. Burtis R.C., Eusam D.A., Bullke C., Davenport L.B., Davies P.,
R. Burtis R.D., Cawley S., Dallke C., Davenport L.B., Davies P.,
R. Burtis R.C., Evangelista C.C., Ferraz C., Ferriera S., Fleischman W.,
R. Ballow R., Googe F., Gorrell J.H., Gu Z., Galbart W.M., Glasser K.,
R. Googer C., Gabriellan A.B., Gary N.S., Galbart W.M., Glasser K.,
R. Googer C., Gabriellan A.B., Gary N.S., Galbart W.M., Glasser K.,
A Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kannison J.A., Kerchum K.A.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., Dri V., Lia Z.,
Liasko P., Lei Y., Levitsky A.A., Li J.J., Li Z., Liang Y., Lin X.,
Rabor D., Lei Y., Levitsky A.A., Li J.J., Wai M.Phy Y., Nesee M.G.,
Rabor D. R., Moyl W., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Rabor D. R., Nixon K., Nusskern D.R., Parly V., Rese M.G.,
Rabor B.C., Siden-Kiamos I., Simpson M., Stupski M.P., Smith T.,
Shue B.C., Solder-Kiamos I., Simpson M., Stupski M.P., Smith T.,
Rabor R., Woseager T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zhon Q.A.,
Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zhon Q.A.,
R. The genome sequence of Drosophila melanogaster.",
----SKDTFIKPVFKKIEEKKEEENKPTFDVSKKK--DNPQVNHSQLNESHRKEDLQR 110
                                                                                                                 727 NVSEGSSKENPVK-----EIKKETPK---SVSPKKFEKKPPVKSSPVKSPVKSPPIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Hēxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                               EEHSQKSDSTKDVTATVLDKNNISSKSTTNNP 142
                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                               943 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arsenite-resistance protein 2 homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVISIONS, AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                               DROME
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ARS2_DROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291 MOSVKEVEKTINSPKEEMSEADPVSTORKPVRPVNSDGENWDDDAENSAPKKELAEDSK 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 IQNGKEMSSTI-----VSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSK
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01-APR-1990 (Rel. 14, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Microtubule-associated protein 1B (MAP 1B) (Neuraxin) (Contains: MAP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                                                                                   "Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the rat microtubule-
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FlyBase; FBgn0033062; CG7843.
Pfam; PF04959; ARS2; 1.
Hypothetical protein; Alternative splicing.
VARSPLIC 47 50 /FTIG=VSP_000327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OCIAFOSE02E8AB0B CRC64;
                                                                                                                                                                                                                                                                                                                                                 Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=2;
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"Isolation and sequencing of the 5' end of t
associated protein (MAPIB)-encoding cDNA.";
Gene 172:307-308(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 2459 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBOId=Q9V9K7-2; Sequence=VSP 000327; SIMILARITY: BELONGS TO THE ARSZ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=09V9K7-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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STRAIN=Sprague-Dawley; TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Sprague-Dawley; TISSUE=Test
MEDLINE=96257242; PubMed=8666295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE003784; AAM68343.1; -.
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Query Match

Best Local Similarity

Local 32; Conservative 2
                                                                                                                                                                                                                                                                                                                          systematic review.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Long;
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                                                                                                                                                                                                                              Lewis S.E.;
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11D MAPB

MAPB

DT 01-50

DT 01-60

DT 02-70

DE MAPI

OC MAPI

OC EUKA

OC MAPI

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MEDLINE-97405699; PubMed-9260743;

MEDLINE-97405699; PubMed-9260743;

MEDLINE-97405699; PubMed-9260743;

MEDLINE-97405699; PubMed-9260743;

MEDLINE-97405699; PubMed-9260743;

MEDLINE-97405699; PubMed-9260743;

In rat CNS and PNS during development.";

J. Neurosci. Res. 49:319-332(1997).

I. FUNCTION: The function of brain MAPS is essentially unknown.
Phosphorylated MAPIB may play a role in the cytoskeletal changes that accompany neurite extension. Possibly MAPIB Binds to at least two tubulin subunits in the polymer, and this bridging of subunits might be involved in nucleating microtubule polymerization and in stabilizing microtubules.

I. SUBUNIT: 3 different light chains, LC1, LC2 and LC3, can associate with MAPIA and MAPIB proteins.

C. I. TISSUB SPECIFICITY: Nervous system (spinal cord, brain stem, cerebellum and cerebrum). Not expressed in liver, spleen, kidney,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -! DEVELOPMENTAL STAGE: In cerebral cortex, spinal cord and sciatic nerve levels are high early in development but decrease during postnatal development and are low in adulte. In dorsal root ganglia levels remain high throughout development.
-! DOMAIN: Has a highly basic region with many copies of the sequence KKEE and KKEI/V, repeated but not at fixed intervals, which is responsible for the binding of MAPIB to microtubules.
-! FM: LCI is coexpressed with MAPIB. It is a polypeptide generated from MAPIB by proteolytic processing. It is a polypeptide generated both MAPIB By similarity).
-! GAMTION: A G-terminal fragment of this protein (residues 1597 to CAMTION: A G-terminal fragment of this protein (residues 1597 to CAMTION: A G-terminal fragment of this protein (residues 1597 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its meeb by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                               TISSUE-Spinal cord;
MEDLINE=90059871; PubMed=2555150;
Rienitz A., Grenningloh G., Hermans-Borgmeyer I., Kirsch J.,
Littauer U.Z., Prior, Gundelfinger E.D., Schmitt B., Betz H.;
"Neuraxin, a novel putative structural protein of the rat central nervous system that is immunologically related to microtubule-
                                                                                                       domains on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2459) was originally described as neuraxin in Ref.3.
                                                                                                                                                                                             SEQUENCE OF 1541-2459 FROM N.A., AND TISSUE SPECIFICITY
                  SEQUENCE OF 96-2459 FROM N.A., DOMAIN, AND INDUCTION. STRAIN-Sprague-Dawley; TISSUE-Brain, and Glial tumor; MEDLINE-92347374; PubMed=1639092;
                                                                               Zauner W., Kratz J., Staunton J., Feick P., Wiche G. "Identification of two distinct microtubule binding recombinant rat MAP 1B.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAPI LIGHT CHAIN LC1.
MAPIB 1.
MAPIB 2.
MAPIB 3.
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InterPro; IPR000102; MAPIB neuraxin.
Pfam; PF00414; MAPIB neuraxin. 10.
PROSITE; PS00230; MAPIB NEURAXIN; 8.
Microtubules; Repeat; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X60370; CAC16162.1; -. X16623; CAA34620.1; ALT_SEQ.
                                                                                                                                                Eur. J. Cell Biol. 57:66-74(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; US2950; AAB17068.1; -.
                                                                                                                                                                                                                                                                                                                                              аввосіатей protein 5.";
ЕМВО J. 8:2879-2888(1989).
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                                                                                                                                                                                                                                                                                                                                   70 -KIEEKKEEENKPIFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVL 128
                                                                                                                                                                                                                                                                                                                                                   10 GKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFK 69
                                                                                                                                                                                                                                                                                               Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.; "The nucleotide sequence of Saccharomyces cerevisiae chromosome XIII.";
                                                                                                         CONTAINS MANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Pungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Hypothetical 32.4 kDa protein in TAF40-ERV25 intergenic region.
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                                                                                                                                                                                                                            DB 1; Length 2459;
                                                                                                                                               127 127 M -> V (IN REF. 1).
140 140 T -> S (IN REF. 1).
2112 212 R -> K (IN REF. 3).
2159 2169 L -> I (IN REF. 3).
2459 AA; 269497 MW; 2E3F6872DEDBBBA2 CRC64;
MAPIB 4.
MAPIB 5.
MAPIB 6.
MAPIB 7.
MAPIB 9.
MAPIB 9.
MAPIB 10.
CLU-RICH HIGHLY BASIC, CC
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M -> V (I)
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(Rel. 34, Last seq
(Rel. 42, Last ann
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SGD; S0004476; YML014W.
               1953
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STRAIN=S288c / AB972;
PubMed=9169872;
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YMB4_YEAST
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InterPro; IPR001601; Methyltransf.

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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                               41 WEISGFEGKKDAGYVINLSKOTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLN 100
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01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase) (GS).
GLNA OR PF0450.
Pyrococcus furiosus.
                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Bukarycta; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
WCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Maia e Silva A., Bossier P., Vilela C., Fernandes L., Soares H.,
Guerreiro P., Rodrígues-Pousada C.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                       01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Hypothetical 47.4 kDa protein in PASI-MSTI intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91 NPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSK 136
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                                              Query Match 11.0%; Score 82; DB 1; Length 279; Best Local Similarity 28.9%; Pred. No. 16; Matches 24; Conservative 14; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.0%; Score 82; DB 1; Length 427; 27.4%; Pred. No. 25; ive 18; Mismatches 43; Indels
            Hypothetical protein.
SEQUENCE 279 AA; 32438 MW; 2F8795BB3C640D3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
SEQUENCE 427 AA; 47416 MW; 44386D250DE5DE4 CRC64;
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                                                                                                                                               101 ESHRKEDLQR-EEHSQKSDSTKD 122
                                                                                                                                                             200 PKERSEYLQRWKEEQQRSKSLDD 222
 InterPro; IPR000051; SAM_bind.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105 RALEELEKEGYKAYIGPEPEFYLFKKNGTWELEIPDVGGYFDILTLDKARDIRREIAEYM 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------ 91
Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN=Vcl / DSM 3638 / ATCC 43587 / JCM 8422;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBJ/GenBank/DDBJ databases.
-! - CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----POVNHSOLNESHRKEDLQREEHSQKSD---STKDVTATVLDKNNI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 PSFGLIPEVLHHEVGKAQHEIDFRYDEALKTADNIVSFKYITKAVAEMHGL 215
                                                                                                                                                                                                                                                                                                                                            Brown J.R., Masuchi Y., Robb F.T., Doolittle W.F.; "Evolutionary relationships of bacterial and archaeal glutamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N (IN REF. 1).
G (IN REF. 1).
S (IN REF. 1).
THE STATE OF THE STATE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42; Indels
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E -> G (IN REF. 1).
A -> S (IN REF. 1).
MPKDTK -> IPPDTE (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY).
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                                                                                                                                                                                                                                                STRAIN-VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
MEDLINE=94365840; PubMed=7916055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.0%; Score 82; DB 3
18.1%; Pred. No. 26;
tive 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 KIEEKKEEEN-----KPTFDVSKKKDN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UNDER
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K -> G (IN
M -> L (IN
A -> S (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L12410; AAA71968.1; -.

18281; AE010168; AAL80574.1; -.

18281; P06201; LLGR.

INTERPO: IPR001681; GIN synth.

INTERPO: IPR001681; GIN adenyltn.

Pfam; P00120; gln-synt, 1.

Pfam; PF03951; gln-synt, 1.

PROSITE; PS00180; GLNA.1; 1.

PROSITE; PS00180; GLNA.1; 1.

PROSITE; PS00180; GLNA.1; 1.

IJGASE; Complete proteome.

BINDING 358 358 AMP (UND)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   I -- I
                                                                                                                                                                                                                                                                                                                                                                                                                                                        synthetase genes.";
J. Mol. Evol. 38:566-576(1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

Query Match

Best Local Similarity

Local 31; Conservative 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               439 AA;
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L-glutamine.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profilt institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 KIEEKKEEEN-----KPTFDVSKKKDN-------
                                                                                        01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Glutamine synthetase I (EC 6.3.1.2) (Glutamate--ammonia ligase) (GSI)
                                                                                                                                                                                                                                                                                                      Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae; Pyrococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tiboni O., Cammarano P., Sanangelantoni A.M.; "Cloning and sequencing of the gene encoding glutamine synthetase I from the archaeum Pyrococcus woesei: anomalous phylogenies inferred from analysis of archaeal and bacterial glutamine synthetase I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Bacteriol. 175:2961-2969(1993).
-!- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----PQVNHSQLNESHRKEDLQREEHSQKSD---STKDVTATVLDKNNI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42; Indels 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              358 358 AMP (UNDER CONDITIONS OF ABUNDANT GLUTAMINE) (BY SIMILARITY).
439 AA; 50066 MW; C503B43B790BD25C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L-glutamine.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 439;
                               439 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 11.0%; Score 82; DB 1
Best Local Similarity 18.1%; Pred. No. 26;
Matches 31; Conservative 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P06201; 1LGR.
InterPro; 1PR001691; GLN synth.
InterPro; 1PR004809; GlnÄ.
InterPro; IPR001637; GlnA_adenyltn.
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=93259940; PubMed=8098326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00120; gln-synt; T. Pfam; PF03951; gln-synt_N; 1. ProDom; PD0010057; Gln synt_C; 1. TIGRPAMS; TIGR00653; GlnA; 1. PROSITE; PS00180; GLNA_1; 1. PROSITE; PS00181; GLNA_ATP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X60161; CAA42730.1; -. PIR; A36911; A36911.
                               STANDARD;
                                                                                                                                                                                                                                                                             Pyrococcus woesei.
                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=2262;
                            GLNA PYRWO P36687;
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BINDING
GLNA PYRWO
                                                                   STATE 
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REC STRAIN-168;

KRAIN-168;

KREAN-168;

RA Borriss R., Boursier I., Brans A., Bardun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., RA Choi S.K., Codani J.J., Fornertoft A., Ehrlich S.D., Emmerson P.T., RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., RA Ghims S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., A., Henaut A., R., Haiden J., Harwood C.R., Henaut A., R., Holbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., RA Guiseppi G., Guy B.J., Haga K., Haiden J., Harwood C.R., Henaut A., R., Hosappel S., Hosono S., Hullo M.F., Itaya M., Jones L., RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., Koetter P., Koningstein G., Lauber J., Lazarevic V., RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., None D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., RA Presecan E., Pujic P., Purnelle B., Ropoport G., Rey M., Reynolds S., Riveger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y., Racconi E., Pujic P., Purnelle B., Rapoport G., Rey M., Tanconi E., Takahashi H., Takemaru K., Tanaka T., Takahashi H., Takemaru K., Aschiuch J., Sekowska A., Seroc S.J., Serroceter R., Yoshikawa H., Tanaka T., Tarakanen F., Vasarotti A., Yanahott R., Wedler E., Wedler
01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Penicillin-binding protein 1A/1B (FBP1) [Includes: Penicillin-insensitive transglycosylase (EC 2.4.2.-) (Peptidoglycan TGase);
Penicillin-sensitive transpeptidase (EC 3.4..-) (DD-transpeptidase)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99389671; PubMed=9721295;
Murray T., Popham D.L., Setlow P.;
"Bacillus subtilis cells lacking penicillin-binding protein 1 require
increased levels of divalent cations for growth.";
J. Bacteriol. 180:4555-4563(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence analysis of the Bacillus subtilis chromosome region between the serA and kdg loci cloned in a yeast artificial chromosome."; Microbiology 142:2005-2016(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sorokin A.V., Azevedo V., Zumstein E., Galleron N., Ehrlich S.D.,
                                                                                                                                                                                                                                                                                                             Popham D.L., Setlow P.; "Cloning, nucleotide sequence, and mutagenesis of the Bacillus subtilis port operon, which codes for penicillin-binding protein (PBP) 1 and a PBP-related factor."; J. Bacteriol. 177:326-335(1995).
                                                                                                                                                               Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus NCBI_TaxID=1423;
                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 499-515
                                                                                                                                                                                                                                                                       STRAIN=168;
MEDLINE=95113769; PubMed=7814321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=168 / Marburg;
MEDLINE=96349105; PubMed=8760912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GROWTH REQUIREMENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=168 / Marbu
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SUBCELLULAR LOCATION.

Ą 914

PBPA_BACSU 1D PBPA_BACSU STANDARD; AC P3793; DT 01-FEB-1995 (Rel. 31, Created)

RESULT 31

STRAIN=168

149 IQNSS------AKEAVISGVQPGSV---YKFEVTAVSD-DGKSTASTSYEVPKAEDDED 797

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1. Bacteriol, 181:3201-3211(1999).

1. FUNCTION: CELL WALL FORMATION. SYNTHESIS OF CROSS-LINKED

PEPTIDOGLYCAN FROM THE LIPID INTERMEDIATES. THE ENZYME HAS A
FENICILLIN-INSENSITIVE TRANSCLYCOSYLASE N-TERMINAL DOMAIN

(FORMATION OF LINEAR GLYCAN STRANDS) AND A PENICILLIN-SENSITIVE
TRANSFEPTIDASE C-TERMINAL DOMAIN (CROSS-LINKING OF THE PEPTIDE
SUBBUNITS) (BY SIMILARITY).

-!- PATHWAY: Peptidoglycan synthesis; final stages.
-!- PATHWAY: PEPTIDAE CELLS.
-!- DEVELOPMENTAL STAGE: EXPRESSION IS CONSTANT DUBLING GROWTH,
DECREASES DURING SPORULATION AND IS INDUCED APPROXIMATELY IS MIN
INTO SPORE GERMINATION.
-!- PTM: THE PRODUCT EXPRESSED FROM THE TRANSLATION OF THE SPECIFIC AMINO
APPEARS AS TWO BANDS ON A GEL (1A AND 18), BUT THE SPECIFIC AMINO
ACID SEQUENCE OF EACH PROTEIN IS UNKNOWN.
-!- MSCELLANBOUG: CELLS ACKING THE PROTEIN REQUIRE INCREASED LEVELS
-!- MSCELLANBOUG: CELLS ACKING THE PROTEIN REQUIRE INCREASED LEVELS
-!- MSCELLANBOUG: CELLS ACKING THE PROTEIN SYNTHESIS: INCREASED LEVELS
-!- PATHY: THE PROTEIN CONTAIN ABNORMAL FTSZ RINGS,
C C CELLS WITHOUT THE PROTEIN CONTAIN ABNORMAL FTSZ RINGS,
-- SIMILARITY: CONLAINS I SECTION; BELONGS TO THE
-- PATHY: PATHY: THE PROTEIN CONTAIN BELONGS TO THE
-- SIMILARITY: COLLAINS I SECTION; BELONGS TO THE
-- PATHY: PATHY: THE PROTEIN NAME SECTION; BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptidoglycan synthesis; Cell wall; Transferase; Glycosyltransferase; Hydrolase; Multifunctional ensyme; Transmembrane; Signal-anchor; Antibiotic resistance; Complete proteome (POMAIN 1 37 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    329 662 TRANSPEPTIDASE.
706 784 FIBRONECTIN TYPE-LIII.
390 390 ACYLATED BY PENICILLIN (BY SIMILARITY)
914 AA; 99562 MW; 6978E33DFE2423E6 CRC64;
                  Pedersen L.B., Angert E.R., Setlow P., "Septal localization of penicillin-binding protein 1 in Bacillus subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.0%; Score 82; DB 1; Length 914; 22.7%; Pred. No. 56; tive 31; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSGLYCOSYLASE FAMILY.
SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE
TRANSPEPTIDASE PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FOIENTIAL).
EXTRACELLULAR (POTENTIAL)
TRANSGLYCOSYLASE.
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PIR; 140529; 140529.
Subtilist; BG10954; ponA.
InterPro; IPR001361; FW_III.
InterPro; IPR001264; Glyco_trans_51.
InterPro; IPR001460; Transpeptdse.
Pfam; PF00912; Transpeptidse.
Pfam; PF00915; Transpeptidses.
Pfam; PF00915; Transpeptidses.
ProDom; PD001895; Glyco_trans_51; 1.
ProDom; PD001895; Glyco_trans_51; 1.
Prodom; PN001895; Glyco_trans_51; 1.
MEDLINE=99255546; PubMed=10322023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U11883; AAA64947.1; -.
EMBL; L47838; AAB38459.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 22.74
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACT SITE
SEQUENCE
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                                 857
                                                                                                                                                                                                                                                                                                                                                                                                                           65 KPVFKKIEEKKEEENK----------PTFDVSKKKDNPQVNHSQLN
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-99120557; PubMed=9923682;
MEDLINE-99120557; PubMed=9923682;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown B.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Tummino P.J., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
Trust T.J.;
                                                                                                                                                                                                                             Translation initiation factor IF-2.

INFB OR JHP0377.

Helicobacter pylori J99 (Campylobacter pylori J99).

Bacteria, Proteobacteria, Epsilonproteobacteria; Campylobacterales;
                                                                              858 NQDQSNDNDNDNDNSNNQDTSDGDSNSGKNDSTG--SDTNKNKTDTSNKTQTNS 907
                                                            ------ESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNN 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS01176; IF2; 1. -
Initiation factor; Protein biosynthesis; GTP-binding;
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
POLY-GLU.
                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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PIR, E71940; E71940.
HAMAP; MF 00100; -; 1.
InterPro; IPR0000795; EF GTPbind.
InterPro; IPR0006178; IF2.
InterPro; IPR006847; IF2.
Pfam; PP00109; GTP EFTU; 1.
Pfam; PP03144; GTP EFTU; 1.
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TIGRFAMs; TIGR00487; IF-2; 1.
TIGRFAMs; TIGR00231; small_GTP; 1.
                                                                                                                                                            STANDARD;
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503
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NP_BIND
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7 IONGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDA--GYVINLSKDTFI

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01-OCT-1993
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SEQUENCE
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                                                                                           60 KDTFIKPVFKKIEEKKEEENKPTFDVSKKKD------NPQ-VNHSQLNES 102
                                                                                                              Conley C.A., Fritz-Six K.L., Almenar-Queralt A., Fowler V.M.; "Leiomodins: larger members of the tropomodulin (Tmod) gene family."; Genomics 73:127-139 (2001).
                                                             32; Gaps
                                                                                                                                                                                                                                                                                             01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Leiomodin I (Leiomodin, muscle form) (64 kDa autoantigen D1) (64 kDa autoantigen D3) (7hyroid-associated ophthalmopathy autoantigen) (Smooth muscle leiomodin) (SM-Lmod).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SUBCELLULAR LOCATION: CYTOSKELETON.
-1- TISSUE SPECIFICITY: SMOOTH MUSCLE (HEART, SKELETAL MUSCLE, COLON AND SMALL INTESTINE), A SUBSET OF STRIATED MUSCLE FIBERS, AND AT LOW LEVEL IN THYROID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISEASE: RECOGNIZED BY PATIENTS WITH AUTOIMMUNE THYROID DISEASE. SIMILARITY: BELONGS TO THE TROPOMODULIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dong Q., Ludgate M., Vassart G.;
Cloning and sequencing of a novel 64-kDa autoantigen recognized by
patients with autoimmune thyroid disease.";
J. Clin. Endocrinol. Metab. 72:1375-1381(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conley C.A., Fowler V.M.; "Localization of the human 64kD autoantigen D1 to myofibrils in
                             DB 1; Length 949;
                                                             20; Indels
105961 MW; FA8969B0C64B3278 CRC64;
                                                                                                                                                         103 HRKEDLOREEHSOKSDSTKDVTATVLDKANISSKSTTNNPN 143
                                                                                                                                                                                      155 --KOKLÓEIOKSREA------LINKLTOSNTNTTNNAN 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conley C.A.; "Leiomodin in smooth muscle."; "Leiomodin and tropomodulin in smooth muscle."; Am. J. Physiol. 280:C1645-C1656 (2001).
                             Query Match 11.0%; Score 82; DB Best Local Similarity 28.7%; Pred. No. 58; Matches 29; Conservative 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                subset of extraocular muscle fibers.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21218919; PubMed=11318603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99451105; PubMed=10520227;
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MEDLINE=91225220; PubMed=2026759;
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                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                             (Human)
949 AA;
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P29536;
 SEQUENCE
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159 KEEEKKGGDRNTGLSRDKDKKREEMKEVAKKEDDEKVKGERRNTDTRKEGEKMKRAGGNT 218
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"Sequence analysis of the CEN12 region of Saccharomyces cerevisiae on a 43.7 kb fragment of chromosome XII including an open reading frame homologous to the human cystic fibrosis transmembrane conductance regulator protein CFTR.";
Yeast 12:693-708(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.
5 X 4 AA APPROXIMATE TANDEM REPEATS.
; D4B42F8E0523DE94 CRC64;
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MEDLINE-39087480; PubMed=1454790;
Ripmaster T.L., Varbhu G.P., Woolford J.L. Jr.;
"A putative ATP-dependent RNA helicase involved in Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 DLOREEHSOK----SDSTKDVTAT----VLDKNNISSKSTTNNPNK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219 DMKKEDEKVKRGTGNTDTKKDDEKVKKNEPLHEKEAKDDSKTKTPEK 265
                                                                                                                                                                                                                                                                                                                                                                                            X APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 KEEENK-----PIFDVSKKKDNPQVNHSQLNESHRKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cerèvisiae ribosome assembly.";
Proc. Natl. Acad. Sci. U.S.A. 89:11131-11135(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.9%; Score 81.5; Dl
22.8%; Pred. No. 37;
ive 21; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
                                                                        GO; GO:0005624; C:membrane fraction; TAS.
GO; GO:0009405; P:pathogenesis; TAS.
InterPro; IPR004934; Tropomodulin.
InterPro; IPR003124; WH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-SEP-2003 (Rel. 42, Last annotation upor Probable ATP-dependent RNA helicase DRS1 DRS1 OR YLL008W OR L1345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=S288c / FY23;
MEDLINE=96405918; PubMed=8810043;
                                                                                                                                                                                                                                      Pfam; PF03250; Tropomodulin; 1. Pfam; PF02205; WH2; 1. SMART; SM00246; WH2; 1.
                                                                                                                                                                                                                                                                                                                       SMART; SMUUZTO; ....., Antigen; Repeat; Cytoskeleton.
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(Rel. 34, Last seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38; Conservative
Genew; HGNC:6647; LMOD1.
MIM; 602715; -.
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STRAIN=S288c / AB972;
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carboxypeptidase precursor (EC 3.4.16.4) (DD-

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D-alanyl-D-alanine
MEDLINE=97313267; PubMed=9169871;
A Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W., Johnston M., Hillier L., Riles L., Dubois E., Duesterhoeft A., Benes V., Brueckner M., Ooffeau A., Hebling U., Heumann K., Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P., Louis E.J., Messenguy F., Mewes H.-w., Miosga T., Moestl D., Ameller-Auer S., Nenrwich U., Obermaier B., Piravandi E., Pohl T.M., Portetle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M., Scharfe M., Schooller P., Schooller P., Schwager C., Schwarz S., Norendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E., Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D., Marture 387:87-90(1997).
                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 VSEGDNLDEDVHEDLDAGFKFDLDADDTTSNFQGWNFLAEGESNKDDAEAFV--KKDVDL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 KPVFKK------PEEKKEEENKPTFDVSKKKDN--------PQVNHSQLNE 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 VSEEDFILPVYKGELEKGYQFD------GWEI--SGFEGKKDAGYVINLSKDTFI 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> MTKKSRLRRL I (IN REF. 1).
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10.9%; Score 81.5; DB 1; Length 752;
Best Local Similarity 21.0%; Pred. No. 50;
Matches 30; Conservative 26; Mismatches 48; Indels 39; Gaps
                                                                                                                                                                                                                                                                     FUNCTION: PROBABLE HELICASE INVOLVED IN RIBOSOME ASSEMBLY. SUBCELLULAR LOCATION: Nuclear. SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KKRKGKNNKKKVSEGDNLDEDVHEDLD -> MT
RRSGRVRITRKRLVRGITSMRMFMRTWT (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L00683; AAA34666.1; -.
EMBL; X91489; CAA62783.1; -.
EMBL; Z73113; CAA97452.1; -.
PIR; S64750; S64750.
HSSP; Q58083; 1HV8.
SGD; S0003931; DRSJ.
InterPro; IPR001410; DBAD.
InterPro; IPR001659; DEAD_box.
InterPro; IPR001659; DEAD_box.
InterPro; IPR001659; Helicase_C.
Pfam; PF00270; DBAD; 1.
SMART; SM00490; DELD; 1.
SMART; SM00490; HELICC; 1.
PROSITE; PS00039; DRAD_ATP_HELICASE; 1.
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ATP (POTENTIAL).
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DACA BACSU
ID DACA BACSU
AC P08750;
DT 01-AUG-1988
DT 28-FEB-2003
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(Rel. 08, Created)
(Rel. 30, Last sequence update)
(Rel. 41, Last annotation update)

01-AUG-1988 01-OCT-1994 28-FEB-2003

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Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

R. Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

R. Azevedo V., Berron M.G., Bessieres P., Bolotin A., Borchert S.,

Roriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

Bornilse S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

R. Bornisor E., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

R. Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

R. Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

R. Fritz C., Fujtta M., Fujte Y., Fabret C., Ferrari E., Foulger D.,

R. Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

R. Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

R. Albert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

R. Kobayashi Y. Y. Koetter P., Koningstein G., Krogh S., Kumano M.,

R. Kohayashi Y., Koetter P., Koningstein G., Medigue C.,

R. Kohayashi Y., Koningstein G., Moestl D., Nakai S., Noback M.,

R. Mediado R.P., Milado R.P., Milano M., Moestl D., Nakai S., Noback M.,

R. Menlado R.P., Milano M., Moestl D., Nakai S., Noback M.,

R. Menlado R.P., Milano M., Moestl D., Nakai S., Noback M.,

R. Reger M., Rivolta C., Rocha E., Rapoport G., Rey M., Reynolds S.,

R. Schiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,

R. Schiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S.,

R. Schiguchi J., Sambubtt R., Wadder H., Wannier F., Vassmotti A.,

R. Alakuchi M., Tamakoshi A., Tanamato K., Yasumoto K., Yatu K.,

R. Winters P., Wipat A., Yamamoto H., Yannier F., Vassmotti A.,

R. Winters P., Wipat A., Yamamoto G. the Gram-positive bacterium Bacillus

R. Wibrii R. Wibri R. Wedler E., Woeller E., Woeller E., Weller H., Waller H., Waller H.,

R. Wibrit R., Weller E., Weller E., Weller H., Waller H., Waller H.,

R. Wibrit R., Wipat R., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,

R. Wibrit R. Weller E., Weller E., Weller H., Waller H., Waller H.,

R. Wibrit R. Wibrit R., Yoshikawa H.F., Zumstein E., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Reduced heat resistance of mutant spores after cloning and mutagenesis of the Bacillus subtilis gene encoding penicillin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIINE-80182289; PubMed=6768745; Waxman D.J.; Strominger J.L.; Sequence of active site peptides from the penicillin-sensitive Dalamine carboxypeptidase of Bacillus subtilis. Mechanism of penicillin action and sequence homology to beta-lactamases."; J. Biol. Chem. 255:3964-3976 (1980).
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MEDLINE=56051385; PubMed=7584024;
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Syasawara N., Nakai S., Yoshikawa H.;
"Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chromosome containing the replication origin.";
DNA Res. 1:1-14(1994).
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MEDLINE=81117303; PubMed=6780559;
Waxman D.J., Strominger J.L.;
"Primary structure of the COOH-terminal membranous segment of penicillin-sensitive enzyme purified from two Bacilli.";
J. Biol. Chem. 256:2067-2077(1981).
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Todd J.A., Roberts A.N., Johnstone K., Piggot P.J., Winter G.,
                                                                                             Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                    peptidase) (DD-carboxypeptidase) (CPase) (PBP5)
                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=168;
MEDLINE=98044033; PubMed=9384377;
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SEQUENCE FROM N.A.
                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                    Bacillus subtilis.
                                                                                                            NCBI_TaxiD=1423;
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MEDLINE=97128274; PubMed=8972867;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Rodriguz-Cousino N., Lill R., Neupert W., Court D.A.;
"Identification and initial characterization of the cytosolic protein
FUNCTION: REMOVES C-TERMINAL D-ALANYL RESIDUES FROM SUGAR-PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  370 TAPVKKGTKVGK------LTAEYTGDEKDYGFLNSDLAGVDLVTKENVEKAN 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 IKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSD 118
                                                                     -i- PATHWAY: Peptidoglycan synthesis; final stages.
-i- SUBCELULAR LOCATION: Membrane associated.
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY 311; ALSO KNOWN AS THE
D-ALANYL-D-ALANINE CARBOXYPEPTIDASE 1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D-ALANYL-D-ALANINE CARBOXYPEPTIDASE.
ACYLATED BY PENICILLIN.
E -> Q (IN REF. 3).
E -> Q (IN REF. 4).
DAGCSB0307D7C117 CRC64;
                       CELL WALL PRECURSORS.
CATALYTIC ACTIVITY: D-alanyl-D-alanine + H(2)O = 2 D-alanine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carboxypeptidase; Peptidoglycan synthesis; Cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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Ballesta J.P.G., Franco L., Hoenicka J., Jimenez A., Remacha
Sanz E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.8%; Score 81; DB 1; Length 443; 24.3%; Pred. No. 31; tive 20; Mismatches 41; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomycetales, Saccharomycetaceae, Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    327 TISVDKGKEKEVGIVTNKAFSLPVKNGE-EKNYKAK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Topoisomerase II-associated protein PAT1.
PAT1 OR YCRO77C OR YCR77C.
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01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
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Pfam; PF00768; Peptidase S11; 1.
PRINTS; PR00725; DADACBPTASE1.
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Membrane; Signal; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D26185; BAA05246.1; -.
EMBL; Z99104; CAB11786.1; -.
EMBL; M13766; AAA22375.1; -.
PIR; S66040; S66040.
MEROPS; S11.001; -.
SubtiList; BG10074; dacA.
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67
100
227
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[3]
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227
443 AA;
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Best Local Similarity
Matches 28; Conserv
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26
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PIR, S53590; S53590.
SGD; S0000673; PAT1.
GG; GG:0005843; C:Cytosolic small ribosomal subunit (sensu Eu. . .; IDA. GG; GO:0007059; P:chromosome segregation; IMP. GG; GG:000644; P:regulation of translational initiation; IGI. DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  293 SQIVTEDPYNEDFYFQVYKIIQRGGITSESNKGLIARAYLEHSGHRLGGRYKRTD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kern L.;
"The URK1 gene of Saccharomyces cerevisiae encoding uridine kinase.";
Nucleic Acids Res. 18:5279-5279(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STIVSE----EDFILPVYK-----GELEKG-----YQFDGWEISGFEGKKDAGYVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Wang X., Watt P.M., Louis E.J., Borts R.H., Hickson I.D.;
"Patl: a topoisomerase II-associated protein required for faithful
chromosome transmission in Saccharomyces cerevisiae.";
Nucleic Acids Res. 24:4797(1996).
-i- FUNCTION: NECESSARY FOR ACCURATE CHROMOSOME TRANSMISSION DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Pungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58; Indels 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YCG1 YEAST STANDARD; PRT; 853 AA.
P25588; P25589; P27513; P87003;
01-MAY-1992 (Rel. 22, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
Hypothetical 97.9 kDa protein in CHA1-KRR1 intergenic region.
YCL061C OR YCL61C/YCL60C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.8%; Score 81; DB 1; Length 797; 25.8%; Pred. No. 58; tive 21; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rasmussen S.W., von Wettstein D.;
Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gromadka R.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2A54F39AE3E75ECE CRC64;
                                                                                                                                                                                                                                            CELL DIVISION. INTERACTS WITH TOPOISOMERASE TOP2.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: TO S.POMBE SPBC19G7.10C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 DLO--REEHSQKSDSTKDVTATVLDKNNISSKSTT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 384-596 FROM N.A.
STRAIN=ATCC 28383 / FL100;
MEDLINE=90384830; PubMed=2169608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .797 AA; 88487 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 25.8%
nes 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4932;
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MEDLINE=21848401; PubMed=11859360;

MEDLINE=21848401; PubMed=11859360;

MEDLINE=21848401; PubMed=11859360;

MOOD V., GAUlliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

MOOD V., GAulliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

A Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

A Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

A James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

A Mooney P., Moule S., Saunders D., Seeger K., Sharp S.,

Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

Rad Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      283 KEKRREKLEENDFOLNAHDSGSDSGSESSGFALSGNEIADYESSGSENDNRRESDSEKED 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          343 DEIILKQKKSHHVKHIINESDSDTEVEAKP----KEKADESLPKRIAINLGHYGDNI--- 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21
                                                                                                                                                                                                                                                           GO:0006347; P:chromatin silencing at HML and HMR (sensu S. . .; IGI. GO:0006348; P:chromatin silencing at telomere; IGI. GO:000076; P:DNA replication checkpoint; IGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 KEMSSTIVSEEDFILPVY-----KGELEKGYQFDGWEISGFEG------KKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34;
                                                                                                                                                                                                                                                                                                                                                                                                                            10.8%; Score 81; DB 1; Length 853; 21.7%; Pred. No. 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                      97946 MW; 16E09FCC0BF248D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 EHSQKSDSTKDVTATVLDKNNI----SSKSTTNNPNK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68;
                                                                                                                                                                                                                                                                                                                                              L -> V (IN REF. 3).
MISSING (IN REF. 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein C23D3.06c in chromosome I. SPAC23D3.06C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1325 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Mismatches
                                                                                                                                                                            EMBL; XS9720; CAA42405.1; -.
EMBL; XS998; -; NOT_ANNOTATED_CDS.
PIR: $74279; $74279.
SGD; S0000566; YCL061C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 21.7%
Matches 34; Conservative
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                                                                                                                                                                                                                                                                                                                                              505
567
                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                505 5
567 5
853 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    685 WGASTFOSKPOPSFSFGLTLDDKSNTPGKNFSIFGKTAETQVEOKKPENNVLTKPFSFAP 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKK-----KDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Loucas M., Rochet M., Caillardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Shpakovski GV., Ussery D., Barrell B.G., Nurse P.;
Shpakovski GV., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 WEISGFEGKKDAGYVINLSKD------TFIKPVFKKIEEKKEEEN---KP-TFDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96180278; PubMed=8603916; Benian G.M., Tinley T.L., Tang X., Borodovsky M.; Tinley T.L., Tang X., Borodovsky M.; The Caenorhabditis elegans gene unc-89, required for muscle M-line assembly, encodes a giant modular protein composed of Ig and signal transduction domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UN89 CAEEL STANDARD; PRT; 6632 AA.
001761, 017362,
15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
Muscle M-line assembly protein unc-89 (Uncoordinated protein 89)
UNC-89 OR C09D1.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 1325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 1325 AA; 145776 MW; EEFD952FB7F0E6BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISIONS.
Waterston R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Bristol N2;
Du Z., Le T.T., Wilson R.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 23.3%; Pred. No. 99; Aatches 35; Conservative 19; Mismatches
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TIAKQNDKSSKSEGKASVANMSALNKSTNN 827
                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.8%; Score 81; 23.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                               GeneDB SPombe; SPAC23D3.06c; -. Pfam; PF03093; Nucleoporin_FG; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Cell Biol. 132:835-848(1996)
                                                                                                                                                                                                                                                                                                                                                              EMBL; Z64354; CAA91241.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 TVLDKNNISSKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                   PIR; S62497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 VIVIIONGKEMSSTIVSEEDF--ILPVYKGELEKGYOFDGWE---ISGFEGKKDAGYVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.8%; Score 81; DB 1; Length 6632; 21.6%; Pred. No. 5.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IN REF. 1)
| IG-LIKE C2-TYPE 17. |
| IG-LIKE C2-TYPE 19. |
| IG-LIKE C2-TYPE 19. |
| IG-LIKE C2-TYPE 20. |
| IG-LIKE C2-TYPE 21. |
| IG-LIKE C2-TYPE 21. |
| IG-LIKE C2-TYPE 23. |
| IG-LIKE C2-TYPE 24. |
| IG-LIKE C2-TYPE 24. |
| IG-LIKE C2-TYPE 26. |
| IG-LIKE C2-TYPE 27. |
| IG-LIKE C2-TYPE 27. |
| IG-LIKE C2-TYPE 31. |
| IG-LIKE C2-TYPE 41. |
| IG-LIKE C2-TYPE 41. |
| IG-LIKE C2-TYPE 41. |
| IG-LIKE C2-TYPE 42. |
| IG-LIKE C2-TYPE 43. |
| IG-LIKE C2-TYPE 44. |
| IG-LIKE C2-TYPE 44. |
| IG-LIKE C2-TYPE 45. |
| IG-LIKE C2-TYPE 46. |
| IG-LIKE C2-TYPE 47. |
| IG-LIKE C2-TYPE 48. |
| IG-LIKE C3-TYPE 48. |
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Matches 32; Conservative
   6632 AA;
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                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
   FUNCTION: Structural component of the muscle M-line. Myofilament lattice assembly begins with positional cues laid down in the basement membrane and muscle cell membrane. UNC-89 responds to these signals, localizes, and then participates in assembling an
                                                                 M-line.
--- TISSUE SPECIFICITY: Localizes to the middle of A-bands.
--- SIMILARITY: Contains 1 DBL-homology (DH) domain.
--- SIMILARITY: Contains 1 fibronectin type III domain.
---- SIMILARITY: Contains 49 immunoglobulin-like C2-type domains.
---- SIMILARITY: Contains 1 PH domain.
---- SIMILARITY: Contains 5 RCSD domains.
---- SIMILARITY: Contains 1 SH3 domains.
                                                                                                                                                                                                                                                                                                                                          IG-LIKE C2-TYPE 7.
IG-LIKE C2-TYPE 8.
IG-LIKE C2-TYPE 9.
IG-LIKE C2-TYPE 10.
IG-LIKE C2-TYPE 11.
IG-LIKE C2-TYPE 12.
IG-LIKE C2-TYPE 13.
IG-LIKE C2-TYPE 14.
IG-LIKE C2-TYPE 14.
IG-LIKE C2-TYPE 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SH3.

DH.

PH.

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 4.

IG-LIKE C2-TYPE 6.

THR-RICH.

RCSD 1.

RCSD 2.

RCSD 3.

RCSD 3.

RCSD 5.
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11; Gaps

38; Indels

11; Mismatches

23; Conservative

Matches

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
58 LSKDTFIKPV----FKKIEEKK--EEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQRE 111
                                                                                                                                                                                                                                                                                                                                   STRAIN=Pm25;
Tarrago R., Badiola I., Barbe J.;
"Pasteurella multocida tonB gene, complete cds, and exbD gene, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                     There are no restrictions on ng as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEMBRANE VIA ITS N-TERMINAL SIGNAL-LIKE SEQUENCE, SPANS THE
                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                membrane; Periplasmic;
                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL-ANCHOR (POTENTIAL)
PERIPLASMIC (POTENTIAL).
PEFOD4E73577D193 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: ANCHORED TO THE CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
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PRINTS; PR01374; TONBROTEIN.
TIGREMMs; TIGR01352; tonB_Cterm; 1.
Transport; Protein transport; Inner membrane; Per Transmembrane; Signal-anchor; Complete proteome.
Transmembrane; Signal-anchor; Complete proteome.
                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                   256 AA
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SIMILARITY: BELONGS TO THE TONB FAMILY.
                                                                      1260 IAQQVKEASPEATTTITMETSLTSTKTT 1287
                                                      112 EHSQKSDSTKDVTATVLDKNNISSKSTT 139
                                                                                                                                                   PRT;
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28306 MW;
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                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                       TonB protein.
TONB OR PM1188.
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09ZH79;
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10.8%; Score 80.5; DB 1; Length 256; 27.7%; Pred. No. 19;

Query Match Best Local Similarity

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        Qy
        61 DTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDST 120

        Db
        83 DPTVKPEPPKEPEKFKEPERP------KEKPKEKPKKEKPKKEQRDLPKSDRQIDSN 135

        Qy
        121 KDVTATVLDKANISSKSTTANPN 143

        Db
        136 SSINQQATTTGNI---TTNNPN 154

        Search completed: February 10, 2004, 10:49:52

        JOb time: 8.69436 secs
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SEQUENCE FROM N.A.
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Q94mm streptococc
Q95pis plasmodium
Q95pis plasmodium
Q95pis plasmodium
Q85pros plasmodium
Q87785 plasmodium
Q77355 plasmodium
Q97785 plasmodium
Q9784 gallus gall
Q25995 plasmodium
Q81j55 plasmodium
Q81j55 plasmodium
Q81j55 plasmodium
Q81j59 arabidopsis
Q9644 plasmodium
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                                                                    February 10, 2004, 10:48:44; Search time 25.4955 Seconds (without alignments) 1457.493 Million cell updates/sec
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                                                                                                                                 748
1 HRVTVTIQNGKEMSSTIVSE.....ATVLDKNNISSKSTTNNPNK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                            830525 seqs, 258052604 residues
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                                                                                                                      US-10-067-385-8_COPY_630_773
                                               - protein search, using sw model
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Q8DQP7
Q9S4M8
Q95PI5
Q9UGG0
Q25705
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O77355
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Q815F3
Q9FJK9
Q9U6C4
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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sp_bacterlap:*
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	O96229 plasmodium	O44016 GICTYOBTELL	14	Q91h98 arabidopsis	Q9v7j0 drosophila	Q9v7i9 drosophila	Q9gg82 drosophila		Q9ppl5 campylobact		P91488 caenorhabdi	Q8ic27 plasmodium	Q8i3a0 plasmodium	Q9vqv0 drosophila	Q8ihw3 plasmodium	Q95893 drosophila	Q8i5t1 plasmodium	Q9stn4 arabidopsis	Q8i2z6 plasmodium	Q8i426 plasmodium	Q8ie35 plasmodium	O14712 homo sapien		Q93zg2 arabidopsis	N	U	덮	Q8ils9 plasmodium	
026019	096229					_			16 Q9PPL5				Q813A0					10 Q9STN4					6 Q8E5X9	0 093202	.0 Q9M1D2 ·	Q17595	.6 Q98QA1	OBILS9	
380 5													2563 5										635 1	641 1	644 1	535 5	622 1	3026 5	
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104.5	104	Z. 501	103.5	102.5	101.5	101.5	101.5	101	100	100	66	66	66	96	97.5	97.5	97	97	96		96	95.5	95.5	95.5	95.5	92	95	95	
17	18	۲,	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41		43	44	45	

## ALIGNMENTS

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Q9AHTS

AC OPAHTS

D7 O1-UNA-2001 (TrEMBLrel. 17, Created)
D7 O1-UNA-2001 (TrEMBLrel. 17, Last sequence update)
D8 Serine procease (Fragment).
D8 Serine procease (Fragment).
C9 Serine procease (Fragment).
C0 Serine procease (Fragment).
C1 Streptcocccus
C2 Streptcocccus
C3 Streptcocccus
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C9 Strep

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2140 AA;
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                                                                                                                                                                                                                                                                                           HRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSK
                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                               .;
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                                                                                                                                                                                                 Length 2119;
                                                                                                                                                                                                                                             Indels
                                                                                                                                                        2119 AA; 238226 MW; 517F9B7F6B960A6A CRC64;
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Last annotation update)
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                                                                                                                                                                                             ; Score 748; DB 2;
; Pred. No. 9.4e-49;
0; Mismatches 0;
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                    PROSITE; PSS0840; PA; 1.
PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00138; SUBTILASE ESR; 1.
PROSITE; PS00678; WD_REPEATS 1; 1.
Cell wall; Peptidoglycan-anchor; Protease.
SEQÜENCE 2119 AA; 238226 MW; 517F9B7F61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00746; Gram pos_anchor; 1.
Pfam; PF02225; PA; I.
Pfam; PF02225; PA; I.
PRINTS; PR00723; SUBTILISIN:
TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
PROSTIE; PS50847; GRAM_POS_ANCHORING; 1.
  PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2062 KDVTATVLDKNNISSKSTTNNPNK 2085
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PSO0138; SUBTILASE SER; 1.
PSO0678; WD_REPEATS_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2001 (TrEMBLrel. 18, Created 01-OCT-2001 (TrEMBLrel. 18, Last 80 01-MAR-2003 (TrEMBLrel. 23, Last an Serine protease, subtilase family.
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MEDLINE=21357209; PubMed=11463916;
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InterPro; IPR000209; Peptidase_S8
InterPro; IPR001680; WD40.
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EMBL; AE007373; AAK74791.1; -.
MEROPS; SOB.064; -.
                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%;
Matches 144; Conservative 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1313;
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1963 HRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSK 2022
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                                                                                                                                  Gaps
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MEDLINE=21429245; PubMed=11544234;
Meokins J., Alborn W.B. Jr., Arnold J., Blaszczak L.C., Burgett S. DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E., LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P., McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I., Noris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P., Sun P.-M., Winkler M.B., Yang Y., Young-Bellido M., Zhao G., Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P...
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J. Bacteriol. 183:5709-5717(2001).
BMBL; ABO08434; AAK99365.1; -.
Hydrolase; Complete proteome.
SEQUENCE 2144 AA; 240436 MW; 8C1B4B1DBC503A0C CRC64;
                                                               Length 2140;
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01-MAR-2003 (TrEWBLrel. 23, Last sequence update)
01-MAR-2003 (TrEWBLrel. 23, Last annotation update)
Cell Wall-associated serine proteinase PrtA (EC 3.4.21.-).
PRTA OR SPR0561.
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240426 MW; FA44AD8E2938B334 CRC64;
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
                                                               Query Match 100.0%; Score 748; DB 16; Best Local Similarity 100.0%; Pred. No. 9.5e-49; Matches 144; Conservative 0; Mismatches 0;
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99.3%; Pred. No. 1.6e-48;
tive 1; Mismatches 0;
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Matches 143; Conservative
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Matches
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Hisaeda H., Saul A., Long C.A., Miller L.H., Stowers A.W.;
"Merozoite Surface Protein 3 and Protection Against Malaria in Aotus
                                                                                                                                                                                                                                                                           pneumoniae.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
AN AMIDE BOND (BY SIMILARITY).
EMBL; APT27143; AAD48399.1; -.
HSSP; P00782; 2SBT.
                                                                                                                                                                                                                            Bethe G., ten Thoren E., Bongaerts R.J.M., Heinz H.-P., Zysk G.; "Cloning and sequencing of a novel surface protease of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CELL WALL-ASSOCIATED SERINE PROTEINASE
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Merozoite surface protein 3 (Fragment).
Plasmodium falciparum.
Eukaryota, Alveolata; Apicomplexa, Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.5%; Score 744; DB 2; Length 21.
98.6%; Pred. No. 1.9e-48;
ive 2; Mismatches 0; Indels
                                                                                         Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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2144 AA; 240724 MW; 2052511470741331 CRC64;
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Cell wall-associated serine proteinase PrtA precursor.
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InterPro; IPR001899; LPXTG.
InterPro; IPR001897; PA.
InterPro; IPR001209; Peptidase_S8.
InterPro; IPR001680; WD40.
Pfam; PP00746; Gram pos_anchor; 1.
Pfam; PP00082; PA; I.
Pfam; PP00082; Peptidase_S8; 2.
PRINTS; PR00723; SUBTILISIN.
TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
PROSITE; PS50847; GRAM POS_ANCHORING; 1.
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PROSITE; PS50840; PA; I.S.
PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00678; WD REPEATS 1; 1.
PROSITE; PS00678; WD REPEATS 1; 1.
Cell wall; Peptidoglycan-anchor; Signal.
19
PROSITE: PS00678; PS0140919.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 98.6
Matches 142; Conservative
                                                                    Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  MEROPS; S08.064;
                                                                                                                 Streptococcus.
NCBI_TaxID=1313;
                                                                                                                                                                                                      STRAIN=3.B;
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Q95PI5
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242
                                                                                                                                                                                                                                                                                               57 NLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQK 116
                                                                                                                                                                                                                                                                                                                                                                                           225 SKDKENISKENDDVLDE-KEEEAEETEEELEEKNEEETESEISEDEEBEEEEEKEEE 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 NKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATV-----LDKN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 AEETGEQELEEKNEEETESEINEDEEQEEEEEEEKEEENDNKKEQAKEQSNDQKEDMEAQ 302
                                                                                                                                                                                                                                                              26
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                                                                                                                                                                                                                                                            ----FD---GWEISGF--EGKKDAG----YVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 VYKGELEKGYQFD-GWEISGF---BGKKDAG-----YVINLSKDTFIKPVFKKIEEKKEEE
                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54; Indels 16;
                                                                                                                                                                                                        42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-20146497; PubMed=10960178;
MEDLINE-20146497; PubMed=10960178;
Okenu D.M.N. Thomas A.W., Conway D.J.;
"Allelic lineages of the merozoite surface protein 3 gene in Plasmodium reichenowi and Plasmodium falciparum.";
Mol. Biochem. Parasitell. 109:185-188(2000).
EMBL; AJ552286; CAB65754.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5854;
                                                                                                                                                  15.0%; Score 112; DB 5; Length 361; 23.9%; Pred. No. 0.57; tive 28; Mismatches 48; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match
Local Similarity 26.2%; Pred. No. 0.78;
nes 34; Conservative 26; Mismatches 54; Indels
the EMBL/GenBank/DDBJ databases
                                                                           361 361
361 AA; 41163 MW; 6127A3041587BA74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             346 346
346 AA; 39127 MW; A804B96BDFAFA010 CRC64;
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Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDSTKDVTATVLDKN-----NISSKSTTNN 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                346 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Merozoite surface protein 3 (Fragment)
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-OCT-2002 (TrEMBLrel. 22, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                              28 YKGELEKGYQ------
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(TrEMBLrel. 01, L
(TrEMBLrel. 22, L
                                                                                                                                                                          Local Similarity 23.9%;
hes 37; Conservative 2
Submitted (JUL-2001) to the EMBL; AY044180; AAK94780.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               303 NLISKNONNN 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 NISSKSTINN 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium reichenowi.
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01-NOV-1996 (TrEMBLre
01-OCT-2002 (TrEMBLre
Polymorphic antigen.
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                       Plasmodium falciparum (isolate 3D7)
                                                                                                        Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                           NCBI_TaxID=36329;
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077355
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AC CONTRACTOR SERVING 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----ESH 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 YAĞKVEKDYERAKNAYQKANQAVLKAKEASSYDYILGWEFGGGVPEHKKEENMLSHLYVS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----FD---GWEISGF--EGKKDAG----YVI 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 VTIONGKEMSSTIVSEEDFILPVYK-----GELEKGYOFDGW---EISGFE-----G 48
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Chen Z., Wen Y.;
                                                                                                                                                                                                           Conservation of structural motifs and antigenic diversity in the
                                                                                                                                                                                                                                                                                                                                                                                                                            20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42;
                                                                                                                                                                                                                                    Plasmodium falciparum merozoite surface profein-3 (MSP-3).";
Mol. Biochem. Parasitol. 90:21-31(1997).
EMBL; U08851; AAC47831.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.7%; Score 110; DB 16; Length 775;
                           Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 NLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLN-----
                                                                                                                                                                                                                                                                                                                                                                       DB 5; Length 379;
                                                                                                                                                                                                                                                                                                                                                                                                                         41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE016746; AA004453.1; -.
                                                                                                                                                                                                                                                                                                                379 AA; 43344 MW; DC7AF106887C8AA0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           775 AA; 86354 MW; 4A00563A7BB8777C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 HRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNN 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 RKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNN 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Penicillin-binding protein 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacceria, Firmicutes, Bacillales, Staphylococcus, NCBI TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                     14.7%; Score 110; DB 523.4%; Pred. No. 0.86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              775 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                      30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                            MEDLINE=98156743; PubMed=9497029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 YKGELEKGYQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            684 TKGNGFVTNQSISKGQIIK-
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                                                                                                                                                                                                                                                                                                                                                                                                                         37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43; Conservative
                                                                                                                                                                                  McColl D.J., Anders R.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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Matches 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome. SEQUENCE 775 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                        SEQUENCE FROM N.A.
                                                    NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         625
                                                                                                                                                                                                                                                                                                                SEQUENCE
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3008 AA

PRELIMINARY;

081436

RESULT 9 Q81436 ID Q814:

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54 YVINLSK----DTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQ---LNESHRKE 106
                                                                                                                                                                                                                                  ABDULNE=2225708; PhDMed=12368867;
Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
Mungall K., Bowman S., Akkin R., Baker S., Barcoks K.,
Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
Chillingworth T., Christodoulu Z., Clark L., Clark R., Corton C.,
Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
Peltwell T., Goble A., Goodhead I., Gwilliam R., Hance Z.,
Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
Line A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,
Oliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch E.,
Alaylor K., Samith R., Squares R., Squares S., Stevens K.,
Alaylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
Sequence C. Plasmodium falciparum chromosomes 1, 3-9 and 13.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bowman S., Lawson D., Basham D., Brown D., Chillingworth T., Churcher C.M., Craig A., Davies R.M. Devlin K., Feltwell T., Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T., Horrocks P., Jagels K., Jassell N., Wres S., McLean J., Moule S., Munghl K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A., Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 DLOREEH----SQKSDSTKDVTATVLDKNNISSK-----STTNNPNK 144
                                                                             SEQUENCE FROM N.A. Devlia P., Mungal K., Berriman M., Pain Devlin K., Baker S., Davies P., Mungal K., Berrall B.; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 109; DB 5; Length 3008;
Pred. No. 9.4;
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3008 AA; 356023 MW; 60BCBBEE15C599B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.4%; Pred. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum (isolate 3D7).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=3D7;
MEDLINE=99376085; PubMed=10448855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 419:527-531(2002).
EMBL; AL929351; CAD51431.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical 71.7 kDa protein.
PFC0465C, MAL3P4.20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
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36;
                                                                                                                                             STRAIN=NFS4
                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                 Antigen.
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                                          255995
                               025995
         RESULT 12
Q25995
                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                               595 KPETKTIVAEKDV-----TTKEEQLGKSETSEKQASEKQDVKPKVTKEKSVKKEVKA 646
                                                                                                                                                                           60 ILGFEDDILYEYCISQLKOSKEKK---DGEEDKYLNAKKLKINLTGFIGNKKSDIFIEEL 116
                                                                                                                                                                                                  68 FKKI--EEKKEE-----SINKPTFDVSK-KKDNPQVNHSQLNE-----SHRK 105
                                                                                                                                                                                                                                          E-----DLQREEH----SQKSDSTK----DVTATVLDKNNISSKSTTN 140
                                                                                                                                                                                                                                                       17 IVSEEDFILPVY-----KGELEKGYQFDGWEISGFEGKK----DAGYVINLSKDTFIKPV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQRE----EHSQKSDSTKDV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claustrin.
Gallus gallus (Chicken).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 KEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Brain;
MEDLINE=94157526; PubMed=7906711;
MEDLINE=9457526; PubMed=7906711;
"Claustrin, an antiadhesive neural keratan sulfate proteoglycan, is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
Whitehead S., Woodward J.R., Newbold C., Barrell B.G.; "The complete nucleotide sequence of chromosome 3 of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1038;
                                                                                                                                     61;
                                                                                                                 DB 5; Length 600;
                                                                                                                                   47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           structurally related to MAP1B.";
J. Neurobiol. 25:1-22(1994).
EMBL; X67778; CA8479881.; SEQUENCE 1038 AA; 117112 MW; 213D694A5B510927 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cole G.J.;
Submitted (OCT-1992) to the EMBL/GenBank/DDBJ databases
                                                                                   .l protein.
600 Aa; 71663 MW; 57EAB42565CAD64C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.5%; Score 108.5; D 28.6%; Pred. No. 3.3;
                                                                                                               14.5%; Score 108.5; D
29.3%; Pred. No. 1.8;
tive 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                Created)
                                         EMBL, AL008970; CAA15610.2;
InterPro, IPR002483; PWI.
Pfam; PF01480; PWI; 1.
SWART; SM00311; PWI; 1.
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01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-451 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 28.6
Matches 34; Conservative
                                                                                                                                      54; Conservative
                     falciparum .";
Nature 400:532-538(1999)
                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE=Brain;
                                                                                                                                                                                                                                                                                    141 NPNK 144
                                                                                                                                                                                                                                                                                                        KTNK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus.
NCBI_TaxID=9031;
                                                                                   Hypothetical
                                                                                                                                                                                                                                           106
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                                                                                             SEQUENCE
                                                                                                                 Query Match
                                                                                                                            Local
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181 VLKAKEASS----YDYIL------GWEFGGGVPEHKKEENMLSHLYVSSKD 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222 KENISKENDDVLDEKEEEAETEEELEEKNBEETESEISEDEEEEEEEKKEEENDKKK 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23
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Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 IQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGF--EGKKDAG----YVINLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McColl D.J., Silva A., Foley M., Kun J.F., Favaloro J.M.,
Thompson J.K., Marshall V.M., Coppel R.L., Kemp D.J., Anders R.F.;
"Molecular variation in a novel polymorphic antigen associated with
Plasmodium falciparum merozoites.";
                                                                                                                                                                                                                                                                                                                                                                         Plasmodium falciparum (isolate NF54).
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.4%; Score 108; DB 5; Length 354; 23.2%; Pred. No. 1.1; ative 29; Mismatches 46; Indels 'ative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Conservation of structural motifs and antigenic diversity Plasmodium falciparum merozoite surface protein-3 (MSP-3)." Mol. Biochem. Parasitol. 90:21-31(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              354 AA; 40119 MW; 3A7256152F48B527 CRC64;
                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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0-1-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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354
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PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=NF54;
MEDLINE=98156743; PubMed=9497029;
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PF10 0345.
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PRELIMINARY;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                           NCBI_TaxID=3702;
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                                                                                                                 01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000
01-MAY-2000
                                                                            01-MAR-2001
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                                                                                                01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                 Tabata S.;
                                                                                                                                                                                                         eurosids
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                                                                                                                                                                                                                                                                      SEQUENCE
                                       Q9FJK9
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                                                                                                                                                                                                                                                                                      KDTFIKPVFKKIEEKKEE-----ENKPTFDVSKKKDNPQVNHSQLNESHRKE 106
                                                                                                                                                                                                                                                                                                            76 EEENKPT-------FDVSKKKDN-PQVNHSQLNESH-RKEDLQREEHSQKSDS 119
                                                                                                                                                                                                                                                 181 VLKAKEASS----YDYIL-----GWEFGGGVPEHKKEENMLSHLYVSSKD 221
                                                                                                                                                                                                           7 IQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGF--EGKKDAG----YVINLS 59
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Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
Elsen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M.-S., Nene V., Shallon S.J., Suh B., Peterson J., Angluoli S.,
Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
Martin D.M.A., Fairlanb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                 Length 354;
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Fraser C.M., Barrell B.; "Genome sequence of the human malaria parasite Plasmodium
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                                                                                                                                                                      46; Indels
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                                                                          EMBL; AE014834; AAN35542.1; -.
SEQUENCE 354 AA; 40119 MW; 3A7256152F48B527 CRC64;
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EMBL, AE014848; AANS6341.1; -.
Hypothetical protein.
SEQUENCE 829 AA; 98816 MW; EF2675E301B2CE93 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                        282 EQEKEQSNENNDQKKDMEA----QNLISKNQNNN 311
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14.4%; Score 108; DB 5;
Best Local Similarity 23.2%; Pred. No. 1.1;
Matches 36; Conservative 29; Mismatches 46,
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Best Local Similarity 24.8
Matches 36; Conservative
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                                                        Nature 419:498-511(2002)
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207 VLKAKEASS----YDYIL-----GWEFGGGVPEHKKEENMLSHLYVSSKD 247
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                                                                                                                                                                                                 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                             "Structural analysis of Arabidopsis thaliana chromosome 5. VII. Sequence features of the regions of 1,013,767 bp covered by sixteen physically assigned Pl and TAC clones."; DNA Res. 5:2797-308 (1998). EMBL, AB015468; BAB166941; -. SEQUENCE 470 AA; 53758 MW; 6D686CE72E35AC54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                              Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.,
                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Li X.R., Yu X.B., Luo S.H., Shan Z.X., Fang J.M., Xu J.; "Sequence of Plasmodium falciparum secreted polymorphic antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45;
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NCBI_TaxID=5833;
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SEQUENCE 379 AA; 43316 MW; C152A54E1F9D5F25 CRC64;
                                                                    Last sequence update)
Last annotation update)
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Last annotation update)
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24.5%; Pred. No. 2.3;
ive 28; Mismatches
  470 AA
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  PRT;
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                                               (TrEMBLrel. 16, (TrEMBLrel. 16, I
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PRELIMINARY;
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Best Local Similarity
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Query Match
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SEQUENCE FROM N.A.
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---ESHRKE 106
            208 VLKAKEASS----YDYIL------GWEFGGGVPEHKKEENMLSHLYVSSKD 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                       MEDLINE=95198774; PubMed=7891748; McColl D.J., Silva A., Foley M., Kun J.F., Favaloro J.M., Thompson J.K., Marshall V.M., Coppel R.L., Kemp D.J., Anders R.F.; Thompson J.K., warshall V.M., Coppel R.L., Kemp D.J., Anders R.F.; Molecular variation in a novel polymorphic antigen associated with plasmodium falciparum merozoites."; Mol. Biochem. Parasitol. 68:53-67(1994).
                                                                                                                                                                                                                                                                                                                                                                     McColl D.J., Anders R.F.;
"Conservation of structural motifs and antigenic diversity in the plasmodium falciparum merozoite surface protein-3 (MSP-3).";
Mol. Biochem. Parasitol. 90:21-31(1997).
EMBL; L07944; AAC09378.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5; Length 380;
                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-CCT-2002 (TrEMBLrel. 22, Last annotation update)
Polymorphic antigen precursor.
Plasmodium falciparum.
Bukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum (isolate 3D7).
Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=36329;
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KDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLN---
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Last sequence update)
Last annotation update)
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                                                       107 DLOREEHSOKSDSTKDVTATVLDKNNISSKSTTNN 141
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(TrEMBLrel. 23, I
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01-MAY-1999
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SIGNAL
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58 LSKDTFIKPVFKKIEEKKE-----EENKPTFD----VSKKKDNPQVNHSQLNESH 103
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                                                                                                                                                                                                                                                                                                                                                                                                     Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Elsen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nenher V., Shallom S.J., Sub B., Peterson J., Angluoli S., Pertea M., Allen J., Selangut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., Worder J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B., Genome sequence of the human malaria parasite Plasmodium
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                       Gardner M.J., Tettelin H., Carucci D.J., Cummings L.M., Aravind L., Koonin E.V., Shallom S., Mason T., Yu K., Fujii C., Pederson J., Shan K., Jing J., Aston C., Lai Z., Schwartz D.C., Pertea M., Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O. Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.; "Chromosome 2 sequence of the human malaria parasite Plasmodium
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EMBL, AE001410; AAC71925.2; -.
Hypothetical protein.
SEQUENCE 951 AA; 112486 MW; AC8D889358A84F4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 RKEDLQR-EEHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    orcryoscellum discoideum (Slime mold).
Bukaryota; Mycetozoa; Dictyostellida; Dictyostellum.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 103.5; DB 5;
Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.9%; Score 104; DB 25.9%; Pred. No. 6.6; Live 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           325 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22255705; PubMed=12368864;
WEDLINE=99021743; PubMed=9804551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.8%;
                                                                                                                                                                                                                                                      Science 282:1126-1132(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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STRAIN=Columbia;
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                                                                                                                                                                                                                                                                                                              ----ESHRKE 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 KENISKENDDVLDE-KEEEAEETEEELEEKNEEETESEISEDEEEEEEEEEKEEENDKKK 306
                                                                                                                                                                                                                                                                                                                                                                                                                                 71 --IEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKE-----DLQREEHSQKSDSTK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 IQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGF--EGKKDAG----YVINLS 59
                                                                                                                                                                      57 HRTITSIKN -- RFSVKKIGDEEKLFRISKNGELIVLNELEFDNFHIK-- EGKHLRKSKMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Conservation of structural motifs and antigenic diversity in the blasmodium falciparum merozoite surface protein-3 (MSP-3)."; Mol. Biochem. Parasitol. 99:21-31(1997).

EMBL; U08852; AAC47832.1; -.
63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45;
                                                                                       1 HRVTVTIQNGKEMSSTIVSEEDFILPVYK-GEL--EKGYQFDGWEISGFEGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum.
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
                                                                                                                                                                                                                                                              50 ---KDAGYV-----INLSKDTFIKPV------FKK-----
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        832.1; -.
43302 MW; ABF9D54E1ED91A24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 KDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spermatophyta, Magnoliophyta, eudicotyledons, core e
eurosida II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last annotation update)
    50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               307 EQEKEQSNENNDQKKDMEA----QNLISKNQNNN 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 DLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNN 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomic DNA, chromosome 3, BAC clone: T19N8. Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28; Mismatches
    25; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-cs12;
MEDLINE-98156743; PubMed-9497029;
McColl D.J., Anders R.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C1. C (TrEMBLrel. 01, C 01-OCT-2002 (TrEMBLrel. 22, Le Polymorphic antigen. Prince of the prince of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 24.5
Matches 38; Conservative
        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           379 AA;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 D 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000
01-OCT-2000
        43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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Q9LH98
        Matches
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NETAINSERERELY;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,

Adamstides P.G., Scherer S.E., Li P.W., Hookins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

A brid J.F., Agbayani A., Hardrews-Pfannkoch C., Baldwin D.,

A brid J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

Ballew R.W., Basu A., Baxendale J., Bayraktaroglu L., Beasaley E.M.,

Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Blothakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan W.S., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

A Durbin K.J. Evangelista C.C., Ferraz C., Ferriera S., Pleischmann W.,

RA Posler C., Gabrielian A.E., Garrell J.H., Gu Z., Guan P., Harris M.,

A Horsin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wel M.-H., Ibegwam C.,

A lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liasko P., Lei Y., Levitsky A.B., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPerson D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1709 STKESSKDGKINEIHGDKEATMEEGSKDGGTNSTGKDSKKSVEINGVKDDSLKDDSKN 1768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 YVINLSKDTFIKPVFKKIEEKKEEENKP--TFDVSK-KKDNPQVNHSQLNESHRKEDLQ- 109
                                                                                                                                                                                                                                        Nakamura Y.;
"Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the regions of 4,251,695 bp covered by ninety Pl,
Sato S., Nakamura Y., Asamizu E., Tabata S.; to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10; Length 2081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neoptera; Endopterygota; Diptera; Brachycera; Muscomorphā;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 TVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKD
                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AP002057; BAB03174.1; -.
SEQUENCE 2081 AA; 232851 MW; D3603E1F85EFFF29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13, Created)
01-CT-2000 (TrEMBLrel. 13, Created)
01-CT-2002 (TrEMBLrel. 22, Last sequence update)
01-CT-2002 (TrEMBLrel. 22, Last annotation update)
CG6421 protein (Aspartyl beta-hydroxylase variant 2)
ASPH OR CG8421 OR CG18658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDINEINNGKEDSVKDNVTEIQGNDNSLTNSTSSEPN 1805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.7%; Score 102.5; 27.4%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                MEDLINE=20363099; PubMed=10907853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 27.49
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                    TAC and BAC clones.";
DNA Res. 7:217-221(2000)
        Kaneko T., Kato T., S
Submitted (MAY-2000)
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Merkulov G., Milahina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.K., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G., Pollard J., Puri V., Reses M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng I.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                Celniker S.E., Adams M.D., Kronmiller B., Wan K.H.; Holt R.A.,
A Evans C.A., Gocayne J.D., Amanatides P.G., Rarandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J. Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
A Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
I begwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
A McIncosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
A Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
Milliam S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
Sequencing of Drosophila melanogaster genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20564328; PubMed=10956665;
Dinchuk J.E., Henderson N.L., Burn T.C., Huber R., Ho S.P., Link J.,
O'Neil K.T., Focht R.J., Scully M.S., Hollis J.M., Hollis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.. Hradecky P., Huang Y., Kaminker J.S., Prochnik S.B., Smith C.D., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.B., Smith C.D., Clamp M., Drysdale R., Emmert D., Frise B., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith B., Smuth E., Smuth E., Smuth E., Muhiffield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Aspartyl beta -Hydroxylase (Asph) and an Evolutionarily Conserved
Isoform of Asph Missing the Catalytic Domain Share Exons with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter C.J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Vente
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Biol. Chem. 275:39543-39554(2000).

EMBL; AE003808; AAF58065.2; -

EMBL; AF289494; AAG40007.1; -.

Flyase; Fanon034075; Asph.

SEQUENCE 382 AA; 43287 MW; 60E5C03AEBFCGE8B CRC64;
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EDLDTPLSESRFSK--VFDGWVDEHRDEHDGHDVQEPSGBALDDHDEHDDHDDHEDEDEE 135

EDFILPVYKGELEKGYQFDGW-----EISGFEGKKDAGYVI------NLSKDTFIK

9

Gaps

DB 5; Length 382;

Local Similarity

Query Match

Matches

21

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RAMEDINE-2019 80066; Pubbed-1073132;

RAMADINE-2019 80066; Pubbed-1073132;

RAMADINE-2019 80066; Pubbed-1073132;

RAMADINE-2019 80066; Pubbed-1073132;

RAMADINE-2019 8006; Pubbed-1073132;

RAMADINE, Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Batiluw R.M., Basu A., Baxendall U., Bayarkaraglu L., Basalsy E.M., Beeson K.Y., Bencen D.A., Buller H., Cadieu E., Center A., Chadra I., Raken B. B., Bhandari D., Botchan M.R., Buutler H., Cadieu E., Center A., Chadra I., Rawadin D.A., Buller H., Cadieu E., Center A., Dunn P., Rodon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Bodon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Rodon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Rodon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Rodon K., Doup L.E., Downes M., Dugan-Rocha S., Plater S., M., Ramadina M.B., Gargel C., Rerraz C., Ferraz C., Ferra
PVFKKIEEKKEEENKPT-----FDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDS 119
                          |: ::||: || :|| :|| ::|
136 PLTEELEEELEEEEEEPTEEDEPAADEEYEEDEDEENNA--GENITAEDAEEEEEEEDNDD 193
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                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Brosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequ
01-MAR-2003 (TrEMBLrel. 23, Last anno
                                                                                                                                                                                                                                                        PRT;
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                                                                                          120 TKDVTATVLDKNNISSKST 138
                                                                                                                                        194 EGTVEATVEATTEAT 212
                                                                                                                                                                                                                                                        PRELIMINARY;
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Biol. Chem. 275:39543-39554 (2000)

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SEQUENCE FROM N.A.
    66 PVFKKIEEKKEEENKPT----FDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20564328; PubMed=10956665;
Dinchuk J.E., Henderson N.L., Burn T.C., Huber R., Ho S.P., Link J.,
O'Neil K.T., Focht R.J., Scully M.S., Hollis J.M., Hollis G.F.,
Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
McIntosh T.C., Moy M., Murphy B., Nolson C., Nolson K.A., Nunoo J.,
Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
Sequencing of Drosophila melanogaster genome.",
Sequencing of Drosophila melanogaster genome.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Aspartyl beta -Hydroxylase (Asph) and an Evolutionarily Conserved Isoform of Asph Missing the Catalytic Domain Share Exons with
                                                                                                                                                          Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell R. Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Huradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Carlson J.W., Calniker S.E., Clamp M., Drydalle R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield B., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                           Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 13, Last annotation update)
Aspartyl beta-hydroxylase variant 1 (CG8421-PA).
ASPH OR CG8421 OR CG18658.
Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Atthropoda, Hexapoda, Insecta, Pterygota,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                            Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
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FlyBase; FBgn0034075; Asph.
SEQUENCE 556 AA; 63144 MW; B420980CBD6C357A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51;
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                                                                                                                                                                                                                                                                                                60 KOTPIKPVFKKIEEKKEEENKPTPDVSKKKONPQVNHSQLNESHRKEDLQREEH----- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212 KENISKENDDVLDE-KEEEAEETEEEELEEKONEEETESEISEDEEEEEEKEEEKEEKEEKOAKE 270
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                                                                                                                                                                                                                               21 EDFILPVYKGELEKGYQFDGW-----EISGFEGKKDAGYVI------NLSKDTFIK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29
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Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                         25;
                                                                                                                                                                               Length 785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Allelic lineages of the merozoite surface protein 3 gene in Plasmodium reichenowi and Plasmodium falciparum."; Mol. Biochem. Parasitol. 109:185-188(2000).
EMBL; AJ252287; CAB85901.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=57266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 13.5%; Score 101; DB 5; Length 329; Best Local Similarity 25.3%; Pred. No. 3.6; Matches 38; Conservative 25; Mismatches 47; Indels
                                                                                                                                                                                                         Indels
                                                             to the EMBL/GenBank/DDBJ databases
                                                                      EMBL; AF289433; AAG40806.11; -.
EMBL; AE003808; AAM70947.1; -.
ELYBASS; FBGIN0034075; ASPh.
InterPro; IPR001401; TPR.
InterPro; IPR006025; Zn MTPSPtdse.
PROSITE; PS00142; ZINC PROTEASE; 1.
SEQUENCE 785 AA; 89843 MW; 30A8DFCD6836F7F1 CRC64;
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329 AA; 36916 MW; C5B045DB5E21A159 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Merozoite surface protein 3 (Fragment).
MSP3.
                                                                                                                                                                                                      51;
                                                                                                                                                                               DB 5;
                                                                                                                                                                             13.6%; Score 101.5; D
24.5%; Pred. No. 8.3;
:ive 29; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                              329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Okenu D.M.N., Thomas A.W., Conway D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum (isolate 7G8)
                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-7G8;
MEDLINE-20416497; PubMed=10960178;
                                                                                                                                                                                                                                                                                                                                    120 TKDVTATVLDKNNISSKST 138
                                                                                                                                                                                                                                                                                                                                                              194 EGTVEATVEATTEAT 212
                                                                                                                                                                                                       34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                   FlyBase;
Submitted (SEP-2002)
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                                     SEQUENCE FROM N.A.
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56 INL---SKDTFIKPVFKKIEEKKEEENKPT---FDVSKKKDNP----QVNHSQLNESHRK 105
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MEDLINE=22255705; PubMed=12368864;
MEDLINE=22255705; PubMed=12368864;
MEDLINE=22255705; PubMed=12368864;
MEDLINE=22255705; PubMed=12368864;
MEDLINE=22255705; PubMed=12, Bowman S., Paulsen I.T., James K., Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nene V., Shallom S.J., Sub B., Petrson J., Angluoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., Worfædden G.I., Cummings L.M., Subramanian G.M., Mungall C., Pavis R.W., Fraser C.M., Barrell B., Genome sequence of the human malaria parasite Plassmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 INÇKPLDDDLRDEISSDDILRRRFKKKTPNKFLEELDEEYESKHTKKSNIYLKED---L
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                                                                                                                                                                                                                                                                      STRAIN=NCTC 11168;
MEDILINE-2012, PubMed=10688204;
MEDILINE-2012, PubMed=10688204;
Barkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandraem M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.,
"The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                     Campylobacter jejuni.
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Campylobacteraceae, Campylobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.4%; Score 100; DB 16; Length 312;
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Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI TaxID=36329;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         312 AA; 37221 MW; 0004FA7836A741E8 CRC64;
                         Last sequence update)
Last annotation update)
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
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     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reveals hypervariable sequences.";
Nature 403:665-668(2000).
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01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2002 (TrEMBLrel. 22,
                                                                          Putative membrane protein.
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01-MAR-2003
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                                                                                                                         44 SGFEGKKDAGYV--INLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNE 101
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                                                                                                                                                    568 SFLSGSNDSYRIDRIYLSPDNYFSYSSNRNRNNINDENVEVIQVEETRSDYNESHDETNE 627
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                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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Waterston R.;
Waterston R.;
"Direct Submission.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; Was109; AAB42334.1; -.
WormPep; T2381.5; CE14016.
Hypothetical protein.
SROUENCE 211 AA; 23955 MW; 11B16164A87E5928 CRC64;
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                                        FEGAAFE08C4CCDB6 CRC64;
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Maggi L., Le T.;
"The sequence of C. elegans cosmid T23B3.";
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
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01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 24.0 kDa protein.
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                                                                                               53;
                                                                Query Match 13.4%; Score Luv, C. Best Local Similarity 26.1%; Pred. No. 16; Matches 30; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.2%; Score 99; DB 529.4%; Pred. No. 3.2;
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Nature 419:498-511(2002).
EMBL; AE014829; AAN35244.1; -.
Hypothetical protein.
SEQUENCE 1130 AA; 131697 MW;
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Best Local Similarity 29.4#
Matches 30; Conservative
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PRT; 1859 AA.

PRELIMINARY;

Q81C27 Q81C27;

RESULT 29 Q8IC27

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63 ----FIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 QQDLSFIHSSINKYEKKKEKENK-NYDKNKKSSNINDKSYNITQNDPRKNNQNKEFVDNN 332
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MEDLINE=2225508; PubMed=12368867;

MEDLINE=2225508; PubMed=12368867;

MINIGALINE DATE OF THE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 TIVSEEDFILPVYKGELEKGYQFDGWEISGF------EGKKDAGYVINLSKDT-
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                                                                                                                                                                                                                                                                                                                                                                                            Seeger K., Murphy L., Harris D., Berriman M., Pain A., Hall N., Quail M., Barrell B.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AEM44506, CAD50814.1; -.
Hypothetical protein.
SEQUENCE 1859 AA; 218376 MW; 2266544164BD360C CRC64;
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=36329;
                                                                                                                                                                     Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.2%; Score 99; DB 5; Length 1859; 24.7%; Pred. No. 33; ive 24; Mismatches 60; Indels
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Last sequence update)
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
E1-E2_ATPase/hydrolase, putative.
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EMBL; AL929355; CAD51734.1; -.
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Matches 35, Conservative
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(TrEMBLrel. (TrEMBLrel.
                                                                                                                                PF07_0016.
Plasmodium falciparum
                                                                         Hypothetical protein.
PF07 0016.
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Best Local Similarity
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Gocayne M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Gotago R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Batton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Abatton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Abril J.F., Agbayani A., An H.J., Andrews-Frankoch C., Baldwin D., Ballaw R.M., Basu A., Baxendale J., Baytaktaroglu L., Basaley E.M., Baeson K.Y., Banos P.V., Berman B.P., Bhandari D., Bolshakoy S., Abril J.F., Bouck J., Broketein P., Bottier P., Abattis R.C., Eusam D.A., Bulke C., Davenport L.B., Davies P., Achery J.M., Cawley S., Dallke C., Davenport L.B., Davies P., Achery J.M., Cawley S., Dallke C., Davenport L.B., Davies P., Buckin K.J., Evangelista C.C., Ferraz C., Ferriera S., Pleistchmann W., Robber C., Gabriellan A.E., Gary N.S., Gelbart W.M., Glasser K., Adloden K.J., Evangelista C.C., Ferraz C., Ferriera S., Pleistchmann W., Andrei B.E., Mownes M., Dugan-Rocha S., Dunkov B.C., Dunk P., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchun K.A., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchun K.A., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Mattel B.E., McIntosh T.C., McLeod M.P., McThy M., Nalson K., Murphy E., Murphy L., Wang X., Shien H., Shore E.C., Siden-Kiamos I., Simpson M., Stupski M.P., Shu B., Shiet R., Shan H., Shiet S., Wanger E.W., Rodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Wangaran D.A., Wanganger P., Shore B.C., Shore H., Worley K., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Walliams S.M., Woodage T., Worley K., Cheeler F., Spradling A.C., Stapler C., Stapler C., Stapler C., Stapler C., Stapl
                                         KD---NPQVNHSQLNESHRKEDLQREE-HSQKSDSTKDVTATVLDKNNISSKSTTNNPN 143
                                                                                                                                                                                                                915 KEKDHNSSNDEDNINDSVLKENVKEEEIHESSSNEQSDSYLKKIEKKDNKNISVDNNEN 973
GELEKGYOFDG-WEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y., Baldwin D., Banzon J., Beson K.Y., Busam D.A., Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M., Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
CG31958 protein.
CG31958 OR CG10022.
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                      157 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 13, C
(TrEMBLrel. 22, I
(TrEMBLrel. 23, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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01-OCT-2002
30
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109 VQVV

109 VQVV

109 VQVV

100 VQVV

101 VGA

101 VG
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106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 MSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVI------NLSKDTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MDELSVEEQDLLKNIY-SLLDK-----DNEGAITSKELGMVIRALGRQPNESIAKEEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34; Gaps
Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
Pacleb J., Paragas V., Park S., Patel S., Féteifer B.,
Phousenavong S., Pittman G.S., Puri V., Richfards S., Scheeler F.,
Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,
Sequencing of Drosophila melanogaster genome.,
Sequencing of Lorsophila melanogaster genome.,
                                                                                                                                                                                                            SEQUENCE FROM N.A.

Maitera S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K Hradecky P., Thang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Tupy J.L., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Krommiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mingall C.J., Lewis S.E.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          přil 0413.
Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEGN; PF00036; efhand; 3.
ProDom; PD000012; EF-hand; 1.
SWART; SW00054; EFh; 3.
PROSITE; PS00018; EF HAND; 1.
Calcium; Calcium-binding;
SEQUENCE 157 AA; 18263 MW; 543F0480E11D9EC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
13.1%; Score 98; DB 5;
Best Local Similarity 22.7%; Pred. No. 2.7;
Matches 34; Conservative 29; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 DLDQDNHINFEESNNWMTTPILNYNHTAVK 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DLQREEHSQKSDSTKDVTATVLDKNNISSK 136
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STRAIN=3D7;
MEDLINE=22255705; PubMed=12368864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AE003578; AAF51062.2;
HSSP, P02593; ICTR.
FlyBase; FBgn0051958; CG31958
InterPro; IPR002048; EF-hand.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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194 EGTVEATVEATTEAT 212

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66 PVFKKIEEKKEEENKPT----FDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDS 119
                                                                                                                                                                                                                                                                                                                                                                                                                    110 LKKKRKIIESEEETNINSDDEEEEEYQRKKOKKOKNSNVSTLSLLEKKKKKKRDSESSN 169
                                                                                                                                                                                                                                                                                                                                                                                              11 KEMSSTIVSEEDFILPVY-----KGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 IKPVFKKIE-----SKKKEEE-----NKPTFDV----SKKKDNPQVN
Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K. Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise B., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K. Yu C., Lewis S.E., Rubin G.M., Celniker S., Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                        49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASPH OR CG8421 OR CG18658.
Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta; Pterygota,
Neoptera, Edopterygota; Diptera, Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                            / Match 13.0%; Score 97.5; DB 5; Length 449; Local Similarity 25.1%; Pred. No. 9.3; nes 42; Conservative 28; Mismatches 48; Indels 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :: || :: | :: | :: | :: | :: | 1.0 NNDYNEEYDEDDEQEEEEEEES-----LSKKKSKKKNSTISP 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5; Length 556;
                                                                                                                                                                               "Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 EDFILPVYKGELEKGYQFDGW-----EISGFEGKKDAGYVI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNP
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                                                                                                                                                                                                                                     EMBL, AE014842; AAN35996.1; -.
Hypothetical protein.
SEQUENCE 449 AA; 52812 MW; 85B62272D6257C68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AY060905; AAL28453.1; -. FlyBase; FBgn0034075; Asph. SEQUENCE 556 AA; 63089 MW; 95D82EAC57D11FE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last.sequence update)
Last annotation update)
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1 Similarity 24.5%; Pred. No. 12;
34; Conservative 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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                                                                                                                                                                                                                     Nature 419:498-511(2002)
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Best Local Similarity
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                                                                                                                                                                                                 falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                  55
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Matches
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Matches
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68 FKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNE-------SHRKEDL 108
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                                                                                                                                                                                                                                                               Gardner M.J., Hall N., Pering E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nene V., Shallom S.J., Sub B., Peterson J., Angluoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 QNGKKY1YYNLSKKKNNG1IKGGSKHNGHLF----INNYKKKRNVKYKINKYKPCSIFSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Bevan M., Lennard N., Quail M., Harris B., Rajandream M.A.,
Bevan M., Lennard N., Quail M., Mayer K.F.X., Lemcke K.,
Schueller C.,
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56;
                                                                                                                                                 falciparum (isolate 3D7).
Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 419:498-511(2002).
EMBL; AE014846; AAN36209.1; -.
Hypothetical protein. SEQUENCE 558 AA; 66487 WW; 2ADC29EA69FF90D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-0CT-2002 (TrEMBLrel. 22, Last annotation update) Mypothetical 109.0 kba protein. 128B5.30 OR AT4G08340. Arabidopsis thaliana (Mouse-ear cress).
                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 QREEHSQKSDSTXDVTATVLDXNNISSKSTTNNPNK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 KKKKELQKEEKKTKLTNVLKQNNKNKNNNNKNNNNK 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5;
13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 97;
Pred. No.
                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                    MEDLINE=22255705; PubMed=12368864;
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                                                                                  (TrEMBLrel. 23, (TrEMBLrel. 23,
                                                                  23,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35; Conservative
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                                 PRELIMINARY;
                                                                                                                                                  Plasmodium falciparum
                                                                                                               Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                  Eukaryota; Alveole
VCBI_TaxID=36329;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          falciparum."
                                                                01-MAR-2003
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                                                                                                 01-MAR-2003
                                                                                                                                    PFL0600W
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                                 QSIST1
RESULT 34
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238 AA; 28481 MW; DA175A2B5A109B49 CRC64;
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01-MAR-2003 (
01-MAR-2003 (
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEOUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 37
Q81426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ::|| :: | | :: :| | 442 VEPVGDDVRSSGDMSPNPSAANNVREGPATFDIMESEDNPGRDNVAPMEDHIRSEVQLSP 501
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MEDLINE=22255708; PubMed=12368867;
MAIL N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
Hall N., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
Mungall K., Bowman C., Cherevach I., Chillingworth C.,
Chillingworth T., Christodoulou Z., Clark L., Clark E., Corton C.,
Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
Reltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
Harper D., Hauser H., Hornsby T., Holroyk S., Horrocks P.,
Humphray S., Jaqels K., James K.D., Johnson D., Lennard N.,
Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
Knights A., Maddison M., Mclean J., Mooney P., Moulle S., Murphy L.,
Oliver K., Ormond D., Price C., Quall M.A., Rabbinowitsch B.,
Asjandream M.A., Rutter S., Squares R., Squares S., Stevens K.,
Asjandream M.A., Rutter S., Smith R., Squares S., Stevens K.,
Alston J.E., Craig A., Newbold C., Barrell B.G;
Squence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 NGKEMSSTIVSEEDFILPVYKGELEKGY-----QFDGWEISGFEGKKDAGYVINLSKDTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum (isolate 3D7).
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.0%; Score 97; DB 10; Length 988; 22.1%; Pred. No. 24; tive 31; Mismatches 67; Indels
                                                                                                                          SEQUENCE FROM N.A.
Lennard N., Quail M., Harris B., Rajandream M.A., Barrell
Mewes H.W., Lencke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                               EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL109819; CAB52556.1; -.
EMBL; AL101511; CAB77959.1; -.
InterPro; IPR01760; Opsin.
InterPro; IPR0355; SUMO protease.
Pfam; PR02902; Peptidase __G8; 1.
                                 EU Arabidopsis sequencing project;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .1 protein.
988 AA; 108955 MW; 01C518587D460EAD CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSOKSDSTKDVT--ATVLDKNNISSKSTTNNPNK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | | | | | | | | | | HVL---GAKDVIDVSDPTE 532
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PROSITE; PS50600; ULP PROTEASE; 1.
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EMBL; AL929356; CAD51839.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 22.1%
nes 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical
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Matches
   REPRESENTATIONS OF THE PROPERTY OF THE PROPERT
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58 LSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDN--PQV--NH--SQLNESHRKED---- 107
                                                                                                                                                                                                                                                                                                                                                               57 NLSKDTFIKPVFKKIE--EKKEEEN-KPTFDVSKKKDNPQVNHSQLNE--SHRKEDL--- 108
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MEDLINE=22255788; PubMed=12368867;

MEDLINE=22255788; PubMed=12368867;

MINGALINE=22255788; PubMed=12368867;

MINGALINE, Bowman S., Arkin R., Baker S., Barron A., Brooks K.,

MINGALI K., Bowman S., Arkin R., Baker S., Barron A., Brooks K.,

Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,

Chillingworth T., Christodoulou Z., Clark K., Corton C.,

Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,

Reltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,

Reltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,

Harper D., Haucer H., Hornsby T., Holroyd S., Horrocks P.,

Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,

Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,

Knights A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,

Oliver K., Sharp S., Smith R., Squares R., Squares R., Stanes R.,

Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,

Squaren C., Craig A., Newbold C., Barrell B.G,

Squares C., Craig A., Newbold C., Barrell B.G,
                                                                                                                                                                  8 ONGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISG---FEGKKDA-----GYVIN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 VTIQNGKEMSSTIVSEEDFI-LPVYKGELEKGYQFDGWEI-----SGFEGKKDAGYVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Devlin K., Baker S., Davies P., Mungal K., Berriman M., Pain A., Hall N., Bowman S., Churcher C., Quail M., Barrell B.; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                      30,
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NCBL_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64; Indels
       Length 238;
                                                                                   58; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 LLKLIEKSNKDDNN-----NINNKKNNNQKCDTKNLN 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 -LQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPN 143
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Best Local Similarity 27.7%; Pred. No. 14;
Matches 44; Conservative 27; Mismatches 64
           12.8%; Score 96; DB 5
28.7%; Pred. No. 6.1;
tive 24; Mismatches
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EMBL; AL929351; CAD51442.1; -.
Query Match
Best Local Similarity 28.7%
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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Search completed: February 10, 2004, 10:57:06 Job time: 27.4955 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=216495;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                             137
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Q8E5X9
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 F--KKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                600 FEIKKLEKEKNIDDKENF--GYKKDNNGEN-DKSDENDKSDENDKSDENDKSDEN ---- 651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98043401; PubMed-9383053; MEDLINE-98043401; PubMed-9383053; MEDLINE-98043401; PubMed-9383053; MEDLINE-98043401; PubMed-9383053; Media M. Elledge S.J.; Liegeois N., Horecka J., DePinho R.A., Sprague G.F. Jr., Tyers M., Elledge S.J.; Media 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harris B., Lennard N., Clark L., Line A., Barron A., Corton C., Berrinan M., Pain A., Hall N., Akkin K., Chillingworth C., Doggett J., Ormond D., Sanders M., Hall N., Akkin K., Chillingworth C., Doggett J., Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AL844509; CAD52432.1; -. Hypothetical protein.

SEQUENCE 1795 AA, 205476 MM; BEE12D50079E76F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 12.8%; Score 95.5; DB 4; Length 375; Best Local Similarity 28.9%; Pred. No. 11; Matches 48; Conservative 12; Mismatches 63; Indels 4:
                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.8%; Score 96; DB 5; Length 1795; 24.6%; Pred. No. 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57; Indels
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
PF13_0161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Cell cycle progression restoration 8 protein.
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Best Local Similarity 24.64
Matches 34, Conservative
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Q81E35;
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51 DAG----YVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKE 106
                                                                                                                                                                 89 KGGRGSHRVKNKSKGTFLGSV------KETFDAMKNSTKEFVRHHKEKIKQAKE 136
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BEDLINB=22242508; PubMed=12354221;
Glaser P., Remaniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of Streptococcus agalactiae, a pathogen causing invasive neonatal disease.";
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                                                                                                                                                                                                                             DLOREEHSOKSDST-----KDVTATVLD-KNNISSKSTINNPNK 144
                                                                                                                                                                                                                                                                                DV-KENLKKFSDSVKSTFRHFKDTTKNIFDEKGNKRFNATKEAAEK 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus agalactiae (serotype III).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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EMBL; AL766847; CAD46494.1; -.
SagaList; gbs0850; -.
Hypothatical protein; Complete proteome.

SEQUENCE 635 AA; 72953 MW; 3ASD85E3207159CE CRC64;
9 NGKEMSSTIVSE--EDFILPVYKGELEKGYQF-----DGWE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 23, Last sequence update) (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                   635' AA
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01-MAR-2003 (TrEMBLre
Hypothetical protein.
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February 10, 2004, 10:48:44; Search time 30.4847 Seconds (without alignments) 697.707 Million cell updates/sec
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1 KEMSSTIVSEEDFILPVYKG......ATVLDKNNISSKSTTNNPNK 134
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| SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1994.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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                                                                                                                                    OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMAKIES		Description	S. pneumoniae Sp13	Streptococcus pneu	S. pneumoniae type	Streptococcus pneu	S. pneumoniae SP04	Drosophila melanog	Plasmodium falcipa	Novel human diagno	Arabidopsis thalia
		ΩI	AAB48343	AAY81710	ABU01020	AAW55096	ABP54590	ABB61977	AAB18278	ABG16636	AAG47777
		DB	22	21	24	19	23	22	21	22	21
		Length	773	2120	2140	117	117	564	665	2519	484
	de	Query e Match Length DB ID	100.0		100.0						
		Score	969	969	969	615	615	101.5	98	92.5	91
		Result No.	1	7	٣	4	Ŋ	9	7	60	6

Chlamydia pneumoni Shrimp white spot Candida albicans e	Human protein sequence of the	s. epidermidis ope Staphylococcus epi		Human protein SEQ	Drosophila melanog	Human polypeptide	Plasmodium falcipa	Plasmodium falcipa	Human sodium chann	Human sodium chann	Candida albicans e	Arabidopsis thalia	Arabidopsis.thalia	rabidopsis th	u	. epidermidis	<ol> <li>S. epidermidis ope</li> </ol>	Staphylococcus epi	Plasmodium falcipa	Tetrodotoxin-sensi	Tetrodotoxin-sensi	Streptococcus poly	Streptococcus poly		. Zea mays protein f		m	Candida albicans e		Staphylococcus epi		Yeast selected int
	AAB9458	AAG81779 ABP39023	•			AAM3995	AAB1817			-						-	•	-	AAB18268		-	•				AAB35803	AAG35426	ABP73309	ABJ19106	ABP56879	AAB98612	ABJ11001
222	222	2 2	22	22	22	22	21	21	21	23	23	21	21	21	23	22	22	23	21	13	19	23	23	21	21	21	21	23	24	24	22	23
511	258	778	817	817	281	607	635	2485	1980	1980	884	329	339	358	465	472	720.	728	1166	1978	1988	157	161	309	361	390	416	434	645	654	2663	215
	12.6				12.5	•		12.4	12.4	•	12.3	12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.1	12.1	12.1	12.1	12.1	12.1	12.1	12.1	12.1	12.1	12.1
88.0 88.0 8.0 8.0	8 8 6	æ æ	88	88	87	87	87	86.5	98	98	85.5	85	85	85	85	85	82	85	85	82	85	4.	4.	4.	4.	84.5	4.	4.	4.	4.	4.	84
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## ALIGNMENTS

Immunogenic, Sp128; Sp130; pneumococcal, otitis media, nasopharyngeal, bronchial; lung; blood; infection; immune response; immunotherapy; antibacterial; auditory; vaccine. AAB48343 standard; Protein; 773 AA S. pneumoniae Sp130 polypeptide. 99US-0138453. 09-JUN-2000; 2000WO-US15925. 20-APR-2001 (first entry) Streptococcus pneumoniae. (MEDI-) MED IMMUNE INC Choi GH; WPI; 2001-112197/12. N-PSDB; AAC84742. WO200076540-A2. 10-JUN-1999; 21-DEC-2000. Adamou JE, AAB48343; AAB48343
IID AAB4
XX AAC AAB4
XXX XXX XXX
XXX CO-1
XXX Immn
XXX Immn
XXX Immn
XXX Immn
XXX ATL

New vaccines comprising Sp128 or Sp130 polypeptides, for treating and

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Fraser C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU01020 standard; Protein; 2140 AA.
         Page 41-42; 76pp; English.
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Matches 134; Conservative
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                                                                                                                                                                                                                                                      2120 AA;
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          Claim 2;
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                                                                                                from S. pneumoniae. Vaccines comprising the polypeptides are useful for the treatment and prevention of pneumococal infections, particularly infections caused by Streptococcus, such as otitis media, nasopharyngeal, bronchial, lung or blood infections. The antigens are used as immunogenic
                                                                                                                                                                                                                                                                                                                                  61 IEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDK 120
                                                                                                                                                                                                                                                                                                                                                                                     100 IEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDK 759
                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                agents to stimulate an immune response. The antisera and antibodies may also be used in diagnosing and treating pneumococcal infections. Recombinant polypeptides serve as a mechanism for stimulating production of antibodies for use in passive immunotherapy, diagnostic reagents, and as reagents in other processes such as affinity chromatography. The present sequence represents the S. pneumoniae Spilo polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae infection; immunogen; antigen; diagnosis; AIDS;
                                                                                      The invention relates to novel immunogenic polypeptides, Sp128 and Sp130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bacterial pneumonia; asplenia; heart disease; lung disease; alcoholism; kidney disease; diabetes; immunosuppressive disorder; otitis media; pneumococcal septicaemia; sinusitis; meningitis; therapy.
                                                                                                                                                                                                                                                                                                                    1 KEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKK
                                                                                                                                                                                                                                                                                            Gaps
preventing pneumococcal infections, particularly infections caused Streptococcus, e.g. otitis media, nasopharyngeal, bronchial, lung oblood infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcal proteins and polynucleotides useful for diagnosis, treatment and prophylaxis of bacterial infections
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                                                                                                                                                                                                                                                                Length 773;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY81710 standard; Protein; 2120 AA.
                                                            8; Page 51-54; 54pp; English
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99US-0125329.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                           773 AA;
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                                                                                                                                                                                                                                           Sequence
                                                            Claim
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This sequence represents a Streptococcus pneumoniae protein of the invention. The proteins (or their homologues, derivatives and/or fragments) are useful as immunogens or antigens. Immunogenic or antigenic compositions comprising the proteins are useful as vaccines and also in diagnostic assays. The sequences are useful for the detection or diagnostic assays. The sequences are useful for the detection or diagnostic assays. The sequences are useful for the detection or the function or expression of the protein or polypeptide are useful in the function. As the sequences can be used to treat S. pneumoniae infection, they can be used to treat bacterial pneumonia, which has high rates in young children, the elderly, and in patients with predisposing conditions or with immunosuppressive disorders, especially AIDS. They can also be used to treat pretences and kidney disease, diabetes, alcoholism, or with immunosuppressive disorders, especially AIDS. They can also be used to treat pneumococcal septicaemia, otitis media, sinustis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2013 IEEKKEEERNFTFDVSKKKONPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDK 2072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KEMSSTIVSBEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKK
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ear infection; antiinflammatory; antibacterial; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 696; DB 21;
100.0%; Pred. No. 1.3e-62;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  auditory, respiratory; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae type 4 strain.
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Streptococcus pneumoniae; epitope; vaccine; antigenic protein; antibacterial; Streptococcal infection; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S. pneumoniae SP043 protein sequence SEQ ID NO:68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP54590 standard; Protein; 117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JAN-2001; 2001US-0765272.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-SEP-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae.
                                                                                                                                                                                                    WPI; 1998-272224/24.
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(KUNS/) KUNSCH C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                            N-PSDB; AAV27357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2002061545-A1.
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                                                                31-OCT-1996;
                   30-OCT-1997;
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ABP54590
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                                                                          The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS56454. Also included are an antibody which binds one of the camposition), a kit comprising first and second primers, which are the nucleic acid cited above or fragments between nucleotides carried are nucleic acid cited above or fragments between nucleotides which are the nucleic acid cited above or fragments between nucleotides carget sequence contained within a Streptococcus nucleic acid sequence, where the first primer is substantially complementary to the target sequence and the second primer is substantially complementary to the complement of the target sequence, and where the parts of the primers complement of the target sequence, and where the parts of the primers of having substantial complementarity define the termini of the target sequence to be amplified, assay comprising contacting a test compound with the protein, and determining whether the test compound binds to the protein and a Streptococcus pneumoniae bacterium, where one or more genes encoding the proteins has been rendered inactive. The proteins, cuties media or ear infection. They are also useful in developing vaccines, otities media or ear infection. They are also useful in developing vaccines, otities media or ear infection. They are also useful in developing contactines, diagnostics and antibiotics. The methods are useful for the read and proteins. The methods are useful for the read and proteins. The methods are useful for the read and proteins. The method of the grant formation of the identified coding repeats the definition of the read of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae; antigen; vaccine; infection; diagnosis; detection; pneumonia; otitis media; meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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100.0%; Pred. No. 1.3e-62;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences
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                                           Claim 1; SEQ ID No 1180; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW55096 standard; Protein; 117 AA.
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Best Local Similarity 100.
Matches 134; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2140 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genomic sequence.
or ear infection
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AAW55096 RESULT

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The present sequence represents a protein from Streptococcus pneumoniae.

The nucleic acid sequence encoding the Streptococcus pneumoniae protein

can be useful in vaccines for inducing protective antibodies against
Streptococcus pneumoniae, for treatment or prevention of infection e.g.

are used to detect Streptococcus infection (by usual hybridisation or
amplification methods), also for isolating Streptococcus genes or their

allelic variants. The protein can be used similarly to detect specific
antibodies in standard immunoassays, especially for diagnosing or
monitoring infections. Antibodies which bind the protein are used to
detect corresponding antigens, to purify the protein and for passive
immunisation (optionally coupled to a toxin). Vaccines are administered,
e.g. by injection, orally or through the skin, typically at 0.01-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIESKKEEENKPTFDVSK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 YKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSK
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                                                                                                                                                                                                                                                                                                                                Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis
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                                                                                                                                              Kunsch CA;
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                                                                                                                                                  Johnson LS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 62; 118pp; English.
                                                                       (HUMA-) HUMAN GENOME SCI INC
96US-0029960.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 117; Conservative
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1.8

Gaps

25;

(BARA/) (DILL/) (DOUG/) (FANN/) ROSE/)

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PVFKKIEEKKEEENKPT-----FDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 EDFILPVYKGELEKGYQPDGW-----EISGFEGKKDAGYVI-----NLSKDTFIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 EDLDTPLSESRFSK--VPDGWVDEHRDEHDGHDVQEPSGEALDDHDEHDDHDDHEDEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum chromosome 2 related protein SEQ ID NO:135.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 564;
                                                                                                     Disclosure; SEQ ID NO 12723; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22;
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14.6%; Score 101.5; DE
Best Local Similarity 24.5%; Pred. No. 0.09;
Matches 34; Conservative 29; Mismatches
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194 EGTVEATVEATTEAT 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum
                                                                                                                                                                                                                                                                                                 (ABB57737-ABB72072).
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(CARU/) CARUCCI D.
(GARD/) GARDNER M.
                                                                                                                                                                                                                                                                                                                                                                                                    564 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 YKGELEKGYOFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSK 77
                                                                                                                                                                                                                                                                                                                                                                          ABQ84792 to ABQ84904 represents nucleic acids which encode the Streptococcus pneumoniae antigens given in ABB54557 to ABP54669. The S. pneumoniae antigens have antibacterial activity and can be used in vaccines. The S. pneumoniae antigens can also be used to prevent or attenuate a Streptococcal infection in an animal. The polynucleotides encoding the S. pneumoniae antigens can be used to detect Streptococcus nucleic acids. ABQ84905 to ABQ85130 represent primers used in the cloning of S. pneumoniae ORFs (open reading frames) which are used in an example from the present invention.
                                                                                                                             Fannon MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                      pneumoniae antigens, useful for detecting for preventing or attenuating disease caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match

88.4%; Score 615; DB 23; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.1e-56;
Matches 117; Conservative 0; Mismatches 0; Indels
                                                                                                                           Barash SC, Dillon PJ, Dougherty B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster polypeptide SEQ ID NO 12723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB61977 standard; Protein; 564 AA.
                                                                                                                                                                                                                                                                                                                                        Claim 11; Page 29; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                 Streptococcus infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster
BARASH S C.
DILLON P J.
DOUGHERTY B.
                                                                                                                           Kunsch CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-656860/75.
N-PSDB; ABL06080.
                                                                                                                                                                                         WPI; 2002-479261/51
                                                            FANNON M R.
                                                                                    ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                   New Streptococcus
Streptococcus and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 AA;
                                                                                                                                                                                                             N-PSDB; ABQ84825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200171042-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Venter JC,
                                                                                                                           Choi GH,
Rosen CA;
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RESULT 6

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N-PSDB; AAS80823.
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à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (I) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).

(I) and (II) are useful for the development of vaccines against cartibody raised to immunogens comprising the sequences of (I), are useful in frection. (I) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Purthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in P. falciparum. Sequencing of the Plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand our understanding of parasitic bilecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AMATORIS to AMATORIS and AMATORIS and AMATORIS cepresent mucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                              71 PTFD----VSKKKDNPQVNHSQLNESHRKEDLQR-EEHSQKSDSTKDVTATVLDKNNISS 125
                                                                                                                                                                                                                                                                                                    and protein sequences given in the present invention, but which are not specifically mentioned within the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                          23 EKGYQFDGWEI--SGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKE-----EENK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 KSDDHKVEENKKSDDHKVEENKKSDDHKIEEVKKVEEHEEDEEE------DKKEKKS
                                                                                                                                                                                                                                                                                                                                                                    Query Match
14.1%; Score 98; DB 21; Length 665;
Best Local Similarity 27.1%; Pred. No. 0.26;
Matches 35; Conservative 23; Mismatches 29; Indels 42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy; forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder.
              Disclosure; Page 321-322; 577pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human diagnostic protein #16627.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 KSTTNNPNK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENKOKDENK 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                             665 AA;
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                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
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The invention is gradued to instruct of the invention probes, polymerase chain reaction (FCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymerleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques for identifying expressed genes. (I) is useful in gene therapy techniques correstore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymuclectide sequences have applications in tesponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human can approach this parent disorders the sequence of the this parent dispersion, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48 LSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQRE----E 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 13.3%; Score 92.5; DB 22; Length 2519; Sest Local Similarity 31.0%; Pred. No. 5.9; Aatches 22; Conservative 19; Mismatches 17; Indels 13;
                                                                                                                                                                                                                                                                                   The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana protein fragment SEQ ID NO: 60255.
                                                                                                                                                                                                     Claim 20; SEQ ID No 46995; 103pp; English.
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99US-0123180.
99US-0123548.
99US-0125788.
99US-0126264.
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741 KEEKKEPKKEV 751
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
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99US-0152363.
99US-0153070.
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99US-0154018.
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99US-0151080.
99US-0151303.
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99US-0157753.
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99US-0158029.
99US-0158232.
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13-SEP-1999;
15-SEP-1999;
16-SEP-1999;
20-SEP-1999;
22-SEP-1999;
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04-AUG-1999;
04-AUG-1999;
05-AUG-1999;
99US-0126785.
99US-0128134.
99US-0128134.
99US-0128134.
99US-0130404.
99US-0131449.
99US-0131449.
99US-0132484.
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99US-0132486.
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990S-0135353.
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990S-0136021.
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990S-0137722.
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24-NOV-1999;
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                                                                                                                                                                                                                                                             -----PQVNHSQLNE-----SHRKEDLQREEHS 104
                                                                                                                                                                                                                                                                                                                                                                                                                           Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
                                                                                                                                                                                                                                                     18 YKGELEKGYQFDGWEISGFE-----GKKDAGYVINLSKDTFIKPVFKKIEEKKEEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                    otitis media; erythema nodosum; pharyngitis;
                                                                                                                                                                                                                                      34;
                                                                                                                                                                                                                        Length 484;
                                                                                                                                                                                                                       13.1%; Score 91; DB 21; Length 48
19.3%; Pred. No. 0.89;
tive 29; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Chlamydia pneumoniae transmembrane protein sequence.
                                                                                                                                                                                                                                                                                                                        233 RDQEGVKKTEAKDKDRNKEKKEEKTESINK 262
                                                                                                                                                                                                                                                                                                               OKSDSTKDVTATVLDKNNISSKSTTNNPNK 134
                                                                                                                                                                                                                                                                                                                                                                   AAY35091 standard; Protein; 511 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccine; neutralising epitope.
                                               99US-0159637.
99US-0159584.
99US-0159584.
99US-0160741.
99US-0160767.
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99US-0161404.
99US-0161405.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     sinusitis; purulent
                                                                                                                                                                                                                               Local Similarity
nes 29; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                frames in the complete genome (see AXX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent ottiis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AXX4584-Y35879) can be used infmunospanic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
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to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primary nucleotide sequence of the shrimp white spot Bacilliform (WSBV), useful for producing viral polypeptides that can be used screen for agents that are useful for treating WSBV infection -
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(THIR-) THIRD INST OCEANOGRAPHY STATE OCEANI C A.
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17; Mismatches
                                                                                                                                                                                                                                                                Page 975-976; Disclosure; 1912pp; English
                                                                                                                                       Genome sequence of Chlamydia pneumoniae
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N-PSDB; AAH62788.
WPI; 1999-357842/30.
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comprising modifying

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cells in which both alleles of a gene are modified,
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11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                 225 AA;
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                  The invention provides the primary nucleotide sequence of the WSBV genome (AAH62689), predicted transcript sequences (AAH62689-AAH62839) and encoded proteins (AAG84910-AAG88051) and oligonucleotide sequences (AAH62840-63160) suitable for use as primars or probes. The nucleic acid molecules and proteins of the invention are useful for diagnosis and monitoring viral infection, in screens for antiviral agents and for monitoring viral gene expression or activity during a treatment regimen. The nucleic acid molecules are also useful as antisense constructs to control viral gene expression in infected cells and tissues and to create transgenic viral resistant shrimp.
                                                                                                                                                                                                                                                                                       EKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNN 122
                                                                                                                                                                                                                                                               621 SNVEEEEE------EEEQMEEEEEEVEREGGSDKEDDGDA------PAQBEME 662
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                                                                                                                                                                                                                                       5 STIVSEEDFILPVYKGELEKGYQFDGWEISGFEG--KKDAGYVINLSKDTFIKPVFKKIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fungus, yeast; tetracyclin; promoter; GRACE strain; biosynthesis; signal transduction; DNA replication; cell division; growth; proliferation; Candida albicans; fungicide; antifungal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Constructing strains for identifying gene products as effective for therapeutic intervention, by inactivating in the strain one of a gene and placing other allele of the gene under conditional
                                                                                                                                                                                       Length 1141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Candida albicans essential protein SEQ ID NO 7829.
                                                                                                                                                                                    Query Match 12.7%; Score 88.5; DB 22;
Best Local Similarity 23.3%; Pred. No. 5.2;
Matches 30; Conservative 31; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                               ABP73992 standard; Protein; 225 AA.
Claim 1; Figure 3; 626pp; English.
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20-FEB-2001; 2001US-0792024.
22-AUG-2001; 2001US-314050P.
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                                                                                                                                                                                                                                                                                                                                         123 ISSKSTTNN 131
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N-PSDB; ABZ32542.
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                                                                                                                                                              1141 AA;
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expression
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certs in which both alters of a gene and another, completely modified to a spressible selectable marker and modifying other allele by expressible selectable marker and modifying other allele by concert so that expression of the second allele is regulated by the promoter replacement fragment with a heterologous promoter, so that expression of the second allele is regulated by the promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles modified are useful for identifying a gene that cells in which both alleles modified are useful for identifying a gene that contributes to the survival or growth of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent, an antifungal agent that inhibits the growth of a diploid fungus or and for identifying a therapeutic agent for treatment of a mammalian disease. (M1) is useful for identifying a compound which modulates the activity of a gene product, preferably enzymatic activity, carbon compound catabolism, biosynthetic, transporter, transcriptional, compound catabolism, biosynthetic, identifying a compound having the ability to inhibit growth or proliferation of C. albicans cells and for treating infection by C. albicans. The present sequence is that of an essential candida albicans protein used in the method of the invention. Note: The sequence data for this parent is not represented in the printed to perwent by the compound or sequence information supplied to Derwent by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 YDDDDEFEGFESSNGAAKELNLSESQAIKEWKQRRDLEIEEREKLNSKKKEEIIEKAKS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 YQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKK----IEEKKEEENKPTFDVSKKK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; primer; detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --DNPQVNHSQLNESHRKEDLQREEH---SQKSDSTKDVTATVLDKNN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 TIDDFYENYNSKRDNHQKEILSEQEKFISKRDDFLK--RGTLWDRVN 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 88, DB 23, Length 225, Pred. No. 0.64, 22; Mismatches 43; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saito K, Ya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nishikawa T, Hayashi K, S
T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human protein sequence SEQ ID NO:15383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB94584 standard; Protein; 258 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.6%;
28.0%;
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The present invention describes primer sets for synthesising 5602 (ull-length cDNAs defined in the specification. Where a primer set comptrises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide comprises a 1'-end sequence complementary to a complucation of the 5'-end sequence/3'-end sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the protains encoded by the full-length cDNAs. The primers are also useful for the the full-length without any specialised methods. AA403166 to AA413328 and AA413333 to AA413742 represent human cDNA sequences; AAB92446 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB95893 represent human amino acid sequences, and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 YKGELEKGYQFDGWEISGFEGKKDAGY--VINLSKDTFIKPVFKKIEEKKEEENKPTFDV 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 SKKKDNPQ-----VNHSQLNESHRKEDLQREEHSQKSDSTKDVTATV--LDKNNISSK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 WEGEDEDUVENWEDDEDDEKKEEAEVKPEVKISEK---KKIAEKIKEKERERQOKKRQEEI
Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the

    epidermidis open reading frame protein sequence SEQ ID NO:652.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.6%; Score 88; DB 22; Length 258; 26.3%; Pred. No. 0.77; ive 25; Mismatches 50; Indels
                                                                                                           Claim 8; SEQ ID 15383; 2537pp + CD ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG81779 standard; Protein; 746 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-NOV-2000; 2000WO-US30782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-316495/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258 AA;
                                                                 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200134809-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kimmerly WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-MAY-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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AAG81779
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611 SGTKVLPHSKVMLMTDGELTMP-DMTGWTKEDVLAFEDLTKLKVSTKGNGFVTNQSISKG 669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
                                                                                                                                                      (II), given in AAG8149 to AAG8120, from Staphylococcus pridermidis.

(I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAHS3971 to AAHS5090 represent specifically claimed S. epidermidis genomic DNA polymucleotide sequences from the present invention. AAHS5031 to AAHS5098 represent oligonucleotide sequences and primers which are used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
                                                                                                                                                                                                                                                                                                                                                                                                                                                        N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to
                                                                                                                                           AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 SSTIVSEEDFILPVYKGELEKGYQFDGW---EISGFE-----GKKDAGYVIN--LSKD
                                Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3868.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 12.6%; Score 88; DB 22; Length 746; Local Similarity 25.7%; Pred. No. 3.3; Conservative 21; Mismatches 50; Indels 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             no sequences are present for SEQ ID NO:4455 to 4464
                                                                                                                                                                                                                                                                                                                                                                                                                                         in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 DSTKDVTATVLDKNNISSKSTTNN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           717 SSTKN-----DKSNADSKNDSDD 734
                                                                                               Claim 18; Page 208; 2188pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP39023 standard; Protein; 778 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibacterial, gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-064964P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         746 AA;
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08-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Matches
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05-FEB-2001; 2001WO-US04098
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                                                                       WPI; 2001-476283/51.
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                817 AA;
(HYSE-) HYSEQ INC.
                                                                                     N-PSDB; AAK52451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM79319;
                                                                                                                                                                                                                                                                                                                                                               Sequence
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                       Α,
                                                 Xue AJ,
                        Tang
Zhao (
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AAM79319
                                                                                                                                                                                                                                                                                                                                                                                                               Matches
셤
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                                                                                                                                                                                                                                                                                                                                                                                                                 ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds abla to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                         643 SGTKVLPHSKVMLMTDGELTMP-DMTGWTKEDVLAFEDLTKIKVSTKGNGFVTNQSISKG 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                            Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                          36;
                                                                                                                                                                                                                                                                                                  DB 23; Length 778;
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                                                                                                                                                                                                                                                                                                                                                   4 SSTIVSEEDFILPVYKGELEKGYOFDGW---EISGFE---
                                                                                                                                                                                                                                                                                                  Query Match 12.6%; Score 88; DB 2
Best Local Similarity 25.7%; Pred. No. 3.5;
Matches 37; Conservative 21; Mismatches
                                                                                                  Disclosure, SEQ ID 3868; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSTKN-----DKSNADSKNDSDD 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 DSTKDVTATVLDKNNISSKSTTNN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM79318 standard; Protein; 817 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human protein SEQ ID NO 2964.
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2000US-0654936.
2000US-0663561.
2000US-0693325.
2000US-0728422.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
Bush
                       WPI; 2002-381255/41.
N-PSDB; ABN91568.
Doucette-Stamm LA,
                                                                                                                                                                                                                                                                            778 AA;
                                                                                                                                                                                                                                                   USPTO web site.
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27-APR-2000;
20-JUN-2000;
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20-OCT-2000;
30-NOV-2000;
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAW7832-AAM89302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 -KKDNPQVNHSQLNESHRKED-----LQREEHSQKSDSTKDVTATVLDKNNISSKST 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      256 WKQDTPKSKAGYVQEEHKKQETPKLWPVQLQKEQ-DPKKQTPKSWTPSMQSEQNTTKSWT 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 GELEKGYQFDGWEISG--PEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ma
                                                                                                                                                                                             Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene.therapy -
C, Cao Y,
Wang ZW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 12.6%; Score 88; DB 22; Length 817; 1 Similarity 27.3%; Pred. No. 3.7; 33; Conservative 21; Mismatches 55; Indels
     Chen
     Zhou
Liu C, Drmanac RT, Asundi V, Zhou
Wang D, Wang J, Zhang J, Ren F,
Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                    Claim 20; Page 215; 6221pp; English
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27-APR-2000; 2000US-0560875.
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :::|: | ::|: | :: | | | | | ::| | | | ::| ::| :: | ::| ::| :: | ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ABB57137-ABB72072). The sequent did not form part of the printed The sequence data for this patent did not format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46 INLSKDTFIKPVFKKIEE-KKEEENKPTFDVSKKKDN--------PQVNHSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 LEEMIREYDLDQDNHINFEEFTNMMTTQQDLLKNIYSLLDKDNEGAITSK 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 21276; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 12.5%; Score 87; DB 22; Length 281; Best Local Similarity 21.2%; Pred. No. 1.1; Matches 36; Conservative 32; Mismatches 56; Indels '
                                                                                                                                                                                                                                                           Myers EW;
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                                                                                                                                                                                                                                                           PWD,
                           23-MAR-2001; 2001WO-US09231.
                                                                                           23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                           Venter JC, 'Adams M,
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                                                                                                                                                                                          (PEKE ) PE CORP NY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoded polypeptides (AAM'9333-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, eg. stem cell growth factor activity, nemantopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 -KXDNPQVNHSQLNESHRKED-----LQREEHSQKSDSTKDVTATVLDKNNISSKST 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256 WKQDTPKSKAGYVQEEHKKQETPKLWPVQLQKEQ-DPKKQTPKSWTPSMQSEQNTTKSWT 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.

Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 366 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to polynucleotides (AAK51456-AAK53435) and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy
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                                                                                                                                                                                                                                                                                             C, Cao Y,
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                                                                                                                                                                                                                                                                                      Liu C, Drmanac RT, Asundi V, Zhou P, Xu
Wang D, Wang J, Zhang J, Ren F, Chen R;
Yang Y, Wejhrman T, Goodrich R;
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                              19-JUL-2000; 2000US-0620325.
01-SEP-2000; 2000US-0654336.
15-SEP-2000; 2000US-0653561.
20-OCT-2000; 2000US-053325.
30-NOV-2000; 2000US-0728422.
   2000US-0598075
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N-PSDB; AAK52452.
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20-JUN-2000;
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                                                                                                                                                                                                                                                                                             Tang YT,
Zhao QA,
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Matches

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RESULT 18 **ABB6482**8

45

46; Gaps

88

Venter JC;

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by chromosome 2 of the human malarial parasite, Plasmodium falciparum.

Also described are: (1) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).

(I) and (II) are useful for the development of vaccines against P. falciparum infection. (I) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are riffns or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify arug resistance in P. falciparum. Sequencing of the Plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasite lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            parts of the world, and there is a pressing need for vaccines and new hungs. AAA70078 to AAA70287 and AAAB18144 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202 LQKKYNIQDDEEEDNETIRSDSKIRDIYSDSQSKDIMMSSSPNKEEES-----MSSDNHN 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 LEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDN 81
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                                                                                                                                                                                                                                                                                   Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the
                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes proteins and their fragments (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum chromosome 2 related protein SEQ ID NO:29.
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                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Page 85-86; 577pp; English.
                                                                                                                                                                                                                                                                                                                                     diagnosis of P.falciparum infection
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                      98US-0107131
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                                                                HOFFMAN S.
CARUCCI D.
GARDNER M.
                                                                                                                                           VENTER J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   635 AA;
                   05-NOV-1998;
                                                                                                                                                                                     Hoffman S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB18172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                   (HOFF/)
                                                                                         (CARU/)
(GARD/)
                                                                                                                                           (VENT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 21
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임
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SXEXEXEXEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypucleotide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervopathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, anchritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 SKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSD 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         373 SPDNCCNELFKKKKKKEEEEKKKKEEEEEKKRRRRRKEKREKREEKRREEKRREK 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                            Ren F, Wang D;
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum chromosome 2 related protein SEQ ID NO:33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22; Length 607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28; Indels
                                                                                                                                                                                                                                                                                                            Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                            Asundi V, Chen R, Ma Y,
Wehrman T, Xu C, Xue AJ,
Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 12.5%; Score 87; DB 2;
Best Local Similarity 33.3%; Pred. No. 3.2;
Matches 20; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; SEQ ID NO 3095; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB18176 standard; Protein; 635 AA
                                                                   2000US-0552317.
2000US-0598042.
2000US-0620312.
                                                                                                                                        03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0662191.
19-OCT-2000; 2000US-0693036.
29-NOV-2000; 2000US-0727344.
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26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                           2001-442253/47.
                                                                                                                                                                                                                                                                                                            Liu C, //
Wang Z, //
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   607 AA;
                                                                                                                                                                                                                                                               (HYSE-) HYSEO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAIS9106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200025728-A2
                                                                   25-APR-2000; 209-JUL-2000; 219-JUL-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-NOV-1999;
                                                                                                                                                                                                                                                                                                            Tang YT,
Wang J, 1
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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Human sodium channel 8A (SCN8A) protein sequence.
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AAO14927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (1) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).

(I) and (II) are useful for the development of vaccines against P. falciparum infection. (I) and polyclonal antisers or a monoclonal meful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum. C. infection, or they can be used to identify drug resistance in P. falciparum. Sequencing of the Plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasite biology, a process hampered by the complexity of the parasitic lifesycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito are resistance to insecticides have led to a resurgence to gmalaria in many carrent of the complexity of the parasite resistance to drugs and mosquito are resistance to insecticides have led to a resurgence of malaria in many carrent of the complexity of the parasite resistance to drugs and mosquito are resurgence of malaria in many carrents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1977 ENERGDEKDGYEEMNGGDKNEEMNGGDKNEEMNVGDKNGG--IN------EE 2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 KK----EEENKPTFDVSKKKDNPQVN----HSQLNESHRKEDLQ------REEH---- 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein sequences given in the present invention, but which are not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELEKGYQFDGW------EISGFE-----GKKDAGYVINLSKDTFIKPVFKKIEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57; Gaps
                                                                                                                                                                                                                                                                                                                                                                                          Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.4%; Score 86.5; DB 21; Length 2485; 23.8%; Pred. No. 24; ive 27; Mismatches 31; Indels 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specifically mentioned within the specification
                                                                                                                                                                                                                                                                                                        Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2080 INEEHKNEGINKCIYHMMKNNISNENNYND 2110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 ---SQKSDSTKDVTATVLDKNNISSKSTTNN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 75-82; 577pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB23563 standard; Protein; 1980 AA.
                                                                                                                                                                                                                                                                                                        Gardner M,
                                                                                                           99WO-US26796
                                                                                                                                                 98US-0107131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 23.8
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                        Hoffman S, Carucci D,
                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-365347/31
                                                                                                                                                                                             HOFFMAN S.
CARUCCI D.
GARDNER M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2485 AA;
                                                                                                                                                                                                                                                             (VENT/) VENTER J C.
                    WO200025728-A2
                                                                                                        05-NOV-1999;
                                                                                                                                                    05-NOV-1998;
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                                                               11-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21
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                                                                                                                                                                                               (HOFF/)
                                                                                                                                                                                                                    (CARU/)
(GARD/)
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invention also provides the SCN8A encoding gene sequence and an antibody against the sodium channel. The SCN8A protein alpha subunit and its encoding cDNA can be used in the elucidation of the physiological mechanisms of excitatory cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; sodium channel subunit; SCN12A; SCN12A-e; SCN8A;
human nervous system; chromosome 12q13.1; excitatory cell;
drug development; familial hyperglycaemia; QT extending syndrome type 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 QFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents the human sodium channel SCN8A protein. The
                                                                                                                                                                                                                                                                                                                                      New sodium channel SCN8A useful for the elucidation physiological mechanism participated by excitatory cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1049 TGA-DIHRNGDFQKNGNGTTSGIGSSVEKYIIDEDHM---SFINNPN 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.4%; Score 86; DB 21; Length 1980; 26.2%; Pred. No. 20; vative 23; Mismatches 48; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87 SQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPN 133
Sodium channel 8A; SCN8A; human; excitatory cell.
                                                                                                                                                                                                                                    (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 5-12; 14pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA014927 standard; Protein; 1980 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human sodium channel subunit SCN8A.
                                                                                                                                                                                               99JP-0004645.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAY-2000; 2000JP-0152085.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 26.2%
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  motor endplate disease.
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                                                                                                                                                                                                                                                                            WPI; 2000-545978/50.
N-PSDB; AAA93791.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1980 AA;
                                                                            JP2000201684-A.
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                                                                                                                                                                                               11-JAN-1999;
                                                                                                                                                         11-JAN-1999;
                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                    25-JUL-2000.
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25-MAR-1999;
29-MAR-1999;
01-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 QFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNH 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
                                                                                                                                  Sodium channel alpha subunits SCN12A and SCN8A of human nervous stogether with splicing variants, useful in studying physiological mechanism relating to excitatory cells and in drug development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 12.4%; Score 86; DB 23; Length 1980; Best Local Similarity 26.2%; Pred. No. 20; Matches 28; Conservative 23; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 SQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPN 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Candida albicans essential protein SEQ ID NO 7212.
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                                                                                                                                                                                                                                                                              Claim 3; Page 97-110; 118pp; Japanese.
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20-FEB-2001; 2001US-0792024.
22-AUG-2001; 2001US-314050P.
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                                WPI; 2002-393394/42.
N-PSDB; AAL42751.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1980 AA;
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combination, of a promoter replacement fragment with a heterologous promoter. (MI) is useful for constructing a strain of diploid fungal cells in which both alleles of a gene are modified. The diploid fungal cells in which both alleles modified are useful for identifying a gene that cells having both alleles modified are useful for identifying a gene that is essential to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent that inhibits the growth of a diploid fungus of an entifungal agent that inhibits the growth of a diploid fungus of an entifungal agent that inhibits the growth of a diploid fungus of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent that inhibits the growth of a diploid fungus of a gene product, preferably enzymatic activity, carbon disease. (MI) is useful for identifying a compound which modulates the activity of a gene product, preferably enzymatic activity, carbon compound catabolism, biosynthetic, transporter, transcriptional, transduction, DNA replication and cell division activity. The method is useful for identifying a compound having the ability to inhibit growth or proliferation of C. albicans cells and for treating infection by C. albicans. The present sequence is that of an essential Candida albicans protein used in the method of the invention. Note: The sequence data for this patent is not represented in the printed to berwent by the property of a process of the invention.
                                                                             The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 SGFEGKKDAGYVINLSKDTFIKPVFKKIE---EKKEEENKPTFDVSK--KKDNPQVNHSQ 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 SGQEVIONITNQTSELSKEEKLRKRREQLELWRQKKQQQQQEQEEVQNKAKKTEDSTNNTS 73
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Claim 44; SEQ ID NO 7212; 167pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                     / Match 12.2%; Score 85; DB 21; Length 329;
Local Similarity 23.8%; Pred. No. 2.2;
Nes 24; Conservative 22; Mismatches 33; Indels 22; Gaps
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99US-0129845.
99US-0130077.
99US-0130449.
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  99US-0159330
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          14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
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23-APR-1999;
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09-MAR-1999;
23-MAR-1999;
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29-MAR-1999;
01-APR-1999;
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Matches
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AAG08294
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990S - 0145218.
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990S - 0145919.
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9905 - 0148131
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9905 - 014864
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99US-0156596.
99US-0157117.
99US-0157753.
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99US-0159329.
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99US-0154018
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99US-0154779
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                                                                                       -JUL-1999;
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5-OCT-1999;
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16 PVYKGELEKGYQFDGWEISGFEGKXDAGYVINLSKDTFIKPVFKKIEBKKEEENKPTFDV 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                              Gaps
                                                           22;
Match 12.2%; Score 85; DB 21; Length 339; Local Similarity 23.8%; Pred. No. 2.3; es 24; Conservative 22; Mismatches 33; Indels
                                                                                                                                                                                                                                                        76 SKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTAT 116
                                                                                                                                                                                                                                                                                             268 SNEEDEEE-----EEEEKQDMSEEDDKEEEDEQEEEEKT 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana protein fragment SEQ ID NO: 5773.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG08294 standard; Protein; 358 AA
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99US - 0144814.
99US - 0145086.
99US - 0145088.
99US - 0145087.
99US - 0145087.
99US - 0145145.
99US - 0145145.
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99US-0145276.
99US-0145913.
99US-0145918.
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99US-0151438.
99US-0151930.
99US-0152363.
99US-0153070.
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99US-0146388.
99US-0146389.
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99US-0149930.
99US-0150566.
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99US-0151065.
99US-0151066.
99US-0151080.
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99US-015139.
99US-015139.
99US-0155486.
99US-0155486.
99US-0155659.
99US-0157753.
99US-0157763.
99US-0157763.
99US-0157865.
99US-0157865.
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99US-0147204
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99US-0147260
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99US-0147935
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99US-0148684
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99US-0149722
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99US-0149929
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01-SEP-1999;
07-SEP-1999;
10-SEP-1999;
13-SEP-1999;
16-SEP-1999;
16-SEP-1999;
20-SEP-1999;
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05-AUG-1999;
05-AUG-1999;
06-AUG-1999;
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11-AUG-1999
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99US-0139457.
99US-0139458.
99US-0139458.
99US-0139461.
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99US-0139461.
99US-0139463.
99US-013989.
99US-0140354.
99US-0140391.
99US-0140391.
99US-0142390.
99US-0142390.
99US-0142390.
99US-0142363.
99US-0130891.
99US-0131449.
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99US-0135124.
99US-0135629.
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99US-0139452.
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99US-0144325.
99US-0144331.
99US-0144333.
99US-0144334.
99US-0144335.
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Gaps

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61 IEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQ-----REEHSQKSDS--- 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.

(II) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) wis the production of vectors containing them which are used to produce hosts cells which express the polypeptides. (II) (and/or nucleic acids) may then be polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55091 to
                                                                                                                                                                                                                                                                      3 MEENKNQPNKE--NMSNKDDNA----THINDSHRNEDLELFRRNKNARQRRRRRIDNQSK 56
             antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life (CC) or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S. epidermidis open reading frame protein sequence SEQ ID NO:658.
 The S. epidermidis sequences have
                                                                                                                                                                                    12.2%; Score 85; DB 23; Length 465;
32.6%; Pred. No. 3.5;
ive 15; Mismatches '21; Indels 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis.
                                                                                                                                                                                                                                                                                                                 TKDVTAT-----VLDKNNISSKSTTNNPNK 134
                                                                                                                                                                                                                                                                                                                                             57 EKDATSTOSOLETKPMDKFIDNHKS--HNONK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 18; Page 210; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                          AAG81782 standard; Protein; 472
 given in ABP35124 to ABP37960.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus epidermidis
                                                                                                                                                                                                                   30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-316495/33.
                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                        465 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAH52632
                                                                                                                           USPTO web site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200134809-A2.
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                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences
                                                                                                                                                                                                                                                                                                                                                                                                             16 PVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDV
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3856.
                                                                                                                                                                                                                                                                                                                                                                            22;
                                                                                                                                                                                                                                                                                                                                                Length 358;
                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTAT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | ::| : | :: | :: | SNEEDEEEEEET 320
                                                                                                                                                                                                                                                                                                                                                                              33;
                                                                                                                                                                                                                                                                                                                                            12.2%; Score 85; DB 21;
llarity 23.8%; Pred. No. 2.5;
Conservative 22; Mismatches 33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP39011 standard; Protein; 465 AA
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                                                                                       99US-0160814.
99US-0160815.
99US-0160980.
99US-0160981.
99US-0159638.
99US-0159584.
99US-0160741.
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99US-0160768.
99US-0160770.
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99US-0161404.
99US-0161405.
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99US-0161360.
99US-0161361.
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99US-0161992.
99US-0161993.
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N-PSDB; ABN91556.
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                                                                                                                                                                                                                                                                                                                                                          Local Similarity
hes 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US6380370-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      287
                                                                                                                                                                                                                                                                                                                                                Query Match
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CCCXXXLLXXBXLXBXLXBXBXBXXXXXXXXXXXXXXCCCC
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AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.

(I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the september of the polypeptides (II) was the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to raise antibodies against the bacteria activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent expecifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55091 to the present invention. AAH55091 to the present invention.
                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                        61 IEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQ------REEHSQKSDS--- 109
                                                                                                                                                                                                                                                                                                      3 MEENKNQPNKE--NMSNKDDNA----THLNDSHRNEDLELFRRNKNARQRRRRRIDNQSK 56
                  in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4465 to 4464.
AAH55098 represent oligonucleotide sequences and primers which are used
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptides from Staphylococcus epidermidis, against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epidermidis open reading frame protein sequence SEQ ID NO:2058.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   epidermidis SR1 strain; infection; diagnosis;
                                                                                                                                                                                            12.2%; Score 85; DB 22; Length 472; 32.6%; Pred. No. 3.6;
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                       110 TKDVTAT-----VLDKNNISSKSTTNNPNK 134
                                                                                                                                                                                                                                                                                                                                                                                             86
                                                                                                                                                                                                                                   30; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             Claim 18; Page 558; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG82482 standard; Protein; 720 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0164258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccination; endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding useful for vaccinating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-316495/33.
                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAH53332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200134809-A2
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                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG82482;
                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to sorten for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed
N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4455 to 4472,
                                                                                                                                                                                                                                               38 LEBEGIKALDKKFKASQAKDTNKQNTQNNHQKSNNKQNSNDKEKQQSKNNSKPTKKKEQN 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printer specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid encoding a Staphylococcus epidermidis
polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4968
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                                                                                                                                           DB 22; Length 720;
                                                                                                                                                                            36; Indels
                                                                                                                                                          6.4;
                                                                                                                                                                              15; Mismatches
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                                                                                                                                           Score 85;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 85;
Pred. No.
                                                                                                                                                                                                                                                                                                        113 VTATVLDKNNISSKSTTNNPNK 134
                                                                                                                                                                                                                                                                                                                                                                                                            ABP40123 standard; Protein; 728 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.2%;
28.0%;
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28.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus epidermidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibacterial, gene therapy
                                                                                                                                                            Best Local Similarity 28.0%
Matches 23; Conservative
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Best Local Similarity
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                                                                                                            720 AA;
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The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (I) incleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).

(I) and (II) are useful for the development of vaccines against P. falciparum infection. (I) and polyclonal antisera or a monoclonal entibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in P. falciparum. Sequencing of the Plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito are the world and those is a prosest in many are of the world and the parasitic process.
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                                                                 61 IEEKKEEENKPTFDVSKKKD----NPQVNHSQLNESHRKEDLQREEHSQKSDSTK----D 112
                                                                                                            : | | : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine;
   8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum chromosome 2 related protein SEQ ID NO:125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antimalarial; malaria; protozoacide; infection; insecticide
36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             specifically mentioned within the specification
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Mismatches
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                                                                                                                                                                                                      113 VTATVLDKNNISSKSTTNNPNK 134
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15;
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23; Conservative
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CARUCCI D.
GARDNER M.
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Matches
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                                                                                 stroke and brain
                                                                97
                                                              38 GKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein in tissues. The antibodies can also be used to isolate the protein. The protein is used as a therapeutic target for compounds to treat disorders of the nervous system, such as epilepsy, stroke and br injury, diabetic neuropathy, and AIDS-associated neuropathy, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 QFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNH
                                                                                                                                                                                                                                                                                                                                                                         Tetrodotoxin-sensitive sodium channel; rat; PN4 sodium channel; strok nervous system disorder; epilepsy; brain injury; diabetic neuropathy; AIDS-associated neuropathy; therapy.
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- for detecting inhibitors which alleviate pain, and treating
nervous system disorders, e.g. epilepsy, stroke, diabetic and
21; Length 1166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 19; Length 1978; 26;
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                                                                                                                            98 L--QREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPN
                                                                                                                                                           656 KNDÓEEKNDÓEEKNDKEEKNDKEEKNDOEKKNDOEEKN
Score 85; DB 2
Pred. No. 12;
16; Mismatches
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                                                                                                                                                                                                                                            AAW69361 standard; Protein; 1978 AA
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                           ,16;
12.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 25.23
Matches 27; Conservative
                                Conservative
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N-PSDB; AAV58420.
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               Best Local Similarity
Matches 28; Conserv
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 Query Match
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RESULT 34 AAW69362

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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 548 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a binds to biological sample. (I) is are used to determine whether a compound binds to biological sample. (I) is used to determine whether a compound binds to used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                         Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 EGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKE 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.1%; Score 84.5; DB 23; Length 157; 26.2%; Pred. No. 0.9; tive 23; Mismatches 31; Indels 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Masignani V, Margarit Ros YI,
                                              Streptococcus polypeptide SEQ ID NO 8632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 3975; 4525pp; English
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                                                                                                                                                                                                                                                                                                                                                                           27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
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  02-JUL-2002 (first entry)
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                                                                                                                                                                                          Streptococcus agalactiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
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N-PSDB; ABN70359.
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Best Local Similarity
Matches 21; Conserv
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                                                                                                                                                                                                                                                                                    02-MAY-2002
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ABP26418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence is encoded by the rat PN4 sodium channel cDNA clone of the invention. The DNA sequence was isolated from a peripheral nerve from a rat dorsal ganglia. The PN4 sodium channel sequences are tetrodoctoxin-sensitive sodium channels. The protein is used in assays for detecting inhibitors of tetrodoctoxin-sensitive sodium channels, which alleviate pain. The probes can be used to detect and isolate the DNA or protein in tissues. The antibodies can also be used to isolate the protein. The protein is used as a therapeutic target for compounds to treat disorders of the nervous system, such as epilepsy, stroke and brain injury, diabetic neuropathy, and AIDS-associated neuropathy, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86
                                                                                                                                                                                                                                                                                                                           Tetrodotoxin-sensitive sodium channel; rat; PN4 sodium channel; stroke; nervous system disorder; epilepsy; brain injury; diabetic neuropathy; AIDS-associated neuropathy; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 QFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New rat tetrodotoxin-sensitive sodium channel alpha subunit and DNI - for detecting inhibitors which alleviate pain, and treating nervous system disorders, e.g. epilepsy, stroke, diabetic and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dietrich PS, Fish LM, Herman RC, Sangameswaran L;
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1047 TGV-DIHRNGDFOKNGNGTTSGIGSSVEKYIIDEDHM---SFINNPN 1089
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                                                                                                                                                                                                                                                                                         Tetrodotoxin-sensitive sodium channel PN4a.
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                                                                                                                                               AAW69362 standard; Protein; 1988
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18-JUN-1999;
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AAG35428;
streptococcus/GBS (Streptococcus agalactise) or group A streptococcus/GBS (Streptococcus/GBS (Streptococcus/GBS (Streptococcus/GBS (Streptococcus/GBS (Streptococcus/GBS (Streptococcus/GBS (Streptococcus)). Given in the proteins have antibacterial and antiinflammatory activity. (1), nucleic acids encoding (1), ABN66044-ABN71526 and antibodies that bind (1) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactise and S. pyrogenes. Nucleic acids encoding (1) are used to detect Streptococcus in a compound binds to (1). A composition composition. The disease caused by cused as avaccine or diagnostic composition. The disease caused by C. Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (1) may be used to recombinantly produce (1) and may be used in gene therapy. Antibodies to (1) are used for affinity contractory immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 12.1%; Score 84.5; DB 23; Length 161;
Best Local Similarity 26.2%; Pred. No. 0.94;
Matches 21; Conservative 23; Mismatches 31; Indels 5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a protein (ABP25413-ABP30895) from group B
                                                                                                                                                                                                                                                                                                                                                                                                     Masignani V, Margarit Ros YI, Grandi G, Fraser C;
                                                 Streptococcus polypeptide SEQ ID NO 2012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 3351; 4525pp; English.
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24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
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                 (first entry)
                                                                                                                                                 Streptococcus agalactiae.
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(GENO-) INST GENOMIC RES.
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N-PSDB; ABN67049.
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                 02-JUL-2002
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Protein identification, signal transduction pathway, metabolic pathway, hybridisation assay, genetic mapping, gene expression control; promoter;
                            Zea mays protein fragment SEQ ID NO: 43275.
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99US-0123180.
99US-0123548.
99US-0126264.
99US-0126264.
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99US-0128234.
99US-0128714.
99US-0129845.
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990S-0130449.
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99US-0139492.
99US-0139454.
                                                                                         termination sequence; corn.
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18-OCT-2000 (first entry)
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99US-0139463.
99US-0139750.
99US-0139750.
99US-0139817.
99US-0140354.
99US-0140354.
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14-JUL-1999;
15-JUL-1999;
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RESULT 38 AAG35427 ID AAG35427 standard, Protein; 361 AA.

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990S-0140354-
990S-0141343-
990S-0141343-
990S-0141331-
                                                              Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                             Zea mays protein fragment SEQ ID NO: 43274
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990S - 0123180
990S - 0125788
990S - 0125788
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990S - 0128714
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990S - 0132865
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99US-0139460.
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                           18-OCT-2000 (first entry)
                                                                                                   Zea mays subsp. mays.
                                                                                                                     EP1033405-A2
                                                                                                                                       06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-JUN-1999
14-JUN-1999
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           AAG35427;
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AAB35803 standard; Protein; 390 AA.

(first entry)

23-FEB-2001

AAB35803;

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99US-0150566.
99US-01510884.
99US-0151066.
99US-0151066.
99US-0151303.
99US-0151438.
99US-0151438.
99US-0152363.
                                                                      990S-0154779
990S-0155139
990S-0155589
990S-015659
990S-0156596
990S-0157117
990S-015765
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990S-015865
990S-015823
990S-0158369
990S-0158369
                                                                                                                                                         99US-0159329.
99US-0159330.
99US-0159331.
99US-0159637.
99US-0159638.
99US-0160741.
99US-0160767.
99US-0160767.
99US-0160767.
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990S-0161359.
990S-0161360.
990S-0161920.
990S-0161992.
990S-0161993.
                                                       99US-0153758.
99US-0154018.
99US-0154039.
                                                                                                                                                                                                                                      99US-0160989
                                                                                                                                                                                                                                           99US-0161404
                                                                                                                                                                                                                                                                                              29-OCT-1999;
                                 31-AUG-1999
                                                                                                                                                                                                                                                                                                        Query Match
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5 193 IPVYK----DNDSFTVKRİSDLQASKESPARAVASÖKĞTPVPSSSSQEKDPVAKTILNKV 248 62 EEKKEBENKPIFDVSKKKDNPQVN-----HSQLNESHRKE------DLQREEH 103 15 LPVYKGELEKGYQFDGWEISGFEGKK-----DAGYVINLS----KDTFIKPVFKKI 35; Length 361; Indels 12.1%; Score 84.5; DB 21; llarity 24.8%; Pred. No. 2.8; Conservative 16; Mismatches 46; 104 SQKSDSTKD 112 309 GRESDRERD 317 Local Similarity nes 32; Conserv Best Loca Matches à 유 ò 셤 ò d

RESULT 39 AAB35803

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CC AAB35806 which are involved in regulating the cell cycle. The protein and AAB35806 which are involved in regulating the cell cycle. The protein and CC also includes oligomorlectides AAC83114 - AAC83139 which are related to DNA sequences have been isolated from Zea mays (corn), and the invention of the cell cycle polymuclectides. The cell cycle polymuclectide sequences are useful for producing transgenic plants such as maize, soybean, corner, sorghum, canola, wheat, alfalfa, cotton, rice, barley and millet with increased levels of cell cycle gene activity, such as curivity of cyclin and cyclin-dependent kinases. The DNA sequences are also useful as probes for detecting deficiencies in the level of mRNA in correening for desired transgenic plants, for detecting mutations in the compounds for monitoring upregulation of expression or changes in enzyme activity in screening assays of compounds, for detecting mutations in the correction of the encoded polypeptides and site-directed contagenesis in eukaryotic cells. The DNA sequences are also useful for recombinant expression of the encoded polypeptides and as immunogens for crecombinant expression of the encoded polypeptides and as immunogens of expression cassette including a cell cycle regulatory gene is useful for expression cassette including a cell cycle regulatory gene is useful for corptain antibodies. The antibodies are useful in assaying expression clevels of contagenesis, for identifying homologues of nucleic acids from other species, and for identifying homologues of collypeptides from other species, and for purification of the proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 IPVYK----DNDSFTVKRISDLQASKESPARAVASDKGTPVPSSSSQEKDPVAKTILNKV 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEKKEEENKPTFDVSKKKDNPQVN-----HSQLNESHRKE------DLQREEH 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 LPVYKGELEKGYQFDGWEISGFEGKK------DAGYVINLS----KDTFIKPVFKKI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polynucleotide sequences AAC83101 - AAC83113 encode proteins AAB35794 -
                                                                                                                                                               Cell cycle regulation; corn; transgenic plant; cyclin; maize; soybean; cyclin-dependent kinase; sunflower; sorghum; canola; wheat; alfalfa; cotton; rice; barley; millet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids useful for producing transgenic plants, preferably maize, with increased cell cycle gene activity, preferably activity of cyclin and/or cyclin-dependent kinase -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.1%; Score 84.5; DB 21; Length 390; 24.8%; Pred. No. 3.1; ative 16; Mismatches 46; Indels 35;
                                                                                                                            Protein involved in cell cycle regulation SEQ ID 38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 16; Page 111-112; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sun Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helentjaris TG, Habben JE,
                                                                                                                                                                                                                                                                                                                                                                                                13-APR-2000; 2000WO-US09975.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 24.89 tes 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-687333/67.
N-PSDB; AAC83110.
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                                                                                                                                                                                                                                                                                                         WO200065040-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                           22-APR-1999;
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                                                                                                                                                                                                                                                                   Zea mays.
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 99US-0139454
                                                                                                                                                                                                                             Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                                                                                                                                               Zea mays protein fragment SEQ ID NO: 43273.
                                                                                                        AAG35426 standard; Protein; 416 AA
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99US-0123180.
99US-0123180.
99US-0125788.
99US-0126785.
99US-0126785.
99US-0126785.
99US-0126785.
99US-0126786.
99US-013077.
99US-013081.
99US-013081.
99US-013081.
99US-013148.
99US-0132486.
99US-0132486.
99US-013486.
                                                                                                                                                                                                                                                                                                                                                                                       25-FEB-2000; 2000EP-0301439
                                                                                                                                                                   18-OCT-2000 (first entry)
                 ::|| :|
364 GRESDRERD 372
104 SQKSDSTKD 112
                                                                                                                                                                                                                                                                                             Zea mays subsp. mays.
                                                                                                                                                                                                                                                                                                                          EP1033405-A2
                                                                                                                                      AAG35426;
                                                                      RESULT 40
AAG35426
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PR 16-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149172.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149923.
PR 23-AUG-1999; 99US-0149923.
PR 23-AUG-1999; 99US-0149923.
PR 23-AUG-1999; 99US-011006.
PR 27-AUG-1999; 99US-011006.
PR 27-AUG-1999; 99US-011006.
PR 27-AUG-1999; 99US-0111006.
PR 27-AUG-1999; 99US-0111006.
PR 27-AUG-1999; 99US-0111313.
PR 27-AUG-1999; 99US-0111313.
PR 21-SEP-1999; 99US-0111313.
PR 21-SEP-1999; 99US-011313.
PR 22-SEP-1999; 99US-011313.
PR 23-SEP-1999; 99US-011313.
PR 23-SEP-1999; 99US-011313.
PR 24-SEP-1999; 99US-0115659.
PR 24-SEP-1999; 99US-015659.
PR 24-SEP-1999; 99US-015659.
PR 24-SEP-1999; 99US-015659.
PR 24-SEP-1999; 99US-015659.
PR 24-CCT-1999; 99US-015933.
PR 11-CCT-1999; 99US-015933.
PR 11-CCT-1999; 99US-015933.
PR 21-CCT-1999; 99US-015933.
PR 21-CCT-1999; 99US-015933.
PR 21-CCT-1999; 99US-015933.
PR 21-CCT-1999; 99US-016098.
PR 22-CCT-1999; 99US-016098.
PR 23-CCT-1999; 99US-016098.
PR 24-CCT-1999; 99US-016098
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Oy 104 SQKSDSTKD 112 ::|| :| Db 364 GRESDRERD 372 Search completed: February 10, 2004, 10:53:52 Job time : 31.6275 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

February 10, 2004, 10:48:45; Search time 9.67557 Seconds (without alignments) 1331.870 Million cell updates/sec Run on:

US-10-067-385-8_COPY_640_773

696 1 KEMSSTIVSEEDFILPVYKG.....ATVLDKNNISSKSTTNNPNK 134 score: Title: Perfect sc Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query	Length	DB	ID	Description
	969		2140	~	F95074	serine proteinase,
7	693	9.66	2144	~	A97942	metalloproteinase
e	110	15.8	558	~	T18467	hypothetical prote
4	108.5	15.6	1038	~	JC5497	υ
ß	66	14.2	211	~	T25911	hypothetical prote
9	98	14.1	665	~	B71609	
7	97.5	14.0	1345	N	S46817	
80	95	13.6	348	~	137271	cylicin II - human
σ	95	13.6	622	~	A90570	lipoprotein [impor
10	94.5	13.6	312	~	G81339	probable membrane
11	94	13.5	210	~	T28771	hypothetical prote
12	94	13.5	535	N	T37189	
13	93	13.4	1397	7	T10466	DNA topoisomerase
14	92.5	13.3	219	~	B72291	
15	92.5	13.3	325	~	T18283	
	91	13.1	253	~	T32879	
17	89.5	12.9	508	~	B81594	
	89.5	12.9	508	7	C72074	
	89.5	12.9	508	~	E86549	
20	89	12.8	528	~	E96795	unknown protein F2
21	89	•	1888	7	T39009	hypothetical prote
22	89	12.8	3724	~	T18427	hypothetical prote
23	88.5	12.7	301	7	T33068	hypothetical prote
24	. 88.5	12.7	371	~	A71683	
25	88.5	12.7	385	~	T20410	hypothetical prote
26	88.5	12.7	540	~	D86432	hypothetical prote
27	œ	12.7	4	~	T47835	hypothetical prote
28	æ	12.7	762	7	G88436	protein T04A8.13 [
29	88.5	12.7	791	7	T24435	hypothetical prote

RESULT 2
A97942

metalloproteinase (EC 3.4.21.-) A [imported] - Streptococcus pneumoniae (strain R6)
c;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Accession: A97942
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E R. R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M Y, P.; Sun, P.M.; Winkler, M.E.
J, Bacteriol. 183, 5709-5717, 2001
J, Bacteriol. 183, 5709-5717, 2001
J,Althors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234

rhoptry protein -	hypothetical prote	probable membrane	IgA-specific metal	hypothetical prote	hypothetical prote	microtubule-associ	ORF MSV230 hypothe	hypothetical prote	serine/threonine-s	ankyrin related pr	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	
T28676	T23451	S67610	A41859	T18477	F71621	QRMSP1	T28391	T49989	H71621	T19006	T33457	T27136	.T27135	T14188	H71609
N	~	~	N	7	~	ч	N	~	Н	7	7	N	7	0	7
2401	276	700	1702	2523	635	2464	670	792	2485	1016	335	867	871	986	1166
12.7	12.6	12.6	12.6	12.6	12.5	12.5	12.4	12.4	12.4	12.4	12.2	12.2	12.2	12.2	12.2
88.5	88	88	87.5	87.5	87	87	86.5	86.5	86.5	98	82	85	82	82	85
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT F95074 serine C;Spec C;Date	RESULT 1 F95074 ereine proteinase, subtilase family [imported] - Streptococcus pneumoniae (strain TIGR4) C.Species: Streptococcus pneumoniae C.Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C;Acc R;Tet on, J nson,	Accession: F30.74  R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, Conson, T.; Hickey, B.K.; Holt, I.E.
A; Aut A; Tit A; Ref	Ajauthors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A.Authors: Loftus, Benome Sequence of a virulent isolate of Streptococcus pneumoniae. A;Reference number: A95000; WUID:21357209; PMID:11463916
A; Acc A; Sta A; Mol A; Res A; Cro A; Exp C; Gen	A;Accession: F930/14 A.Status: preliminary A.Molecule type: DNA A;Molecule type: DNA A;Residues: 1-2140 <kur> A;Cross-references: GB:AE005672; PIDN:AAK74791.1; PID:g14972117; GSPDB:GN00164; TIGR:SP4 A;Experimental source: strain TIGR4 C;Genetics:</kur>
A,Gene: Query Best L Matche	<pre>Gene: SP0641 Query Match Best Local Similarity 100.0%; Score 696; DB 2; Length 2140; Best Local Similarity 100.0%; Pred. No. 2.2e-46; Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre>
ζŏ	1 KEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKK 60
qq	1973 KEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKK 2032
ò	61 IEEKKEEENKPIFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTAIVLDK 120
qq	2033 IEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDK 2092
à	121 NNISSKSTTNNPNK 134
đ	2093 NNISSKATTNNPNK 2106

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Query Match
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                                                                                                                                                                                                                                                                                                   1977 KEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKK 2036
A;Accession: A97942
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2144 «KUR»
A;Cross-references: GB:AE007317; PIDN:AAK99365.1; PID:g15458138; GSPDB:GN00174
C;Genetics:
A;Gene: prth
C;Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                          61 IEEKKEEENKPIFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 ILGFEDDILYEYCISQLKQSKEK--KADGEEDKYLNAKKLKINLTGFIGNKKSDIFIEEL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 LELLINEEKKEEHIADTLNENK-TNDIKKVKNENENINENVYNENKDISNKDKEHVSHQN 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B-----DLOREEH----SOKSDSTK----DVTATVLDKNNISSKSTTN 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 IVSEEDFILPVY-----KGELEKGYQFDGWEISGFEGKK----DAGYVINLSKDTFIKPV 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 FKKI--EEKKEE-----SHRPTFDVSK-KKDNPQVNHSQLNE-----SHRK 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     olaustrin - chicken
N;Alternate names: keratan sulfate proteoglycan
C;Species: Gallus gallus (chicken)
C;Date: 07-Jul-1997 #sequence revision 12-Sep-1997 #text_change 21-Jul-2000
C;Accession: JC5497; PC4334; S37561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein C0465c - malaria parasite (Plasmodium falciparum)
C,Species: Plasmodium falciparum
C,Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 11-Jan-2002
C,Accession: T18467
                                                                                                                                                                                                                                                                           1 KEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                  Gaps
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R;Lawson, D.; Bowman, S.; Barrell, B.
submitted to the EMBL Data Library, November 1998
A;Reference number: Z18937
A;Reference number: Z18937
A;Accession: T18467
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-558 < LAW>
A;Residues: 1-558 < LAW>
A;Cross-references: EMBL:AL008970; NID:e1407852; PIDN:CAA15610.1
C;Genetics:
A;Map position: 3
A;Note: C0465c
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                                                                                                                                                                                        Length 2144;
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                                                                                                                                                                                                                                Indels
                                                                                                                                                                                          ; bb - 3.8e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.8%; Score 110; DB 2; 29.3%; Pred. No. 0.31; ive 23; Mismatches 47;
                                                                                                                                                                                        Query Match 99.6%; Score 693; DB 2; Best Local Similarity 99.3%; Pred. No. 3.8e-46; Matches 133; Conservative 1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2097 NNISSKSTTNNPNK 2110
                                                                                                                                                                                                                                                                                                                                                                                                                                            NNISSKSTTNNPNK 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 54; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96
                                                                                                                                                                                                                                                                                                                                                                                                                                            121
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R.Burg, M.A.; Cole, G.J.
N. Neurobbiol.. 25, 1-22, 1-22
A.Title: Claustrin, an antiadhesive neural keratan sulfate proteoglycan, is structurally
A.Reference number: JC5497; MUID:94157526; PMID:7906711
                                                                                                                                                                                                                                                                                                                                                                                                      C. Comment: This process in inhibits neural cell adhesion and neurite outgrowth in the nervon C. Comment: This process in inhibits neural cell adhesion is keratan sulfate C. Keywords: chondroitin sulfate proteoglycan; glycoprotein; keratan sulfate 2.567-270/Region: cell attachment (R-G-D) motif F:112, 213, 490/Binding site: carbohydrate (Asn) (covalent) #status predicted F:152, 213, 490/Psinding site: chondroitin sulfate (Ser) (covalent) #status predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C;Accession: B71609
R;Gardner, M.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V., Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           595 KPETKTIVAEKDV-----TTKEEQLGKSETSEKQASEKQDVKPKVTKEKSVKKEVKA 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               647 KPEEKKDEKEKPKKEVSKKEEKPLI---KKEEKPKKEDIKKEVKKEVKKESKKEAKKEV 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Cross-references: EMBL:U88309; PIDN:AAB42334.1; GSPDB:GN00019; CESP:T23B3.5 A;Experimental source: strain Bristol N2; clone T23B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KIBEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQRE-----EHSQKSDSTKDV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein T23B3.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 EGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNH----SQLNES
                                                                                                                                                                                                                                          A;Cross-references: EMBL:X67778; NID:g406318; PIDN:CAA47988.1; PID:g406319
A;Accession: PC4334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein PFB0680w - malaria parasite (Plasmodium falciparum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1038;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 HRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: T25911
R;Maggi, L.; Le, T.
submitted to the EMBL Data Library, February 1997
A;Description: The sequence of C. elegans cosmid T23B3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 15.6%; Score 108.5; DB Local Similarity 28.6%; Pred. No. 0.83; Pred. 34; Conservative 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Mismatches
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                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 79-83;299-412;485-502 <BUR2>
A;Experimental source: brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-1038 <BUR1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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A; Residues: 1-211 < MAG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Introns: 30/2; 200/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: T25911
                                                                                                                                      A; Accession: JC5497
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A;Title: The protein complexity of the cytoskeleton of bovine and human sperm heads: the A;Reference number: 137271; MUID:95255491; PMID:7737358
A;Accession: 137271
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A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm: A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: A90570
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R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp A;Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable membrane protein Cj0692c (imported) - Campylobacter jejuni (strain NCTC 11168)
C,Species: Campylobacter jejuni
C,Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                           7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 ENKPTFDVSKKKD----NPQVNHSQLNES--HRKEDLQREEHSQKSDSTKDVTATVLDKN 121
                                                                                                                                                                                                                                                                                                                                                             205 ESEGEKG----GTEKDSKKKKKDS----KKGKDSAIELQAVKADEKKDEDGKKDANKGDE 256
                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Cross-references: GB:AL445566; PID:g14089879; PIDN:CAC13638.1; GSPDB:GN00153
A,Experimental source: strain UAB CTIP
                                                                                                                                                                                                                                                                                                                                                                                                                SK--KKDNPQVNHSQLN-----ESHRKEDLQREEHSQKSDSTKD---VTATVLDKNNI 123
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                                                                                                                                                                                                                                                                                                           19 KGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTF---DV 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lipoprotein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 VSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEE
                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-348 <HES-
A;Cross-references: EMBL:Z46788; NID:g758586; PIDN:CAA86752.1; PID:g758587
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                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                              39;
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                                                                                                                                                                                                         Query Match
13.6%; Score 95; DB 2
Best Local Similarity 30.9%; Pred. No. 2.7;
Matches 38; Conservative 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Pred. No. 5.3; 26; Mismatches
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Best Local Similarity 25.4%
Matches 34; Conservative
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A;Residues: 1-1345 <FAV>
A;Cross-references: EMBL:U10556; NID:9500825; PIDN:AAB68895.1; PID:9500838; MIPS:YHR080q
                                                                                                                                                                              A;Cross-references: GB:AE001410; GB:AE001362; NID:g3845245; PIDN:AAC71925.1; PID:g384524 A;Experimental source: clone 3D7 C;Genetics: A;Genetics: PFB0680w
                             A,Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A,Reference number: A71600, MUID:99021743; PMID:9804551
A,Accession: B71609
A,Status: preliminary; nucleic acid sequence not shown; translation not shown A,Molecule type: DNA
A,Residues: 1-665 <GAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1109 KGAIEKG------SVEGQKVSVDYMLSELRDII-----SRAKSKKPVKKVWK 1149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTFD----VSKKKDNPQVNHSQLNESHRKEDLQR-EEHSQKSDSTKDVTATVLDKNNISS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKGKÓ----DISNSNAENKKD------VKEGVKELEEKKKEEKISDDHKVEENK 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein YHR080c - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 28-0ct-1994 #sequence_revision 28-0ct-1994 #text_change 19-Apr-2002
C;Accession: S46817
R;Favello, T.
submitted to the EMBL Data Library, June 1994
A;Description: The sequence of S. cerevisiae cosmid 9205.
A;Reference number: S46795
A;Accession: S46817
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: 137271; S52774
R;Hess, H.; Heid, H.; Zimbelmann, R.; Franke, W.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 KGELEKGYQFDGWEISGFEGKK-DAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSK
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                     42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 1345;
                                                                                                                                                                                                                                                                                                                                                                                                                        EKGYQFDGWEI --SGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38; Indels
                                                                                                                                                                                                                                                                                                        Score 98; DB 2; Length 665;
Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                                                                                   29; Indels
                                                                                                                                                                                                                                                                                                                                             1 Similarity 27.1%; Pred. No. 3.3; 35; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 14.0%; Score 97.5; D
Best Local Similarity 27.0%; Pred. No. 8;
Matches 33; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                   14:1%;
27.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: SGD:S0001122
             Science 282, 1126-1132, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :: : | |
ENKAKDENK 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KSTTNNPNK 134
                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1202 QK 1203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: 8R
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Si
Matches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                        23
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us-10-067-385-8_copy_640_773.rpr

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DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) II - malaria parasite (Plasmodium falc
C;Species: Plasmodium falciparum
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
C;Accession: T10466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 14
C;Superfamily: eukaryotic type II DNA topoisomerase; phage T4 DNA topoisomerase (ATP-hyd
C;Keywords: ATP; DNA binding; isomerase; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 AAKIISGKD-----BEKKKKVKKEDK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                              -----KKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQ---KSDSTK 111
               A;Cross-references: EMBL:U49945; PIDN:AAC47924.1; GSPDB:GN00029; CESP:C02H7.1
A;Experimental source: strain Bristol N2; clone C02H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C,Species: Thermotoga maritima
C,Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 SSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 VSEEDFIL--PVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEE--
                                                                                                                                                                                                                                                                                                                                                                                                                 64 KKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1397;
                                                                                                                                                                                                       Length 535;
                                                                                                                                                                                                                                                         56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein - Thermotoga maritima (strain MSB8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; DB 2;
5: 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DMA
A;Mosidues: 1-1397 <CHE.
A;Cross-references: EMBL:X79345; NID:g994807
                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, September 1995
A;Reference number: 217031
A;Accession: T10466
                                                                             C;Genetics:
A;Gene: CESP:CO2H7.1
A;Map Position: X
A;Introns: 47/3; 100/3; 149/3; 304/2; 347/3; 458/3
                                                                                                                                                                                                                       23.4%; Pred. .v..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33; Mismatches
                                                                                                                                                                                                       13.5%; Score 94; 23.4%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.4%; Score 93; 24.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1251 FLVNTLNIKKNTNKKTTTSSNN 1272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 DVTATVLDKNNISSKSTTNNPN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 TATVLDKNNISSKSTTNNPNK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSEKSSKEKKKEKSTIDEKPK 210
                                                                                                                                                                                                         Query Match
Best Local Similarity 23.4%
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 24.68
Matches 35; Conservative
  A;Residues: 1-535 <LEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C, Accession: B72291
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A;Accession: G81339
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-312 <PAR>
A;Residues: 1-312 <PAR>
A;Cross-references: GB:AL139076; GB:AL11168; NID:g6968128; PIDN:CAB72966.1; PID:g696814
A;Cross-references: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: Cj0692c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein E03H12.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T28771
R;Nelson, J:; Wolldmann, P.; Sansone, J.
submitted to the EMBL Data Library, June 1997
A;Description: The sequence of C. elegans cosmid E03H12.
A;Reference number: Z20520
A;Reference number: Z20520
A;Reference number: Z20520
A;Reference number: Z20520
A;Reference number: Z20520
A;Reference number: Z20520
A;Reference number: Z20520
A;Reference number: Z20520
A;Resperiments preliminary; translated from GB/EMBL/DDBJ
A;Resperimental source: EMBL:AF000229; PIDN:AAC47980.1; GSPDB:GN00022; CESP:E03H12.5
A;Resperimental source: strain Bristol N2; clone E03H12
A;Gene: CESP:E03H12.5
A;Gene: CESP:E03H12.5
A;Gene: CESP:E03H12.5
A;Hutrons: 30/2; 201/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 ISSDDILRRRFKKKTPNKFLEELDEEYESKHTKKSNIYLKED---LINVKLEEKQSLAKK 94
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T37189
R;Leimbac, D.; Minx, M.
submitted to the RMBL Data Library, February 1996
A;Description: The sequence of C. elegans cosmid CO2H7.
A;Reference number: Z20523
A;Stcession: T37189
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 EGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKE
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                                                                                                                                                                                                                                                                                         25;
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0
                                                                                                                                                                                                                                 Query Match 13.6%; Score 94.5; DB 2; Length 312; Best Local Similarity 25.7%; Pred. No. 2.7; Matches 38; Conservative 30; Mismatches 55; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 210;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 13.5%; Score 94; DB 2; Best Local Similarity 28.6%; Pred. No. 1.9; Matches 28; Conservative 18; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 TKDV--TATVLDKNNISSK--STTNNPN 133
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T37189
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A;Residues: 1-508 <REA>
A;Cross-references: GB:AE002189; GB:AE002161; NID:g7189205; PIDN:AAF38139.1; PID:g718920
A;Experimental source: strain AR39, HL cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; WUID:99206606; PMID:10192388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE001632; GB:AE001363; NID:g4376755; PIDN:AAD18613.1; PID:g437675 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R.Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
                      A;Molecule type: DNA
A;Residues: 1-253 <GAT>
A;Cross-references: EMBL:AF043692; PIDN:AAB97531.1; GSPDB:GN00019; CESP:C17F3.3
A;Experimental source: strain Bristol N2; clone C17F3
C;Genetics:
A;Gene: CESP:C17F3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein CP0281 [imported] - Chlamydophila pneumoniae (strain AR39)
C,Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C,Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                      PVAPKVEEKKEEKKEEKKADDEKKKTEEKDOKKSKKTEEKDKISVKKTQETKSERKDKK 120
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                                                                                                                                                                                                                                                                                                                                      hypothetical protein - Chlamydophila pneumoniae (strain CWL029)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----VSKKKDNPQVNHSQLNESHRK
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                           24;
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                                                                                                                                                                                                                                           Length 253;
                                                                                                                                                                                                                                                                                         33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEKKEDEKKEESKEKSKDEKKKDEVKDKKEDEKK 155
                                                                                                                                                                                                                                                                                                                                                                                                                                         ---KEDLQREEHSQKSDSTKDVTATVLDKNNISSK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 EDLQREEHSQKSDSTKDVTATVLDKNNISSKSTT 129
                                                                                                                                                                                                                                           DB 2;
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                      Score 91; DB 2
Pred. No. 3.9;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.9%; Score 89.5; D
24.5%; Pred. No. 11;
:ive 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 IKPVFKKIEEKKEEENKPTFD-------
                                                                                                                                                                                                                                        13.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                           31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: B81594
A;Status: preliminary
A;Molecule type: DNA
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A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: B81594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: C72074
                                                                                                                                                                       A; Map position: 1
                                                                                                                                                                                                A,Introns: 41/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: CP0281
                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                           95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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C;Accession: T18283
Genetics 148, 1117-1125, 1998
A;Title: Dictyostelium discoideum nuclear plasmid Ddp5 is a chimera related to the Ddp1
A;Reference number: Z14684; MUD:98198836; PMID:9539429
A;Accession: T18283
                                                                                                                 A,Cross-references: GB:AE001771; GB:AE000512; NID:g4981678; PIDN:AAD36218.1; PID:g498168
A,Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                              8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 PTFDVSKKKDNPQVNHSQLNESHRKED----LQREEHSQKSDS------TKD 112
                                                                                                                                                                                                                                                                                                                                           20 GELEKGYQ--FDGWEISG-----FEGKKDAGYVIN-LSKDTFIKPVFKKIEEKKEEENK 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----IEEKKEEENKPIFDV 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:U00796; NID:g2702254; PID:g2702258; PIDN:AAC18634.1
C;Genetics:
A;Introns: 85/1
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hypothetical protein C17F3.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T32879
R;Gattung, S; Scheet, P.
R;Gattung, S; Scheet, P.
A;Description: The sequence of C. elegans cosmid C17F3.
A;Reference number: Z21240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                           Length 219;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein G5 - slime mold (Dictyostelium discoideum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKKKDNPQVNHSQLNESHRKE-----DLQREEHSQKSDSTKD 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 EBEBETPAVSEEKEEBEEEEFTPAVSEEKEEBEQEEDKEKD 233
                                                                                                                                                                                                                                                                                           35; Indels
A; Reference number: A72200; MUID: 99287316; PMID: 10360571
                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-325 <RIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 VSEEDFILPVYK-GEL--EKGYQFDGWEISGFEGK
                                                                                                                                                                                                                                              13.3%; Score 92.5; DE 28.1%; Pred. No. 2.5; ive 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.3%; Score 92.5; Dl
llarity 23.2%; Pred. No. 4;
Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47 NLSKDTFIKPV-----FKK-
                                                                                                                                                                                                                                                                                                36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 VTATVLDK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 VAKTLQEK 210
                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 38; Conserv
                                                                                                A; Residues: 1-219 <ARN>
                                                A; Status: preliminary A; Molecule type: DNA
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                                                                                                                                                                         C,Genetics:
A,Gene: TM1142
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Best Local S
Matches 36
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A;Cross-references: EMBL:298531; PIDN:CAB11064.1; GSPDB:GN00066; SPDB:SPAC6B12.02c A;Experimental source: strain 972h-; cosmid c6B12
                                                                                                                                         64 KKEEENKPIFDVSKKK--DNPQVNHSQLNESHRKEDLQREEH-----SQKSDSIKD- 112
                                                                                                                                                                                                                                                               SSSLTSENPFOLNVAANAVSTIPVYRTTKTKMKKN-RFKYVEVEKLPDLILESYGKKAPK 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 YVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEH 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             449 FLRVFARSSSHIP--KMIRRKRQMDSKKYFSFDKESDRQVIDQVLSDWYSGKHELVQQSH 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: EMBL: Z98547; NID: e1325376; PID: e1325379; PIDN: CAB11104.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein SPAC6B12.02c - fission yeast (Schizosaccharomyces pombe Cispecies: Schizosaccharomyces pombe Cibaceis Schizosaccharomyces pombe Cibace: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000 Ciaccesion: T39009
Rigentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V. Asubmitted to the EMBL Data Library, August 1995
A;Reference number: Z21815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C;Accession: T18427
R;Lawson, D; Bowman, S.; Barrell, B.
A;Reference number: Z18935
A;Accession: T18427
                                                                                                               ELEKGYQFDGW------BISGFEGKKDAG----YVINLSKDTFIKPVFKKIEE
                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Map position: 1
C,Superfamily: Schizosaccharomyces hypothetical protein SPAC6B12.02c
                                                         36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1888;
                                                         51; Indels
  Length 528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 SSTIVSEEDF-----ILPVY---KGELEKGYQFDGWEISGFE-
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A,Molecule type: DNA
A,Residues: 1-3724 <LAM>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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12.8%; Score 89; DB 24.3%; Pred. No. 13; ive 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 12.8%; Score 89; DB 1 Similarity 23.9%; Pred. No. 54; 37; Conservative 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 89;
                                                                                                                                                                                                                                                                                                                                                                                          317 MEEDVVTETVKTETSEDMKLLSON 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-1888 <GEN>
A;Cross-references: EMBL:Z98531;
  Query Match 12.8
Best Local Similarity 24.3
Matches 35, Conservative
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Best Local Similarity
Matches 37; Conserv
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                                                                                                               21
                                                                                                                                                                      200
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: D; S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Species: S;Specie
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                                                                                                                                                                                                                      92 VKGVPKKTPQARPEVSSPRLPSHVQHGQRLPGLEGFRDRIQKRSENPEADLGKMKRSYSD 151
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A;Cross-references: GB:BA000008; NID:g8978843; PIDN:BAA98679.1; GSPDB:GN00142
A;Experimental source: strain J138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --- VSKKKDNPQVNHSQLNESHRK 95
                                                                                                               Gaps
                                                                                                               21;
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                                                      Length 508;
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                                                                                                               33;
                                                      12.9%; Score 89.5; DB 2; 24.5%; Pred. No. 11;
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                                                                                                                                                                                                                                                                                                                  96 EDLQREEHSQKSDSTKDVTATVLDKNISSKSTT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 GDLDRVGHDSNEDSTEDSRS---EGGEPSSKSSS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 EDLOREEHSOKSDSTKDVTATVLDKNNISSKSTT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17; Mismatches
                                                                                                               Mismatches
                                                                                                                                                                      54 IKPVFKKIEEKKEEENKPTFD--
                                                                                                               17;
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Best Local Similarity 24.5
Matches 23; Conservative
                                                                                   l Similarity 24.5
23; Conservative
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A; Map position: 1
A; Gene: CPn0473
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                                                         Query Match
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7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:281053; PIDN:CAB02877.1; GSPDB:GN00023; CESP:E02A10.2 A;Experimental source: clone E02A10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 KKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 EQLNKTIINEE-----FRKOLEQ------EKKKIEGKKTQASEALNKK----LKPIYK 234
                                                                                                                               KIEEKKEE-----ENKPTFDVSKKKDNPQVN---HSQLNESHRKEDLQREEHSQKSDSTK 111
1 KEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKK-DAGYVINLSKDTFIKPVFK 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ypothetical protein E02A10.2 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 12.7%; Score 88.5; DB 2; Best Local Similarity 35.5%; Pred. No. 9.9; Matches 22; Conservative 14; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R)Thomas, K. submitted to the EMBL Data Library, October 1996 A, Reference number: 219271 A, Recession: T20410
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A;Introns: 32/1; 72/1; 85/1; 122/1; 133/1; 220/3
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                                                                                                                                                                                                                                                                                                          287 E---IVSKIEYSKKSKTNDIIINNPN 309
                                                                                                                                                                                                                                                                 112 DVTATVLDKNNISSKSTT----NNPN 133
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Best Local Similarity
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hypotherical protein RP278 - Rickettsia prowazekii

c;Species: Rickettsia prowazekii

c;Species: Rickettsia prowazekii

c;Species: Rackettsia prowazekii

C;Accession: A71683

Racketseson, SGE.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998

A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71683

A;Reference number: A71683

A;Reference prominary; nucleic acid sequence not shown; translation not shown A;Molecule type: DMA

A;Molecule type: DMA

A;Residues: 1-371 cAND>

A;Cross-references: GB:AJ235271; GB:AJ235269; NID:G3868717; PIDN:CAA14739.1; PID:G38608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-301 <GRA>
A;Cross-references: EMBL:AF067216; PIDN:AAC17524.1; GSPDB:GN00019; CESP:C35E7.9
A;Experimental source: strain Bristol N2; clone C35E7
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                                                                                                       6 TIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKK 65
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C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T33068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 GYQFDGWEISGFEGKK-----DAGYVINLSKDTFIKPVFKKI------EE
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                                  32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 301;
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                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Graves, T.; McDonald, R. submitted to the EMBL Data Library, May 1998
A;Description: The sequence of C. elegans cosmid C35E7.
A;Reference number: Z21278
   22.3%; Pred. No. 1.2e+02;
:ive 27; Mismatches 42
                                                                                                                                                A; Status: preliminary; translated from GB/EMBL/DDBJ
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Matches 34; Conservative
      Best Local Similarity 22.3
Matches 29; Conservative
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A;Introns: 30/3; 193/1; 236/2
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1149 NKSDIENENK 1158
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A,Gene: CESP:C35E7.9
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Best Local S
Matches 27
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A;Residues: 1-2401 <SIN>
A;Cross-references: EMBL:U36927; NID:g1041784; PID:g1041785; PIDN:AAB41263.1
A;Cross-references: EMBL:U36927; NID:g1041784; PID:g1041785; PIDN:AAB41263.1
R;Keen, J.; Holder, A.; Playfalr, J.; Lockyer, M.; Lewis, A.
Mol. Biochem. Parasitol. 42, 241-246, 1900
A;Title: Identification of the gene for a Plasmodium yoelii rhoptry protein. Multiple co
A;Reference number: A45521; MUID:91101660; PMID:2270106
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C;Obate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 01-Dec-2000
C;Accession: T28676; A45521
R;Sinha, K.A.; Keen, J.K.; Ogun, S.A.; Holder, A.A.
Rol. Biochem. Parsasteol. 76, 329-332, 1996
A;Titel: Comparison of two members of a multigene family coding for high-molecular mass
A;Reference number: Z20507; MUID:97077455; PMID:8920022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | | : | : | | : | : | : | | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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A;Experimental source: clone T04A8
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T24435
                                                                                                                                                                                                                                                                                          9 SEEDFILPVYKGELEKGYQFDGWEISGFEGK-KDAGYVINLSKDTFIKPVFKKIEEKKEE
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                                                                                                             Gaps
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Length 762;
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A,Introns: 31/3; 212/1; 229/3; 331/3; 406/1; 472/3; 572/1; 651/2
                                                                                                             Indels
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A;Molecule type: DNA
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A;Molecule type: DNA
Query Match
12.7%; Score 88.5; D
Best Local Similarity 25.2%; Pred. No. 21;
Matches 32; Conservative 25; Mismatches
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25.2%; Pred. No. 22;
ive 25; Mismatches
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submitted to the EMBL Data Library, August 1994
A;Reference number: Z19889
A;Recession: T24435
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Best Local Similarity 25.2%
Matches 32; Conservative
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C;Specites: Caenorhabditis elegans
C;Specites: Caenorhabditis elegans
C;Accession: G88436
C;Accession: G88436
C;Accession: G88436
C;Accession: G88436
C;Accession: G88436
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Title: Genome wustl:edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: G88436
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T47835
R;Nyakatura, G; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.; Reference number: Z24475
A;Reference number: Z24475
A;Reference number: Z24475
A;Residues: preliminary
A;Residues: 1-644 <NYA>
A;Residues: 1-644 <NYA>
A;Residues: 1-644 <NYA>
A;Residues: Caltivar Columbia; BAC clone T209
C;Genetics: A;Map position: 3
A;Map position: 3
A;Musterimental source: cultivar Columbia; BAC clone T209
A;Musterimental source: Caltivar Columbia; BAC clone T209
C;Genetics: A;Musterimental Source: Caltivar Columbia; BAC clone T209
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                                                                                                                                                                                                                                                                                                                                        61 --IEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVL 118
                                                                                                                                                                                                                                                                                                                                                                                                       :: | : | | : | | : | : | 511 HQKKSDGNVKKENSKVRRPELRSSTGKKKVEVENNNSKSSSKRKQTKETAEVATGKRGRE 630
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                                                                                                                   2 EMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKK-
                                                                                                                                                                                                                          49 EKSASFKEESDFFADLKESEKK-----ALSDLKSKLEEAIVDN----TLLKTKKKES
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           17; Gaps
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           Indels
           54;
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           25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 24.6% nes 32; Conservative
           31; Conservative
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Best Local S:
Matches 32
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A;Cross-references: SGD:S0002232
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Best Local Similarity
Matches 25; Conserva
                                                                                                                          Best Local Similarity Matches 31; Conserv
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A; Introns: 148/3
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A;Molecule type: DNA
A;Residues: 1-700 «WAM>
A;Cross-references: EMBL:Z74122; NID:g1431087; PID:e253213; PID:g1431088; GSPDB:GN00004;
A;Experimental source: strain S288C
C;Genetics:
                                                                                                                                                                                                                                            947 SEESYINDI-KKELEKAVLESQNNATDINQYLSKIENIY--NILKLNKIKKIIDKVKEYT 1003
                                                                                                                                                                                                                                                                                                                                66 EEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKD------ 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 LSKDTFIKPVFKKIEEKKEEE--NKPTPDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||| : |:| : |107
                                                                                                                                                                                                                 9 SEEDFILPVYKGELEKGY---QFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-276 <WIL>
A;Cross-references: EMBL:281568; PIDN:CAB04590.1; GSPDB:GN00021; CESP:K08E3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable membrane protein YDL074c - yeast (Saccharomyces cerevisiae)
NiAlternate names: hypothetical protein D2483
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Decte: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
C;Accession: S67610
R;Wambutt, R: Wedler, H: Wedler, E.; Scharfe, M.
Bubmitted to the Protein Sequence Database, July 1996
A;Reference number: S67608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                         25;
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                                                                                                                              Length 2401;
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                                                                                                                                                28.4%; Pred. No. ,0;
tive 24; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein K08E3.2 - Caenorhabditis elegans
                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C,Accession: T23451
R,McMurray, A.
Bubmitted to the EMBL Data Library, November 1996
A,Reference number: 219743
A,Accession: T23451
A,Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                              12.7%; Score 88.5; 28.4%; Pred. No. 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 3
A;Introns: 81/3; 102/3; 169/1; 211/2
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1059 LKTYIVNEKNNINT 1072
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A;Gene: SGD:BRE1; MIPS:YDL074c
                                                                                                                                                Best Local Similarity 28.4
Matches 38; Conservative
                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 2260-2401 <KEE>
A;Crose-references: GB:M34281
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A;Gene: CESP:K08E3.2
    A; Accession: A45521
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IGA-specific metalloendopeptidase (EC 3.4.24.13) type 1 precursor - Haemophilus influenz
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R. Bacteriol. 174, 2913-2921, 1992
A.Title. A comparative genetic study of serologically distinct Haemophilus influenzae ty
A.Reference number: A41859; MUID:92234949; PMID:1373717
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                                                                                                                                                                                                                                                                   56 PVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTA 115
                                                                                                                                                                                                                           21 ELEKGYQFDGWEISGFEGKK----IK 55
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C.Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Variety: strain HK715
C,Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Dec-2000
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A;Experimental source: strain HK715
A;Experimental source strated from NCBI backbone (NCBIP:97282)
C;Superfamily: IgA-specific metalloendopeptidase
C;Keywords: hydrolase; metalloproteinase
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A;Molecule type: DNA
A;Residues: 1-2523 <LAW>
A;Residues: 1-2523 <LAW>
A;Cross-references: EMBL:AL008970; NID:e1407852; PIDN:CAA15620.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid A;Residues: 1-1702 <POU>
                                                                                                               DB 2; Length 700;
                                                                                                                                                                        Indels
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A;Map position: 4L
C;Keywords: transmembrane protein
F;69-85/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 -- OKSDSTKDVTATVLDKNNISSKSTTNNPNK 134
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                                                                                                                                          1 Similarity 23.7%; Pred. No. 21, 31; Conservative 24; Mismatches
                                                                                                                  12.6%; Score 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 TVLDKNNISSK 126
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Gaps

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A;Molecule type: protein

A;Molecule type: protein

C;Superfamily: microtubule-associated protein MAPIB

C;Superfamily: microtubule binding; phosphoprotein; tandem repeat

C;Keywords: microtubule binding; phosphoprotein; tandem repeat

F;589-786/Domain: microtubule binding #status experimental <WTB>
F;899-786/Domain: microtubule binding #status experimental <WTB>
F;899-786/Domain: microtubule binding #status experimental <WTB>
F;891-786/Domain: microtubule binding #status experimental <WTB>
F;891-786/Domain: microtubule binding #status pics files phosphate (Thr) (co F;1953),891-1353,1862,1863,1702,1708,1990,2057,2063,2419/Binding site: phosphate (Thr) (co F;1953)/Binding site: phosphate (Thr) (covalent) #status predicted
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C; Genetics:
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R;Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L. J.,Virol. 73, 533-552, 1999
A;Fitle: The genome of Melanoplus sanguinipes entomopoxvirus.
A;Reference number: Z20484; MUID:99102612; PMID:9847359
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 LSKDTFIKPVFK-KIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQRE----
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
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28.4%; Pred. No. 1e+02;
tive 16; Mismatches
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R; Bevan, M.; Bancroft, I.; Mewes,
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Matches 35; Conservative
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Best Local Similarity
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A,Status: preliminary
A,Molecule type: DNA
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C, Date: 30.58p-1991 #sequence_revision 30-Sep-1991 #text_change 01-Sep-2000
C, Date: 30.58p-1991 #sequence_revision 30-Sep-1991 #text_change 01-Sep-2000
C, Accession: S07549; S44387; A33645
B,Noble, M.; Lewis, S.A.; Cowan N.J.
J. Cell Biol. 109; 3367-3376, 1989
A;Title: The microtubule binding domain of microtubule-associated protein MAPIB contains A;Reference number: A33645; MUID:90094539; PMID:2480963
A;Title: The microtubule binding domain of microtubule-associated protein MAPIB contains A;Reference number: S13645; MUID:90094539; PIDN:CAA35761.1; PID:g53000
A;Title: Piper mRNA
A;Nolecule type: mRNA
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Cypaces: A. Salzbergy S.; Zhou, L.; Cutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743; PMID:9804551
A;Accession: F71621
A;Accession: F71621
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-635 cGR>
A;Cross-references: GB:AE001377; GB:AE001362; NID:g3845111; PIDN:AAC71823.1; PID:g384511
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                                                                                                     12.6%; Score 87.5; DB 2; 32.5%; Pred. No. 98;
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Matches 30; Conservative
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                  A;Note: C0485w
                                                                                                          Query Match
                                                                                                                                                                                             Matches
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A;Map position: 2
A;Introns: 27/3; 94/3; 279/3; 352/2; 462/2; 523/3; 569/2; 657/2; 718/3; 766/3; 833/3; 89′
C;Keywords: phosphoric monoester hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Residues: 1-1016 <WIL>
A,Cross-references: BMBL:236719; PIDN:CAA85318.1; GSPDB:GN00020; CESP:C06C3.1
A,Experimental source: clone C06C3
R,Matthews, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 LEKGYQ-----FDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEE---NKPTF 73
                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:Z47809; PIDN:CAA87782.1; GSPDB:GN00020; CESP:C06C3.1
A;Experimental source: clone F42A8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 12.4%; Score 86; DB 2; Length 1016; I Similarity 24.4%; Pred. No. 46; 32; Conservative 30; Mismatches 35; Indels
                      Status: preliminary; translated from GB/EMBL/DDBJ; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 DVSKKKDNPQVNHSQ-LNESHRKEDLQ-REEHSQK--
                                                                                                                                                                                                                                                                      Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                         submitted to the EMBL Data Library, January 1995
A;Reference number: Z19510
A;Accession: T22086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: February 10, 2004, 10:58:31
Job time : 10.6756 secs
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TIVIGENDISA 390
                                                                                                                                                                                                                                                                                                  A,Molecule type: DNA
A,Residues: 1-1016 <WI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: CESP:C06C3.1
A; Accession: T19006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-2485 <CAR>
A;Cross-references: GB:AE001376; GB:AE001362; NID:g3845108; PIDN:AAC71820.1; PID:g384510
A;Experimental source: clone 3D7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: malaria parasite serine/threonine-specific protein kinase PFB0150c; prote
C;Keywords: phosphotransferase
F;2087-2352/Domain: protein kinase homology <KIN>
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                                                                                                                                                                                                                                                                                                                         137 TEKEFVKTSYENGLAKYWEIEKCIMEKQGKVSSLQDEFDEGAVVIEDKEAQILMSTTALK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                    197 SCQEKLEELRDKQEQNVKEVDVSRKQISESTEEFGNLSDALLGDGKGNHEIYSEKEKLES 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 ELEKGYQFDGW------EISGFE-----GKKDAGYVINLSKDTFIKPVFKKIEE 63
                                                                                                                                                                                                                                                                      9 SEEDFILPVYKG-----ELEKGYQFDGWEISGFEGKKDAGYVINLSKD-----TFIK 55
                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ankyrin related protein C06C3.1 - Caenorhabditis elegans
N;Contains: myosin-light-chain-phosphatase (EC 3.1.3.53)
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Mar-2000
C;Accession: T19006; T22086
R;BerKs, M.
Babmitted to the EMBL Data Library, August 1994
A;Reference number: Z19058
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                   31;
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A;Cross-references: EMBL:AL353995; GSPDB:GN00063; ATSP:F12B17.150
A;Experimental source: cultivar Columbia; BAC clone F12B17
                                                                                                                                                           Length 792;
                                                                                                                                                           ; Score 86.5; DB 2; Length 79; Pred. No. 32; 26; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31, Indels
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                                                                                                                                                                                                                                                                                                                                                                                 56 PVFKKIEE--KKEEENKPTFDVSKKKDNPQV--
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Best Local Similarity 22.5%;
Matches 32; Conservative 20
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Best Local Similarity
Matches 36; Conserva
                                                  C,Genetics:
A,Gene: ATSP:F12B17.150
A,Map position: 5
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-SDSTKDVTA 115

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

February 10, 2004, 10:48:44; Search time 6.22948 Seconds (without alignments) 1011.574 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-067-385-8_COPY_640_773
696
1 KEMSSTIVSEEDFILPVYKG......ATVLDKNNISSKSTINNPNK_134

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 segs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0. Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description				P46821 homo sapien		P45384 haemophilus	-		Q8cst4 staphylococ	-		P44969 haemophilus		Q15695 homo sapien	пошо	P42872 haemo										P25644 saccharomyc		_		_		002792 saccharomyc	Q02510 staphylococ
SUMMARIES	qi	YHOO YEAST	CYL2 HUMAN	TOP2_PLAFK	MAPB HUMAN	YDT2_SCHPO	IGA2_HAEIN	MAPB MOUSE	GLNA_PYRKO	IF2 STAEP	DPOM ASCIM	SPT7 YEAST	IGAO_HAEIN	YFK8 YEAST	U2R1 HUMAN	IF31_HUMAN			YMB4_YEAST		GLNA PYRFU	GLNA PYRWO	IF2_HELPJ	LMD1_HUMAN	DRS1_YEAST	MAPB_RAT	PAT1_YEAST	YCG1_YEAST	YAE6_SCHPO	TONB PASMU				LIP_STAEP
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	Match Length	1345	348	1398	2468	1888	1702	2464	443	720	1202	1332	1694	778	479	258	270	439	279	427	439	439	949	572	752	2459	797	853	1325	256	793	914	1006	688
* Ouery	Match	14.0	13.6	13.4	13.3	12.8		12.5	12.4	12.2	12.2	12.1	12.1	12.1			11.9	11.9	11.8	11.8	11.8	11.8	11.8	11.7		11.7	11.6	11.6	11.6			•	11.6	11.5
	Score	•	95	93	92.5	68	87.5	87	98	82	85	84.5	84.5	84	83.5	83	83	82.5	82	82	82	82	B	•	81.5	•	81	81	81		80.5		80.5	80
Result	No.	٦	7	m	4	2	9	7	ω	6	10	11	12	13	14	15	16	17	18		20	21	22	23	24	25	56	27	28	29	30	31	35	33

	P36188 drosophila Q23917 dictyosteli O66695 aquifex aeo				P14400 torpedo cal
IF2P HUMAN CENC HUMAN	TRI DROME REGA DICDI Y372 AQUAE	CYL1_HUMAN DNL1_CAEEL	ARS2_DROME CBX5_HUMAN	SPH STRPY EZRA BACSU	ENP1_TORCA
п п		- г			-
1220	268 793 531	598 847	943 191	376 562	721
11.5	11.4	11.3	11.3	11.2	11.2
80 79.5	79 79 78.5	78.5	78.5	78	78
34 35	36 37 38	39	41	44	45

## ALIGNMENTS

78 KKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLD--KNNISSKSTTN---NP 132

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PRT; 1398 AA

STANDARD;

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TOP2 PLAFK
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DOMAIN
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205 ESEGEKG----GTEKDSKKGKKDS----KKGKDSAIELQAVKADEKKDEDGKKDANKGDE 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SK--KKDNPQVNHSQLN-----ESHRKEDLQREEHSQKSDSTKD---VTATVLDKNNI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           257 SKDAKKDAKEIKKGKKDKKKPSSTDSDSKDDVKKE---SKKDATKDAKKVAKKDTEKESA 313
                                                                                                                                                                                                                                                                                     MEDLINE=92255491; PubMed=7737358;
Hess H., Heid H., Zimbelnann R., Franke W.W.;
Hess H., Heid H., Zimbelnann R., Franke W.W.;
Hess H., Heid H., Zimbelnann R., Franke W.W.;

Heads the identification and characterization of cylicin II.";

Exp. Cell Res. 218:174-182(1995).

-!- PUNCTION: POSSIBLE ARCHITECTURAL ROLE DURING SPERMATOGENESIS. MAY

BE INVOLVED IN SPERMATID DIFFERRATIATION.

-!- SUBCELLULAR LOCATION: CALXX; SPERM HEAD CYTOSKELETAL STRUCTURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 KGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTF---DV
                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytoskeleton, Structural protein, Repeat, Sperm, Spermatogenesis. DOMAIN 25 347 31 X 3 AA REPEATS OF K-K-X. DOMAIN 157 240 3 X APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM: 604035; -.
GO; GO:0005200; F:structural constituent of cytoskeleton; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.6%; Score 95; DB 1; Length 348; 30.9%; Pred. No. 1.6; tive 20; Mismatches 39; Indels
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348 AA; 39079 MW; D86766599C1809E7 CRC64;
                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
CYLC2 OR CYLZ.
CYLC2 OR CYLZ.
                                                                                                                     348 AA
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   1150 SHDKHRPFHSKVE--
                                                                                                                     STANDARD;
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Genew; HGNC:2583; CYLC2.
                                                                                                                                                                                                       Homo sapiens (Human)
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                                                           QK 1203
                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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                                   133 NK 134
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Best Local
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MEDLINE=94316496...

A REDLINE=94316496...

A RAIdey R.G., Kilbey B.J.,

A Ridley R.G., Kilbey B.J.,

A Ridley R.G., Kilbey B.J.,

The gene encoding topoisomerase II from Plasmodium falciparum.";

Nucleic Acids Res. 22:2547-2551(1994).

I The gene encoding to FOPOLOGICAL STATES OF DNA BY TRANSIENT

PERAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPOISOMERASE II

MAKES DOUBLE-STRAND BREAKS.

C -1 CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining

C f double-stranded DNA.

C -1 SUBCELLULAR LOCATION: Nuclear.

C -1 SUBCELLULAR LOCATION: Nuclear.

MISCELLANEOUS: EUKARYOTIC TOPOISOMERASE I AND II CAN RELAX BOTH

MISCELLANEOUS: EUKARYOTIC TOPOISOMERASE I AND STRANDS.

RELAX ONLY NEGATIVE SUPERCOLLS.

RELAX ONLY NEGATIVE SUPERCOLLS.

C -1 SIMILARITY: Belongs to the type II topoisomerase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----KKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQ----KSDSTK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00177; TOPOISOMERASE II; 1.
ISOMERASE; TOPOISOMERASE II; 1.
ISOMERASE; TOPOISOMERASE, DNA-bInding; ATP-binding; Nuclear protein.
NP BIND 144 149 ATP (POTENTIAL).
ACT SITE 830 830 DNA CLEAVAGE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26;
                                                                                                                                                                                     Plasmodium falciparum (isolate X1 / Thailand).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 1398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1398 AA; 161029 MW; BAAD7BEE88FE5BE9 CRC64;
01-FEB-1995 (Rel. 31, Created)
30-FEB-1995 (Rel. 31, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
DNA topoisomerase II (EC 5.99.1.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.4%; Score 93; DB 1
24.6%; Pred. No. 9.8;
ive 33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003594; ATPbind ATPase.
InterPro; IPR003595; GPRA, NYB topis.
InterPro; IPR001241; DNA_CopoisoII.
InterPro; IPR002205; DNA_topoisoIV.
Pfam; PP00204; DNA_GyraseB; 1.
Pfam; PP00518; HATPase_C; 1.
Pfam; PP02518; HATPase_C; 1.
PRINTS; PR00418; TP12FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-ASN.
POLY-ASN.
POLY-LYS.
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SWART; SM00487; HPTPBASE C; 1.
SWART; SM00433; TOP2C; 1.
SWART; SM00434; TOP4C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X79345; -; NOT_ANNOTATED_CDS.
HSSP; P06786; 1BGW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35; Conservative
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                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                     NCBI_TaxID=5839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
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-!- FUNCTION: THE FUNCTION OF BRAIN MAPS IS ESSENTIALLY UNKNOWN.

PHOSPHORYLATED MAPIB MAY PLAY A ROLE IN THE CYTOSKELETAL CHANGES

THAT ACCOMPANY NEURITE EXTENSION. POSSIBLY MAPIB BINDS TO AT LEAST

TWO TUBULIN SUBUNITS IN THE POLYMER, AND THIS BRIDGING OF SUBUNITS

MIGHT BE INVOLVED IN NUCLEATING MICROTUBULE POLYMERIZATION AND IN

STABILIZING MICROTUBULES.

-!- SUBUNIT: 3 DIFPERENT LIGHT CHAINS, LC1, LC2 AND LC3, CAN ASSOCIATE

WITH MAPLA AND MAPIB PROTEINS.

-!- DOWAIN: Has a highly basic region with many copies of the sequence

KKEE and KKEIV, repeated but not at fixed intervals, which is

responsible for the binding of MAPIB to microtubules.

-!- PTW: LC1 is coexpressed with MAPIB. It is a polypeptide generated

from MAPIB by proteolytic processing. It is free to associate with

both MAPIB (By similarity).

-!- SIMILARITY: TO MAPIR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright, It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  1199 EFQRNVELSNREESNK--FKVARKQ-----GPSSMKKKKKKKKLSSDEESEGGDTSDSSE 1251
                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last amnotation update)
Microtubule-associated protein 1B (MAP 1B) (Contains: MAP1 light chain
                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Fetal brain;
MEDLINE=95104835; PubMed=7806212;
Lien L.L., Feener C., Fischbach N., Kunkel L.M.;
"Cloning of human microtubule-associated protein 1B and the identification of a related gene on chromosome 15.";
Genomics 22:273-280(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO:0005875; C:microtubule associated complex; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005875; C:mlcrccccxin.
InterPro; IPR000102; MAPIB neuraxin.
PRam; PF00414; MAPIB neuraxin; 10.
PROSTIE; PS00230; MAPIB NEURAXIN; 6.
Microtubules; Repeat; Phosphorylation.
AMELICAL MAPIB NEURAXIN; 10.
AMELICAL MAPI
                                                                                                                                                                                                    PRT; 2468 AA.
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MAP1B 3.
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                                                                                     1252 FLVNTLNIKKNTNKKTTTSSNN 1273
                                           112 DVTATVLDKNNISSKSTTNNPN 133
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MAP1B
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                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                                                                                                                                                                                    HUMAN
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RECORD V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sagouros U., Peat N., Hayles J., Basham D., Bowman S., Brown D., Brown S., Chillingworth T., Churcher C.M., Grantles M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Genlins M., Connor R., Cronin A., Davis P., Hidalgo J., Hodgson G., A. Hornsby T., Howarth S., Hudche E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., R. Hornsby T., Howarth S., Murphy L., Niblett D., Odell C., Monorey P., Moule S., Mundall K., Murphy L., Niblett D., Odell C., R. Rutter S., Saunders D., Seeger K., Sharp S., Stevens K., Stevens K., Stevens K., Stevens K., Stevens K., Taylor R., Taylor R., Tivey A., Walsh S.V., Grymonprez B., Wodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Wodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Wodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Robel C., Fuchs M., Feilzc C., Holzer B., Mestl D., Mutteher S., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Ber P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Lenand M., Rochet M., Gallardin C., Honze V., Horse S., Galibert E., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Locas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Jucas M., Revuelta J.L., Moreno S., Armetrong J., Forsburg S.L., R. Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; R. Henger H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Perker M., He Genome sequence of Schizosaccharomyces pombe. H., R., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter H., Marter
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                                                                                                                                                                                                                                                                                                                                                                     48 LSKDTFIKPVFKKIEBKKEBENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQRE----E
                                                                                                                                                                                                                                                                             Gaps
LYS-RICH (HIGHLY BASIC, CONTAINS MANY KKEE AND KKEI/V REPEATS).
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                                                                                                                                                                                                                                                                             Indels 13;
                                                                                                                                                                                     DB 1; Length 2468;
                                                                                        2468 AA; 270618 MW; 540839CBDF09D461 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae;
                                                                                                                                                                      Query Match 13.3%; Scot. 2.1, Best Local Similarity 31.0%; Pred. No. 19; Matches 22; Conservative 19; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1998 (Rel. 36, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Hypothetical protein C6B12.02c in chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last seq.
28-FEB-2003 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z98531; CAB11064.1; -. PIR; T39009; T39009.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 HSQKSDSTKDV 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4896;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCHPO
                                                                                             SEQUENCE
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014207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              390 SSSLTSENPFOLNVAANAVSTIPVYRTTKTKMKKN-RFKYVEVEKLPDLILESYGKKAPK 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 YVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEH 103
                                                                                                                                                                                                                                                                                                                                                                                                                            4 SSTIVSEEDF------GKKDAG 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBSTITUTES ATE KNOWN.
SUBCELLULAR LOCATION: Secreted.
DOMAIN: THE SIGNAL PEPTIDE GUIDES THE PRECURSOR TO THE PERIPLASMIC SPACE, AND THE CARBOXY-TERMINAL HELPER DOMAIN ASSOCIATES WITH THE OUTER MEMBRANE TO FORM A PORE FOR EXCRETION OF THE PROTEASE SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              449 FLRVFARSSSHIP--KMIRRKRQMDSKKYFSFDKESDRQVIDQVLSDWYSGKHELVQQSH
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
1-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Immunoglobulin Al protease precursor (EC 3.4.21.72) (IGAl protease)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92234949; PubMed=1373717;
MEDLINE=92234949; PubMed=1373717;
Poulsen K., Reinholdt J., Kilian M.;
Poulsen K., Reinholdt J., Kilian M.;
"A comparative genetic study of serologically distinct Haemophilus influenzae type 1 immnoglobulin Al proteases.";
J. Bacteriol. 174:2913-2921(1992).
-!- FUNCTION: VIRULENDE FATOR; CLEAVES HOST IMMUNOGLOBULIN A PRODUCTION INTACT FC AND FAB FRAGMENTS.
-!- CATALYTIC ACTIVITY: Cleavage of immunoglobulin A molecules at certain Pro-|-Xaa bonds in the hinge region. No small molecule
                                                                                                                                                                                                                                                                                                                                                                              30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellaceae, Haemophilus.
                                                                                                                                                                                                                                                                                                                          Score 89; DB 1; Length 1888; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                  12.8%; Score 69, 23.9%; Pred. No. 27; 23.9%; Indels rive 29; Mismatches 59; Indels rive 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mismatches 29; Mism
                                                                                                                                                                                                                                                                        AA; 217432 MW; 8AD3BBCE32397C29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 SOKSDS-TKDVTATVLDKN----NISSKSTTNN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO PEPTIDASE FAMILY S6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1702 AA.
                                                                                                POTENTIAL. POTENTIAL.
                                                                                                                                                                        POTENTIAL.
POTENTIAL.
POTENTIAL.
                       protein; Transmembrane.
                                                                           POTENTIAL
                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                    POLY-LEU
SPombe; SPAC6B12.02c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=HK715 / Serotype B;
                                                                                                                                                                                                                                                                                                                                                                              37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                           775
886
935
935
1053
1356
1665
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                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                           1033
1336
1645
                                                                                                                                                                                                                                                                              1888
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                         Hypothetical
TRANSMEM (
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SEQUENCE
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EMBL; M87489; AAA24966.1; -.

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1296 INTGSATAITETAEKSDKPQTETAASTEDASQHKANTVADNSVANNSESSEPKSRRRSI 1355
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-!- FUNCTION: THE FUNCTION OF BRAIN MAPS IS ESSENTIALLY UNKNOWN.

--- PHOSPHORYLATED MAPLB MAY PLAY ROLE IN THE CYTOSKELETAL CHANGES
THAT ACCOMPANY NEURITE EXTENSION. POSSIBLY MAPIB BINDS TO AT LEAST
TWO TUBULIN SUBUNITS IN THE POLYMER, AND THIS BRIDGING OF SUBUNITS
MIGHT BE INVOLVED IN NUCLEATING MICROTUBULE POLYMERIZATION AND IN
STABILIZING MICROTUBULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WITH MAPIA AND MAPIB PROTEINS.

WITH MAPIA AND MAPIB PROTEINS.

DOMAIN: Has a highly basic region with many copies of the sequence KKEE and KKEI/V, repeated but not at fixed intervals, which is responsible for the binding of MAPIB to microtubules.

PRIN: LCI IS COEXPRESSED WITH MAPIB: IT IS A POINTEPTIDE GENERATED PROM MAPIB BY PROTEOLYTE PROCESSING. IT IS FREE TO ASSOCIATE WITH BOTH MAPIB AND MAPIB. IT INTERACTS WITH THE AMINO-TERMINAL REGION
                                                                                                                                                                                                                                                                                                                              2 X 8 AA TANDEM REPEATS OF A-K-V-E-K-E-E-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 INLSKDTFIKPVFKKIEEKKEEENKPTPDVSKKKDNPQVNHSQLNESHRKEDLQREEHS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                              InterPro; IPR000710; IgA_S6.
InterPro; IPR000710; IgA_S6.
InterPro; IPR0004899; Pertactin.
Pfam; PF03197; Autotransporter; 1.
Pfam; PF03212; Pertactin; 1.
PRINTS; PR00921; IGASERPTASE.
TIGRFAMs; TYGR01414; autotrans barl; 1.
TIGRFAMs; TYGR01414; autotrans barl; 1.
25 POTENTIAL.
I 25 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND DOMAIN.
STRAIN=Swiss Webster; TISSUE=Brain;
MEDLINE=90094539; PubMed=2480963;
Noble M., Lewis S.A., Cowan N.J.;
"The microtubule binding domain of microtubule-associated protein MAPIB contains a repeated sequence motif unrelated to that of MAP2 and tau.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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01-APR-1990 (Rel. 14, Last sequence update)
28-FSB-2003 (Rel. 41, Last annotation update)
Microtubule-associated protein 1B (MAP 1B) (MAP1.2) (MAP1(X))
Maple OR MTAP1B OR WTAP5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 1702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50; Indels
                                                                                                                                                                                                                                                                                                                                                                       1109 1116 1.
1117 1124 2.
1702 Aa, 186539 MW, 860F70D2667807A6 CRC64;
                                                                                                                                                                                                                                                            IMMUNOGLOBULIN A1 PROTEASE.
HELPER PEPTIDE (POTENTIAL).
PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 -- QKSDSTKDVTATVLDKNNISSKSTINNPNK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Pred. No. 32;
14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.6%; Score 87.5; 27.2%; Pred. No. 32;
                                                            InterPro; IPR005546; Autotransporter.
                     nekurs; 806.001; -.
InterPro; IPR006315; Autotransport
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 27.2%
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
A41859; A41859
                                                                                                                                                                                                                                                                                          1015
288
1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF MAP1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAPB MOUSE
                                                                                                                                                                                                                                                                                                             ACT SITE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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PROPEP
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                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
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SEQUENCE
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BINDING
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IF2_STAEP
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SO TT WE BEAR A BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BUT WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR WAS BEAR W
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                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pyrococcus kodakaraensis.
Archaea; Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97316461; PubMed=9172372;
Adul Rahman R.N.Z., Jongsareejit B., Fujiwara S., Imanaka T.;
"Characterization of recombinant glutamine synthetase from the hyperthermophilic archaeon Pyrococcus sp. strain KODI.";
Appl. Environ. Microbiol. 63:2472-2476 [1997].
-!- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LYS-RICH (HIGHLY BASIC, CONTAINS MANY KKEE AND KKEI/V REPEATS). W; FBD3DD99CFDBDA87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase) (GS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.5%; Score 87; DB 1; Length 2464; 28.4%; Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 -----EHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             687 KKEERKELKKEVKKETPLKDAKKEVKKEEKKEVKKEEKEPKK 728
                                                                                                                                                                                                                                                                                                                                                                                                                  Phosphorylation.
4 MAP1 LIGHT CHAIN LC1.
0 MAP1B 1.
                                                                                                                                                                                                                                                    PIR; S07549; QRMSP1.
MGD; MGI:1306778; Mtaplb.
GO; GO:0016358; P:dendrite morphogenesis; IMP.
GO; GO:0001578; P:microtubule bundling; IMP.
InterPro; IPR000102; MAP1B_neuraxin.
                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00414; MAP1B neuraxin; 10.
PROSITE; PS00230; MAP1B_NEURAXIN; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAPIB
MAPIB
MAPIB
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MAPIB
MAPIB
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                                                                                                                                                                                                                                 EMBL; X51396; CAA35761.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: TO MAPIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1993
2010
2027
2044
589
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                                                                                                                                                                                                                                                                                                                                                                                                                       Microtubules;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLNA PYRKO
008467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=KOD1
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REPEAT
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  셤
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this tatement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- FUNCTION: One of the essential components for the initiation of protein synthesis. Protects formylmethionyl-tRNA from spontaneous hydrolysis and promotes its binding to the 30S ribosomal subunits. Also involved in the hydrolysis of GTP during the formation of the 70S ribosomal complex (By similarity).
-!- SUBCELULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE IF-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z., Chen Z., Wen Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----NPQVNHSQLNESHRKEDLQREEHSQKSD---STKDVTATVLD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMP (UNDER CONDITIONS OF ABUNDANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        443 AA; 50259 MW; 9426DCCFEEF18168 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 YKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-257-4; (2017) (Rel. 42, Created) (15-58P-2003 (Rel. 42, Last sequence update) (15-58P-2003 (Rel. 42, Last annotation update) (Translation initiation factor IF-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLUTAMINE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.4%; Score 86;
17.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                      interPro; IPR001691; GLN synth.
InterPro; IPR004809; GlnA.
InterPro; IPR001637; GlnA_adenyltn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00120; gln.synt; I.
Pfam; PF03951; gln.synt_N; 1.
ProDom; PD001057; Gln synt_C; 1.
TIGRFAMS; TIGR0653; GlnA; 1.
PROSITE; PS00180; GLNA 1; 1.
PROSITE; PS00181; GLNA 2; 1.
                                                                                                                                                                                                                                                                                                                                                EMBL; D86222; BAA20530.1; -. HSSP; P06201; 1LGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  362
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  362
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Pfam; PF03175; DNA_pol_B_2; 1.
SWART; SM00486; POLBC; 1.
PROSITE; PS00116; DNA_POLYMERASE_B; 1.
Transferase; DNA-directed DNA polymerase; DNA replication;
DNA-binding; Plasmid; Mitochondrion.
SEQUENCE 1202 AA; 138279 MW; 51D41FCEBDBF2CDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=S288C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=S288c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=S288C
                                                                                                                                                                                                                                                                                                                                                                                                                    YEAST
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                                                                                                                                                                                                                                                                                                                                       5;
                                                                                                                                                                                                                                                                                                                                                                     61 IEEKKEEENKPTFDVSKKKD----NPQVNHSQLNESHRKEDLQREEHSQKSDSTK---D 112
                                                                                                                                                                                                                                                                                                                                                                                        38 LEEEQIKALDKKFKASQAKDTNKQNTQNNHQKSNNKQNSNDKEKQQSKNNSKPTKKKEQN 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=2/1;
MEDLINE=90066356; PubMed=2573821;
Kempken F., Meinhardt F., Esser K.;
Kempken F., Meinhardt F., Esser K.;
"In organello replication and viral affinity of linear,
"In organello replication and viral affinity of linear,
extrachromosomal DNA of the ascomycete Ascobolus immersus.";
Mol. Gen. Genet. 218:523-530 (1989).
-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- MISCELLANEOUS: THIS DNA POLYMERASE REQUIRES A PROTEIN AS A PRIMER
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY. STRONG, TO DNA POLYMERASE OF OTHER FUNGAL AND PLANTS MITOCHONDRIAL PLASMIDS.
                                                                                                                                                                                                                                                                                                                                       8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Fungi, Ascomycota, Pezizomycotina, Pezizomycetes,
Pezizales, Ascobolaceae, Ascobolus.
NCBI_TaxID=5191;
                                                                                                                                                                                                                                                                                                         DB 1; Length 720;
                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                          TP (BY SIMILARITY).

TP (BY SIMILARITY).

TP (BY SIMILARITY).

07FB5A6A59CF970C CRC64;
                                                 HAMAP; MF_00100; -; 1.

Pfam; PF00009; GTP_EFTU; 1.

Pfam; PF04164; GTP_EFTU D2; 1.

ProDom; PD186100; IF2 N; 2.

ProDom; PD186100; IF2 N: 1.

TIGRFAMS; TIGR00487; IF-2; 1.

TIGRFAMS; TIGR00231; small_GTP; 1.

INITIATION factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                        12.2%; Score 85; DB 1; Les 28.0%; Pred. No. 20; ive 15; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1202 AA
   or send an email to license@isb-sib.ch)
                                                                                                                                                                                                             G-DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probable DNA polymerase (EC 2.7.7.7)
                                                                                                                                                                                                                                                                                                                                                                                                                                     113 VTATVLDKNNISSKSTTNNPNK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 NKGKQQNKNNKTNKNQKNNKNK 119
                                                                                                                                                                                                                            GTP
GTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR006172; DNA_pol_B.
InterPro; IPR004868; DNA_pol_B_2.
                                                                                                                                                                                                                                                           334 G
79343 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1991 (Rel. 19, Created)
                                  EMBL; AE016747; AA004542.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X15982; CAA34106.1; -.
                                                                                                                                                                                                                                                                                                                      Local Similarity 28.0 les 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                            238
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15-DEC-1998 (Rel. 37,
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                                                                                                                                                                                                                                                           331 3
720 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ascobolus immersus.
Mitochondrion.
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                                                                                                                                                                                                Complete proteome.
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                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                           Query Match
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NP_BIND
                                                                                                                                                                                                                            NP_BIND
                                                                                                                                                                                                               DOMAIN
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KGSL----SFDFKPLKTIEGTKYANYTFPIKKDIVVKDINKKINFNGLDLPKTMDLSKWP 427
                                                                                                                                                             72 TPDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNI-----S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gansheroff L.J., Dollard C., Tan P., Winston F.;
"The Saccharomyces cerevisiae SPT7 gene encodes a very acidic protein
important for transcription in vivo.";
                                    20; Gaps
                                                                     19 KGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIE-----EKKEEENK-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The bromodomain: a conserved sequence found in human, Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POSSIBLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   van der Aart Q.J.M., Barthe C., Doignon F., Aigle M., Crouzet M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Sequence analysis of a 31 kb DNA fragment from the right arm of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Andre B., Cziepluch C., Hein C., Jauniaux J.C., Urrestarazu A., Vissers S.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         yeast proteins.";
Nucleic Acids Res. 20:2603-2603(1992).
-!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR OF TY ELEMENTS AND
Length 1202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 463-523 FROM N.A.
MEDLINE=92285152; PubMed=1350857;
Haynes S.R., Dollard C., Winston F., Beck S., Trowsdale J.,
                                    55; Indels
 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1994 (Rel. 28, Last sequence update)
01-007-1996 (Rel. 34, Last annotation update)
Franscriptional activator SPT7.
SPT7 OR YBR081C OR YBR0739.
Query Match 12.2%; Score 85; DB 3
Best Local Similarity 25.6%; Pred. No. 34;
Matches 33; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                          PRT; 1332 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae chromosome II.";
Yeast 10:959-964(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER GENES.
-!- SUBCELLULAR LOCATION; Nuclear.
-!- SIMILARITY; Contains 1 bromodomain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95229044; PubMed=7713415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95076715; PubMed=7985423;
                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1994 (Rel. 28, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-835 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetics 139:523-536(1995)
                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                     | ||:||
SMGNTNDPN 494
                                                                                                                                                                                                                 SKSTTNNPN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Steensma H.Y.;
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EKKEEENKPTFD-----VSKKKD-----NPQVNHSQLNESHRKEDLQR-EEH 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 TIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIK---PVFKKIE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Immunoglobulin Al protease precursor (EC 3.4.21.72) (IGA1 protease).
IGA OR IGA1 OR HI0990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Rd / KW20 / ATCC 51907;

STRAIN=Rd / KW20 / ATCC 51907;

MEDLINE=95350630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F.,

Kerlavage A.R., Bult C.J., Tomb J.F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transcription regulation; NucTear protein; Activator; Bromodomain.
DOMAIN 458 528 BROMODOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27;
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Pasteurellaceae, Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.1%; Score 84.5; DB 1; Length 1332; 24.3%; Pred. No. 41; ive 24; Mismatches 61; Indels 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               083B63624669244F CRC64;
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Submitted (MAY-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1694 AA
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PROSITE; PS50014; BROMODOMAIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGD; S0000285; SFT7.
GO; GO:0000124; C:SAGA complex; Il
InterPro; IPR001487; Bromodomain.
Pfam; PF00439; bromodomain; 1.
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EMBL; X76294; CAA53940.1; -.
EMBL; Z35550; CAA85026.1; -.
EMBL; M87651; AAA55087.1; -.
PIK; S41552; 841552.
HSSP; Q92831; 1B91.
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Matches 36, Conservative
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P44969;
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IGAO_HAEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 INLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHS- 104
                                                                                                                                               -!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: THE SIGNAL PREPRIDE GUIDES THE PRECURSOR TO THE PERIPLASMIC SPACE, AND THE CARBOXY-TERMINAL HELPER DOMAIN ASSOCIATES WITH THE OUTER MEMBRANE TO FORM A PORE FOR EXCRETION OF THE PROTEASE DOMAIN. THE HELPER DOMAIN IS THEN RELEASED BY AUTOPROTEOLYSIS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S6.
                             "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                  certain Pro- |-Xaa bonds in the hinge region. No small molecule
                                                         Science 269:496-512(1995).
-1- FUNCTION: VIRULENCE FACTOR; CLEAVES HOST IMMUNOGLOBULIN A PRODUCING INTACT FC AND FAB FRAGMENTS.
-1- CATALYTIC ACTIVITY: Cleavage of immunoglobulin A molecules at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             э
,
Snehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 1694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase; Serine protease; Transmembrane; Zymogen; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> D (IN REF. 1).
-> G (IN REF. 1).
-> G (IN REF. 1).
-> T (IN REF. 1).
C52427013F93178C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Pred. No. 53;
15; Mismatches 50; Indels
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EN -> GV (IN
G -> A (IN R
G -> E (IN R
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InterPro; IPR005546; Autotransporter.
InterPro; IPR000710; IGA SG.
InterPro; IPR004899; Perfactin.
Pfam; PR03797; Autotransporter; 1.
Pfam; PR02395; IGA1; 1.
Pfam; PR02312; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00921; IGASERPTASE.
FIGRFAMs; TIGR01414; autotrans_barl; 1.
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EMBL; U32779; AAC22651.1; -.
PIR; H64106; H64106.
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1545
A; 185539 N
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1036
1074
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TIGR; H10990; -.
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                  Venter J.C.;
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P43610;
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CONFLICT
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                                              Rd.";
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    A D
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical 88.7 kDa helicase in CDC26-SAPI55 intergenic region.
YFR038W.
                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                  Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M., Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K., Yamazaki M., Tashiro H., Eki T.; "Analysis of the nucleotide sequence of chromosome VI from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; DS0617; BAA09277.1; -.
PIR; S56293; SS6293
SGD; S0001934; YFR038W.
INTERPO; IPR0011910; DEAD.
INTERPO; IPR001050; Helicase_C.
INTERPO; IPR0010510; SNF2_N.
Pfam; PF00171; helicase_C; 1.
Pfam; PF00176; SNF2_N; T.
SMART; SM004987; DEXDC; 1.
Hypothetical protein; Nuclear protein; DNA-binding; Helicase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 778;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 ATP (POTENTIAL).
355 DEGH BOX.
88730 MW; 3E6C0857B5EABD84 CRC64;
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25.5%; Pred. No. 26;
iive 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKKRKTKKKSITDFFKKQKKNEDTT 200
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                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-S288c / AB972;
MEDLINE-95400292; PubMed=7670463;
                                                                                                                                                                                                                                                                                                                                                                                          Nat. Genet. 10:261-268(1995).
                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 12.19
Best Local Similarity 25.55
Matches 37; Conservative
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355
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=S288c / AB972;
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778 AA;
                                                                                                                                                                                    NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 KKWLBEQERKLKEGWKEQORKEREBEBQKQOEKKEKEBAVQKWLDQAENDLENSTTWQNP 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE=96212931; PubMed=8630064;
Pearsall R.S., Shibata H., Brozowska A., Yoshino K., Okuda K.,
Pearsall R.S., Chibata H., Brozowska A., Yoshino K., Okuda K.,
Dejong P.J., Plass C., Chapman V.M., Hayashizaki Y., Held W.A.;
"Absence of imprinting in UZAPBPL, a human homologue of the imprinted
mouse gene UZafbp-rs.";
Biochem Biophys. Res. Commun. 222:171-177 (1996).
--- SUBCELLULAR LOCATION: Nuclear (Potential).
--- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
--- SIMILARITY: Contains 2 C3H1-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EEENKPTFDVSKKKDNPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Isolation and mapping of human homologues of an imprinted mouse gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nuclear protein, RNA-bindīng, Ribonucleoprotein, Zinc-finger, Repeat.
DOMAIN 203 309 RNA-BINDING (RRM)
SEQUENCE 479 AA, 57643 MW, 96F326694BD4E7CO CRC64;
                        Q15695; Q13570;
01-NOV-1997 (Rel. 35, Created)
12-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
UZ small nuclear ribonucleoprotein auxiliary factor 35 kDa subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kitagawa K., Wang X., Hatada I., Yamaoka T., Nojima H.,
Inazawa J., Abe T., Mitsuya K., Oshimura M., Murata A., Monden M.,
                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 29;
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GO, 600534; C:nucleus, NAS.
GO; 600300323; F:RNA binding activity; NAS.
InterPro, IPR000504; RNA_rec_mot.
InterPro, IPR00051; Znf_CCCH.
Pfam, PF00076; rrm; 1.
Pfam; PF00642; zf-CCCH; 2.
479 AA
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SMART; SM00356; ZNF C311; 2.
SMSTITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM RNP_1; FALSE_NEG.
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96163878; PubMed=8586425;
                                                                                                                                                                                                    related-protein 1.
UZAF1-RS1 OR UZAF1RS1 OR UZAFBPL.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D49676; BAA08532.1; -. EMBL; U51224; AAA98669.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U2af1-rs1.";
Genomics 30:257-263(1995).
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   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain;
   U2R1 HUMAN
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EMBL; BC002719; AAH02719.1; -.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhata N.K.,
A Hopkins R.F., Jordan H., Moore T., Mang J., Hsieh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Schautz J., Myers R.M.,
Blakesley R.W., Touchman J.W., Schautz J., Myers R.M.,
Cherin J.W., Krzywinski M.I., Skalska U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length
Human and mouse ColN sequences.",
Full M. A. Schein J. R. S. S., M.
                                                                                                                                                                                                                                                                                                                                                                  Block K.L., Vorniocher H.-P., Hershey J.W.B.; "Characterization of cDNAs encoding the p44 and p35 subunits of human translation initiation factor eIF3."; J. Biol. Chem. 273:31901-31908(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

TISSUB=Ovarian carcinoma;

TISSUB=Ovarian carcinoma;

TISSUB=Ovarian carcinoma;

TISSUB=Ovarian carcinoma;

TISSUB=Ovarian carcinoma;

Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

Ninomiya K., Itavanagi T.,

"NEDO human cDNA sequencing project.";

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: EIF-3 IS COMPOSED OF AT LEAST 12 DIFFERENT SUBUNITS (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIGG. NATI. ACAG. Sci. U.S.A. 99:16899-16903 (2002).
-!- FUNCTION: BINDS TO THE 40S RIBOSOME AND PROMOTES THE BINDING OF METHIONYL-TRNAI AND MRNA.
                                                         TF31 HUMAN STANDARD; PRT; 258 AA.
75822; OSBUD2; OSH8Q2;
30-MAY-2000 (Rel. 39, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
ESSEP-2003 (Rel. 42, Last annotation update)
Eukaryotic translation initiation factor 3 subunit 1 (eIF-3 alpha)
(eIF3 p35) (eIF3j).
                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=99041954; Pubmed=9822659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22388257; Pubmed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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              RESULT 15
TF31 HUMAN
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EMBL; U97670; AAC78729.1; -. EMBL; AK023388; BAB14555.1; -.

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18 YKGELEKGYQFDGWEISGFEGKKDAGY--VINLSKDTFIKPVFKKIEEKKEEENKPTFDV 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 SKKKDNPQ-----VNHSQLNESHRKEDLQREEHSQKSDSTKDVTATV--LDKNNISSK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: INTERACTS WITH OUTER MEMBRANE RECEPTOR PROTEINS THAT CARRY OUT HIGH-AFFINITY BINDING AND ENERGY DEPENDENT UPTAKE INTO THE PERIPHASMIC SPACE OF SPECIFIC SUBSTRATES. IT COULD ACT TO TRANSDUCE ENERGY FROM THE CYTOPLASMIC MEMBRANE NO SPECIFIC ENERGY-REQUIRING PROCESSES IN THE OUTER MEMBRANE, RESULTING IN THE RELEASE INTO THE PERIPHASM OF LIGANDS BOUND BY THESE OUTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                     39 WEGEDEDEDVKDNWDDDDDEKKEEAEVKPEVKISEK---KKIAEKIKEKERQQKKRQEEI
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MEDLINE=55350630; PubMed=7542800;

MEDLINE=55350630; PubMed=7542800;

Relachmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutron G., Fitzhugh W., Fields C.A., Gocayne J.D.,

McGman J.F., Shritey R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heme and
                                                                                                                                                                                                                                                                                                                                         12;
                                      MIM, 603910; - Goukaryotic translation initiation factor 3. GO; GO:0005852; C:eukaryotic translation factor activity; TAS. GO; GO:0003446; P:regulation of translational initiation; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A functional tonB gene is required for both utilization of virulence expression by Haemophilus influenzae type b."; Infect. Immun. 62:2470-2477(1994).
                                                                                                                                                                                                                                                                                                11.9%; Score 83; DB 1; Length 258; 25.4%; Pred. No. 9.6; ative 25; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-94245357; PubMed-8188372;
Jarosik G.P., Sanders J.D., Cope L.D., Muller-Eberhard U.,
                                                                                                                                                                                                                     E -> G (IN REF. 1).
A -> T (IN REF. 2).
8362423542445AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                      Initiation factor; Protein biosynthesis.
                                                                                                                                                                                POLY-ASP.
POLY-LYS.
                                                                                                                                         POLY-ALA.
POLY-GLY.
                                                                                                                                                                                                                                                             29062 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 25.4<sup>§</sup>
Matches 30; Conservative
Genew, HGNC:3270; EIF3S1
GK; 075822; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haemophilus influenzae.
                                                                                                                                           32
57
224
40
141
                                                                                                                                                                                                                                         141 1
258 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TonB protein.
TONB OR HI0251.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hansen E.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TONB HAEIN
P42872;
                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                         CONFLICT
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DOMAIN
DOMAIN
DOMAIN
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TONB_HAEIN
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YMB4 YEAST
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   SO THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE PRESENTATION OF THE
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                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pyrococcus abyssi.
Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interaction interactions of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the
MEMBRANE PROTEINS. REQUIRED FOR HEME UTILIZATION AND VIRULENCE.
                        SUBCELLULAR LOCATION: PERIPLASMIC. ANCHORED TO THE CYTOPLASMIC MEMBRANE VIA ITS N-TERMINAL SIGNAL-LIKE SEQUENCE, SPANS THE PERIPLASM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase) (GS)
GLNA OR PYRAB16090 OR PAB1292.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PERIPLASMIC (POTENTIAL).
4 X 2 AA TANDEM REPEATS OF E-P.
GLU/PRO-RICH.
GLU/LYS/PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.9%; Score 83; DB 1; Length 270 32.1%; Pred. No. 10; ive 16; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A -> V (IN STRAIN TN106).
E -> K (IN STRAIN TN106).
D -> N (IN STRAIN TN106).
G -> E (IN STRAIN TN106).
G -> E (IN STRAIN TN106).
E -> Q (IN STRAIN TN106).
E -> D (IN STRAIN TN106).
E -> K (IN STRAIN TN106).
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                                                                                                            -!- SIMILARITY: BELONGS TO THE TONB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 TKDVTATVLDKNNISSKSTTN 130
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16-OCT-2001 (Rel. 40, Last seqn
15-SEP-2003 (Rel. 42, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29193 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U04996; AAA60460.1; -. EMBL; U32711; AAC21917.1; -. PIR; F64057; F64057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR003538; TonB.
Interpro; IPR006260; TonB_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 32....
Local Schularity 32....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 1
226 2
270 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Огвау;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=29292;
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PubMed=12622808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGR; HI0251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLNA PYRAB
Q9UY99;
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SEQUENCE
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VARIANT
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VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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   g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 VIKRVIEKLAEMGIKAYIGPEPEFYLFKKNGSWELEIPDVGGYFDILTLDKAKDIKREIA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .---- 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C., Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.; "An integrated analysis of the genome of the hyperthermophilic archaeon Pyrococcus abysi.";
Mol. Microbiol. 47:1495-1512(2003).
-! - CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-1996 (Rel. 34, Last sequence update)
15-SBP-2003 (Rel. 42, Last annotation update)
Hypothetical 32.4 kpa protein in TAF40-ERV25 intergenic region.
YML014W OR YM9571.04.
Saccharowyces cerevisiae (Baker's yeast).
Eukaryota: Fungi; Ascomycota; Saccharowycotina; Saccharomycetes; Saccharomycetales; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMP (UNDER CONDITIONS OF ABUNDANT GLUTAMINE) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 439;
                                                                                                                                                                                       L-glutamine.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62CCFD3970A98AF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 VFKKIEEKKEEEN-----KPTFDVSKKKDN------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:| |::::| ::|::||::|| EYMPSFGLVPEVLHEVGKAQHEIDFRYDEALKTADN 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 82.5; DE; Pred. No. 18; 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    279 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; C75009; C75009.
HSSP; P06201; ILGR.
INTERPO; PR001691; GIM synth.
InterPro; IPR001690; GIM.
InterPro; IPR001637; GIM.
Adenyltn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00120; gln-synt; T.
Pfam; PF00351; gln-synt, N; I.
ProDom; PD001057; gln synt C; I.
TIGRPAMs; TIGR00653; GlnA; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last seq
15-SEP-2003 (Rel. 42, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AJ248288; CAB50513.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    439 AA; 49742 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ligase, Complete proteome.
BINDING 358 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28; Conservative
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STRAIN-S288c / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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PubMed=9169872;
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21 ELEKGYQPDGWEISGPEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLNA OR PF0450.
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005907;
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                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED custation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@18b-sib.ch).
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maia e Silva A., Bossier P., Vilela C., Fernandes L., Soares H., Guerreiro P., Rodrigues-Pousada C.; Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
P., Skelton J., Walsh S., Whitehead S., Barrell B.G.; nucleotide sequence of Saccharomyces cerevisiae chromosome
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                                                                                                                  -! - SIMILARITY: TO S. POMBE SPACI3D6.03C AND SOME, TO C. ELEGANS
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01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Hypothetical 47.4 kDa protein in PASI-MST1 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.8%; Score 82; DB 1; Length 279; 28.9%; Pred. No. 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Mismatches 39; Indels
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279 AA; 32438 MW; 2F8795BB3C640D3B CRC64;
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427 AA; 47416 MW; 44386D250DE5DED4 CRC64;
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SGD; S0004476; YML014W.
InterPro; IPR001601; Methyltransf.
InterPro; IPR000051; SAM_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z49810; CAA89938.1; -. PIR; S55105; S55105.
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SGD; $0001678; YKL195W.
                                                                                            Nature 387:90-93(1997)
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P36046;
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STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBL/GenBank/DBDJ databases.
-:- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase) (GS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
MEDLINE=94365840; PubMed=7916055;
Brown J.R., Masuchi YV. Rob F.T., Doolittle W.F.;
"Evolutionary relationships of bacterial and archaeal glutamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABUNDANT
                                                                                                                                  81 NPOVNHSQLNESHRKEDLOREEHSQKSDSTKDVTATVLDKNNISSK 126
                                                                                                                                                                            L-glutamine.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PKDTK -> IPPDTE (IN REF. 1)
96563A8E9A0E0892 CRC64;
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InterPro; IPR004809; GlnA.
InterPro; IPR001637; GlnA_adenyltn.
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HSSP; P06201; 1LGR.
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439 AA;
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01-JUN-1994 (Rel. 29, Last sequence update)
15-DEC-1998 (Rel. 37, Last amnotation update)
Glutamine synthetase I (EC 6.3.1.2) (Glutamate--ammonia ligase) (GSI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequences."; J. Bacteriol. 175:2961-2969(1993). J. Bacteriol. ACTIVITY: ATP + L-glutamate + NH(3) \approx ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tiboni O., Cammarano P., Sanangelantoni A.M.;
"Cloning and sequencing of the gene encoding glutamine synthetase I from the archaeum Pyrococus woosei: anomalous phylogenies inferred from analysis of archaeal and bacterial glutamine synthetase I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 PSFGLIPEVLHHEVGKAQHEIDFRYDEALKTADNIVSFKYITKAVAEMHGL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                82 -----PQVNHSQLNESHRKEDLQREEHSQKSD---STKDVTATVLDKNNI 123
                                                                                          72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     358 . 358 AMP (UNDER CONDITIONS OF ABUNDANT GLUTAMINE). (BY SIMILARITY).
439 AA; 50066 MW; C503B43B790BD25C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L-glutamine.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 11.8%; Score 82; DB 1; Length 439; Best Local Similarity 18.1%; Pred. No. 20; Matches 31; Conservative 26; Mismatches 42; Indels
                     DB 1; Length 439; 20;
                                                                                      42; Indels
                                                                                                                                                                                                                                                                                                       60 KIEEKKEEEN-----KPTFDVSKKKDN-----
Query Match
Best Local Similarity 18.1%; Prec. ...
Marches 31; Conservative 26; Mismatches
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InterPro; IPR001691; GLN synth.
InterPro; IPR004809; GLNA.
InterPro; IPR004809; GLNA.
InterPro; IPR004809; GLNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93259940; PubMed=8098326;
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Pfam; PF03951; gln-synt N; 1.
ProDom; PD001057; Gln synt C; 1.
TIGRFAMS; TIGRE00653; GlnA; 1.
PROSITE; PS00180; GLNA 1; 1.
PROSITE; PS00181; GLNA ATP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR, A36911; A36911.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pyrococcus woesei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=2262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PYRWO
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                                      45 GISFDGSSVPGFQGIEDSDLVFKADPDTYVEVPWDNVARVYGFIYKDNKPYGADPRGILK 104
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MEDLINE=99120557; PubMed=9923682;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown B.D., Doig P.C.,
Smith D.R., Noonan B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                        165 PSFGLIPEVLHHEVGKAQHEIDFRYDBALKTADNIVSFKYITKAVAEMHGL 215
                                                                                                                                                                                                                                                    82 -----PQVNHSQLNESHRKEDLQREEHSQKSD---STKDVTATVLDKNNI 123
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GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
31-MAY-2003 (Rel. 42, Last annotation update)
Translation initiation factor IP-2.
GYQFDGWEISGFEGKKDAGYVINLSKDTFI--
                                                                                                                             60 KIEEKKEEEN-----KPTFDVSKKKDN---
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PEam; PF03144; GTP_EFTU D2; 2.
PEam; PF04766; IF2 N; 1.
Pr0Dom; PD186100; F2; 1.
TIGRPAMS; TIGR00487; IF-2; 1.
TIGRPAMS; TIGR00487; Small_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE001472; AAD05948.1; -. PIR; E71940.
HAMAP; MF_00100; -; 1.
InterPro; IPR000795; BF GTPbind.
InterPro; IPR004161; BFTU_D2.
InterPro; IPR000178; IF2.
InterPro; IPR006847; IF2. N.
InterPro; IPR006847; IF2. N.
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464
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DOMAIN
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                                                                                                                                                                                                                  50 KDTFIKPVFKKIEEKKEEENKPTFDVSKKKD-------NPQ-VNHSQLNES 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conley C.A., Fritz-Six K.L., Almenar-Queralt A., Fowler V.M.; "Leiomodins: larger members of the tropomodulin (Tmod) gene family."; Genomics 73:127-139(2001).
                                                                                                                                                32; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Leiomodin I (Leiomodin, muscle form) (64 kDa autoantigen D1) (64 kDa autoantigen 1D) (64 kDa autoantigen D3) (7hyroid-associated ophthalmopathy autoantigen) (Smooth muscle leiomodin) (SM-Lmod).
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DISEASE: RECCANIZED BY PATIENTS WITH AUTOIMMUNE THYROID DISEASE. SIMILARITY: BELONGS TO THE TROPOMODULIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dong Q., Ludgate M., Vassart G.; "Cloning and sequencing of a novel 64-kDa autoantigen recognized by parients with autoimmune thyroid disease."; J. Clin. Endocrinol. Metab. 72:1375-1381(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARACTERIZATION.
MEDLINE=99451105; PubMed=10520227;
Conley C.A., Fowler V.M.;
"Localization of the human 64kD autoantigen D1 to myofibrils in subsec of extraocular muscle fibers.";
Curr. Eye Res. 19:313-322(1999).
                                                                                     11.8%; Score 82; DB 1; Length 949; 28.7%; Pred. No. 45:
                                                                                                                                                20; Indels
                                                             105961 MW; FA8969B0C64B3278 CRC64;
                                                                                                                                                                                                                                                                                                     HRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPN 133
GTP (BY SIMILARITY). GTP (BY SIMILARITY). POLY-GLU.
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                                                                                                                                                                                                                                                                                                                                                                                                                                572 AA
                                                                                                                                                20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: CYTOSKELETON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHARACTERIZATION.
MEDLINE=21248187; PubMed=11350761;
Conley C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21218919; PubMed=11318603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Thyroid;
MEDLINE=91225220; PubMed=2026759;
                                                                                                                                                29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
507
560
326
503
557
321
349 AA;
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                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                         LMD1_HUMAN
P29536;
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NP_BIND
                                                             SEQUENCE
                                                                                                      Query Match
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                                           DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 X 4 AA APPROXIMATE TANDEM REPEATS.
D4B42F8E0523DE94 CRC64;
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"A putative AFP-dependent RNA helicase involved in Saccharomyces cerevisiae ribosome assembly.";
Proc. Natl. Acad. Sci. U.S.A. 89:11131-11135 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 DLQREEHSQK----SDSTKDVTAT----VLDKNNISSKSTTNNPNK 134
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                                                                                                                                                                                                                                                                                                                                                             X APPROXIMATE TANDEM REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 KGELEKGYQFDGWEISGFEGK--KDAGYVINLSKDTFIKPVFKK----
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01-0CT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Probable ATP-dependent RNA helicase DRSI.
DRSI OR YLL008W OR L1345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              752 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.7%; Score 81.5; D
22.8%; Pred. No. 29;
:ive 21; Mismatches
                                                                                                                      MIM; 602715; -.
GO; GO:0005624; C:membrane fraction; TAS.
GO; GO:0009405; P:pathogenesis; TAS.
InterPro; IPR004934; Tropomodulin.
InterPro; IPR003124; WH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast):
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96405918; PubMed=8810043;
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MEDLINE=93087480; PubMed=1454790;
                                                                                                                                                                                                                                                       Pfam; PF03250; Tropomodulin; 1. Pfam; PF02205; WH2; 1.
                                                                                                                                                                                                                                                                                                          SMART; SM00246; WH2; 1.
Antigen; Repeat; Cytoskeleton.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63737 MW;
                                                EMBL; X54162; CAA38101.1; -.
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                                                                                              Genew; HGNC:6647; LMOD1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 480 4
572 AA;
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Best Local Similarity
Matches 38; Conserv
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                                      STRAINS288C / AB972;

MEDLINE-97313267; PubMed-9169871;

MEDLINE-97313267; PubMed-9169871;

A Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W., Benes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A.,

Benian K.-D., Floeth M., Goffeau A., Hebling U., Heunann K.,

Heuse-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P.,

Louis E.J., Messenguy F., Mowes H.-W., Miosga T., Mosett D.,

Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,

Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M.,

Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S.,

Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P.,

Wierendeels F., Voet M., Volckaert G., Voss H., Mambutt R., Wedler E.,

Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.;

"The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                     Nature 387:87-90(1997).
-!- FUNCTION: PROBABLE HELICASE INVOLVED IN RIBOSOME ASSEMBLY.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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RRSGRVRITRKRLVRGITSMRMFMRTWT (IN REF. 1).
60747607A6E5E4AB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L00683; AAA44666.1; -
EMBL; X91488; CAA62783.1; -
EMBL; X91488; CAA62783.1; -
EMBL; X91488; CAA62783.1; -
EMBL; S44750; S64750.
HSSP, Q58083; 1HV8.
SGD; S0003931; DRS1.
InterPro; IPR001410; DEAD.
InterPro; IPR001650; Helicase_C.
Ffam; PF00270; DBAD; 1.
Ffam; PF00271; helicase_C; 1.
SWART; SM00487; DEXDC; 1.
SWART; SM00487; DEXDC; 1.
FROSITE; PS00039; DEAD ATP HELICASE; 1.
RPCSITE; PS00039; DEAD ATP HELICASE; 1.
RPCSITE; PS00039; DEAD ATP HELICASE; 1.
PROSITE; PS00039; DEAD ATP HELICASE; 1.
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                    SEQUENCE FROM N.A
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SITE
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PRT; 2459 AA.

MAPB RAT STANDARD; PF P15205; Q62958; Q9ER21; Q9QW92;

RESULT 25 MAPB_RAT ID MAPB AC P152

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MEDLINE=97405699; PubMed=2260743; MADLINE=97405699; PubMed=2260743; MADLINE=97405699; PubMed=2260743; MADLINE=97405699; PubMed=2260743; MADLINE=97405699; PubMed=2260743; MADLINE=97405699; PubMed=2260743; MADLINE=97405699; PubMed=2260741; MADLINE=97405699; MAPLIA and PNS during development."; J. Neurosci. Res. 49:319-332(1997).

1. Neurosci. Res. 49:319-332(1997).

2. FUNGTION: The function of brain MAPS is essentially unknown. Prosphorylated MAPLB may play a role in the cytoskeletal changes that accompany neurite extension. Possibly MAPLB Binds to at least two tubulin subunits in the polymer, and this bridging of subunits might be involved in nucleating microtubules.

2. SUBUNIT: 3 different light chains, LCI, LC2 and LC3, can associate with MAPLB and MAPLB proteins.

3. WITH MAPLA and MAPLB proteins.

4. TISSUE SPECIFICITY: Nervous system (spinal cord, brain stem, cerebellum and cerebrum). Not expressed in liver, spleen, kidney,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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DEVELOPMENTAL STAGE: In cerebral cortex, spinal cord and sciatic nerve levels are high early in development but decrease during postnatal development and are low in adults. In dorsal root ganglia levels remain high throughout development.

INDUCTION: By nerve growth factor.

DOWAIN: Has a highly basic region with many copies of the sequence KKEE and KKEI/V, repeated but not at fixed intervals, which is responsible for the binding of MAPIB to microtubules.

FTW. LCI is coexpressed with MAPIB. It is a polypeptide generated from MAPIB by proteolytic processing. It is free to associate with of MAPIB (By similarity).
       16-UCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Microtubule-associated protein 1B (MAP 1B) (Neuraxin) (Contains: MAP1
                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
NCBI TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- PTM: Phosphorylateu.
-!- SIMILARITY: TO MAPIA.
-!- CAUTION: A C-terminal fragment of this protein (residues 1597
-!- CAUTION: A C-terminal described as neuraxin in Ref.3.
2459) was originally described as neuraxin in Ref.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90059871; PubMed=2555150;
Rienitz A., Grenningloh G., Hermans-Borgmeyer I., Kirsch J.,
Littauer U.Z., Prior P., Gundelfinger E.D., Schmitt B., Betz H.;
"Neuraxin, a novel putative structural protein of the rat central nervous system that is immunologically related to microtubule-
                                                                                                                                                                                                                                                                                                                                             of the rat microtubule-
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 96-2459 FROM N.A., DOMAIN, AND INDUCTION.
STRAIN=Sprague-Dawley; TISSUE=Brain, and Glial tumor;
MEDLINE=92347374; PubMed=1639092;
Zauner W., Kratz J., Staunton J., Feick P., Wiche G.;
"Identification of two distinct microtubule binding domains on recombinant rat MAP 1B.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1541-2459 FROM N.A., AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                          Liu D., Fischer I.;
"Isolation and sequencing of the 5' end of t
associated protein (MAPIB)-encoding cDNA.";
Gene 172:307-308(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEVELOPMENTAL STAGE, AND PHOSPHORYLATION.
                                                                                                                                                                                                                                                   SEQUENCE OF 1-142 FROM N.A.
STRAIN=Sprague-Dawley; TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eur. J. Cell Biol. 57:66-74(1992).
                                                                                                                                                                                                                                                                                                     MEDLINE=96257242; PubMed=8666295;
(Rel. 14, Created)
(Rel. 40, Last seq
(Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   associated protein 5.";
EMBO J. 8:2879-2888(1989).
                                                                                                                                         Rattus norvegicus (Rat).
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YCG1_YEAST
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                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REVISIONS, AND CHARACTERIZATION.
MEDINE=5933222; Pubmed=7645349;
Rodriguz-Cousino N., Libil R., Neupert W., Court D.A.;
"Identification and initial characterization of the cytosolic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28; Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONTAINS MANY
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Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ballesta J.P.G., Franco L., Hoenicka J., Jimenez A., Remacha M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.7%; Score 81.5; DB 1; Length 2459; 27.8%; Pred. No. 1.3e+02; ive 18; Mismatches 28; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M -> V (IN REF. 1).
T -> S (IN REF. 1).
R -> K (IN REF. 3).
L -> I (IN REF. 3).
W; 2E376872DED88A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sanz E.;
Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LYS-RICH (HIGHLY BASIC, KKEE AND KKEI/V REPEATS)
LYS-RICH.
                                                                                                                                                                                                                                                          MĀP1 LIGHT CHAIN LC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1992 (Rel. 22, Created)
101-NOV-1995 (Rel. 32, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Topoisomerase II-associated protein PATI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        797 AA
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the European Bioinformatics Institute.
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MAPIB 3.
MAPIB 4.
MAPIB 5.
MAPIB 6.
MAPIB 7.
MAPIB 7.
MAPIB 9.
MAPIB 9.
                                                                                                                                                                                                    Pfan, PF00414; MAPIB neuraxin; 10.
PROSITE; PS00230; MAPIB NEURAXIN; 8.
Microtubules; Repeat; Phosphorylation.
                                                                                                                                                                   PIR; A56577; A56577.
InterPro; IPR000102; MAP1B_neuraxin.
                                                                                                                                                                                                                                                                                 MAP1B 1
                                                                                                                             EMBL; X60370; CAC16162.1; -. EMBL; X16623; CAA34620.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269497 MW;
                                                                                                             EMBL; U52950; AAB17068.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                              2038
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"The URK1 gene of Saccharomyces cerevisiae encoding uridine kinase.";
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                        Wang X., Watt P.M., Louis E.J., Borts R.H., Hickson I.D.;
"Patl: a topoisomerase II-associated protein required for faithful
chromosome transmission in Saccharomyces cerevisiae.";
Nucleic Acids Res. 24:4797(1996).
-!- FUNCTION: NECESSARY FOR ACCURATE CHROMOSOME TRANSMISSION DURING
CELL DIVISION. INTERACTS WITH TOPOISOMERASE TOP2.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: TO S.POMBE SPBC19G7.10C.
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Bukaryota, Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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P25589; P25513; P87003;
30-WAY-1992 (Rel. 22, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
30-WAY-2000 (Rel. 39, Last annotation update)
Hypothetical 97.9 kba protein in CHAl-KRR1 intergenic region.
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Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      797 AA; 88487 MW; 2A54F39AE3E75ECE CRC64;
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MEDLINE=97128274; PubMed=8972867;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X59720; CAA42266.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                   283 KEKRREKLEENDFQLNAHDSGSDSGSESSGFALSGNEIADYESSGSENDNRRESDSEKED 342
                                                                                                                                                                                                                                                                                                                                                                                                                               AGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQRE 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                  343 DEIILKOKKSHHVKHIINESDSDTEVEAKP----KEKADESLPKRIAINLGHYGDNI--- 395
                                                                                                                                                                                                                                                                                                                                              34; Gaps
                                                                                                                                                     EMBL; X53998; -; NOT ANNOTATED CDS.
PIR; S74279; S74279.
SGD; S0000566; YCL061C.
GG; GO:0000547; P:chromatin silencing at HML and HMR (sensu S.
GO; GO:0006348; P:chromatin silencing at telomere; IGI.
GO; GO:000076; P:DNA replication checkpoint; IGI.
                                                                                                                                                                                                                                                                                                                  DB 1; Length 853;
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567 MISSING (IN REF. 3).
97946 MW, 16E09FCCOBF248DI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein C23D3.06c in chromosome I. SPAC3D3.06C.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 EHSQKSDSTKDVTATVLDKNNI----SSKSTTNNPNK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----GEDTDKFQETNVLDTQNIEEVMAERNTIENEVK 428
                                                                                                                                                                                                                                                                                                                                              68;
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(Rel. 33, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                           21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1325 AA
                                                                                                                                                                                                                                                                                                                  Score 81;
Pred. No.
Nucleic Acids Res. 18:5279-5279(1990)
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                                                                                                                                                                                                                                                                                                                  11.6%;
21.7%;
                                                                                                                                           EMBL; X59720; CAA42405.1; -.
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Best Local Similarity 21.7%;
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567
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567 5
853 AA;
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01-FEB-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 WEISGFEGKKDAGYVINLSKD------TFIKPVFKKIEEKKEEEN---KP-TFDV 75
Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimmez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P., "The genome sequence of Schizosaccharomyces pombe.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       685 WGASTFQSKPQPSFSFGLTLDDKSNTPGKNFSIFGKTAETQVEQKKPENNVLTKPFSFAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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-!- FUNCTION: INTERACTS WITH OUTER MEMBRANE RECEPTOR PROTEINS THAT CARRY OUT HIGH-AFFINITY BINDING AND ENERGY DEPENDENT UPTAKE INTO THE PERIPLASMIC SPACE OF SPECIFIC SUBSTRATES. IT COULD ACT TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :95
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Pasteurellaceae; Pasteurella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GeneDB_SPombe; SPAC23D3.06c; -.
Pfam; PF03093; Nucleoporin_FG; 10.
Hypothetical protein.
SEQUENCE 1325 AA; 145776 MW; EEFD952FB7F0EGBD CRC64;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z64354; CAA91241.1; -. PIR; S62497; S62497.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.6%; 23.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FonB protein.
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and for

Usage by

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modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                          LIPID
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                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPOVNHSQLNESHRKEDLOREEHSQKSDST 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSDUCE ENERGY FROM THE CYTOPLASMIC MEMBRANE TO SPECIFIC ENERGY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids Res. 24:4420-4449(1996).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                        SUBCELLUJAR LOCATION: ANCHORED TO THE CYTOPLASMIC
MEMBRANE VIA ITS N-TERMINAL SIGNAL-LIKE SEQUENCE, SPANS THE
PERIPLASM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycoplasma pneumoniae.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
                        REQUIRING PROCESSES IN THE OUTER MEMBRANE, RESULTING IN THI
RELEASE INTO THE PERIPLASM OF LIGANDS BOUND BY THESE OUTER
MEMBRANE PROTEINS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transport; Protein transport; Inner membrane; Periplasmic; Transmembrane; Signal-anchor; Complete proteome.

DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).

TRANSMEM 9 29 SIGNAL-ANCHOR (POTENTIAL).

DOMAIN 30 256 PERIPLASMIC (POTENTIAL).

SEQUENCE 256 AA; 28306 MW; PEF0D4E73577D193 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.6%; Score 80.5; DB 1; Length 25
27.7%; Pred. No. 15;
:ive 11; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Hypotherical lipoprotein MPNS06 precursor (P02_orf793).
MPNS06 OR MP336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE MG185 / MG260 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       793 AA
                                                                                                                                                               SIMILARITY: BELONGS TO THE TONB FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 KDVTATVLDKNNISSKSTTNNPN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR01374; TONBPROTEIN.
TIGRFAMs; TIGR01352; tonB_Cterm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; PubMed=8948633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,11;
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF070473; AAC83227.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE006158; AAK03272.1; -. InterPro; IPR003538; TonB. InterPro; IPR006260; TonB_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 27.7
Les 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF03544; TonB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Herrmann R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YF06 MYCPN '
P75280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pneumoniae."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YFOG_MYCPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 30
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Penicilin-binding protein 1A/1B (PBP1) [Includes: Penicillin-
insensitive transglycosylase (EC 2.4.2.-) (Peptidoglycan TGase);
Penicillin-sensitive transpeptidase (EC 3.4.2.-) (DD-transpeptidase)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 SGFEGKKDAGYVINLSKDTFIKPVFKKIEE-----KKEEENKPTFDVSKKKDNPQVNHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serror P.; "Sequence analysis of the Bacillus subtilis chromosome region between the serA and kdg loci cloned in a yeast artificial chromosome."; Microbiology 142:2005-2016(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27; Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Borxiss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96349105; PubMed=8760912;
Sorokin A.V., Azevedo V., Zumstein E., Galleron N., Ehrlich S.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Popham D.L., Setlow P.; "Cloning, nucleotide sequence, and mutagenesis of the Bacillus subtilis pona operon, which codes for penicillin-binding protein (PBP) 1 and a PBP-related factor."; J. Bacteriol. 177:326-335(1995).
                                                                                                                                                                                                                                                                                                                                                                                                         1 22 POTENTIAL.
23 793 HYPOTHETICAL LIPOPROTEIN MPNSO6.
23 23 N-ACYL DIGLYCERIDE (POTENTIAL).
793 AA; 87493 MW; 331C6F077A718970 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                       PIR; $73662; $73662.
InterPro; IPR004890; Lipoprotein_10.
InterPro; IPR004894; Lipoprotein_X.
Pfam; PF03202; Lipoprotein_10; 1.
Pram; PF03305; Lipoprotein_10; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       914 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 499-515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 31.0%; Pred. No. 48; nes 27; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.6%; Score 80.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 -- QLNESHRKEDLOREEHSQKSDSTKD 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 LVOLKOTQEKTĎ----DSÓDTKNSDĎ 262
   entities requires a license agreement (
or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95113769; PubMed=7814321;
                                                                                                     EMBL; AE000032; AAB95984.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995 (Rel. 31, Created)
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                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus subtilis
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Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
R. Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
R. Guiseppi G., Guy B.J., Haga K., Haich J., Harwood C.R., Henaut A.,
Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
R. Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
R. Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
R. Jee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
R. Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
R. Medina N., Pohl T.M., Porteelle D., Porwollik S., Prescott A.M.,
R. Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Sanlan E., Schleich S., Schroeter R., Scoffone F.,
Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sekjuchi J., Sekowska A., Seros S.J., Serror P., Shin B.S., Soldo B.,
R. Sekjuchi J., Tanaka T., Taraka T., Tarakanu K.,
Tosato V., Uchiyama S., Vandenbol M., Vannier F., Yosasarotti A.,
Minters P., Wipat A., Yamamoto H., Yamane K., Yasamoto K., Yata K.,
Whiters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
Whiters P., Wipat A., Yamamoto H., Yamane K., Yasumoto R., Waterillus R., Welliss R., Welliss R., Woelliss R., Woelliss R., Woelliss R., Welliss R., Woelliss                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNITS) (BY SIMILARITY).

STHWAY: Peptidogalycan synthesis; final stages.

SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN, PROBABLY FOUND ALL OVER THE WHOLE CELL AT LOW CONCENTRATIONS. ALSO LOCALIZES TO THE DIVISION SITE IN VEGETATIVE CELLS.

DEVELOPMENTAL STAGE: EXPRESSION IS CONSTANT DURING GROWTH, DECREASES DURING SPORULATION AND IS INDUCED APPROXIMATELY 15 MIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISCELLANBOUS: CELLS LACKING THE PROTEIN REQUIRE INCREASED LEVELS OF MG(2+) OR CA(2+) FOR GROWTH AND GERMINATION. APPROXIMATELY 50% OF CELLS WITHOUT THE PROTEIN CONTAIN ABNORMAL FYSZ RINGS, SUGGESTING IT IS INVOLVED IN SEPTUM SYNTHESIS; INCREASED LEVELS OF MG(2+) OR CA(2+) ONLY PARTIALLY ELIMINATE THE SEPTATION DEFECTS. SIMILARITY: Contains I fibronectin type III domain. SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murray T., Popham D.L., Setlow P.;
"Bacilus subtilis cells lacking penicillin-binding protein 1 require
increased levels of divalent cations for growth.";
J. Bacteriol. 180:4555-4563(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTO SPORE GERMINATION.

THE TRANSLATION OF THE PONA GENE
APPEARS AS TWO BANDS ON A GEL (1A AND 1B), BUT THE SPECIFIC AMINO
ACID SEQUENCE OF EACH PROTEIN IS UNKNOWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Bacteriol. 181:3201-3211(1999).

-I- FUNCTION: CELL MALL FORMATION. SYNTHESIS OF CROSS-LINKED
PEPTIDOGLYCAN FROM THE LIPID INTERMEDIATES. THE ENZYME HAS A
PENICILLIN-INSENSITIVE TRANSCLYCOSYLASE N-TERMINAL DOMAIN
(FORMATION OF LINERA GLYCAN STRANDS) AND A PENICILLIN-SENSITIVE
TRANSPEPTIDASE C-TERMINAL DOMAIN (CROSS-LINKING OF THE PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99255546; PubMed=10322023;
Pedersen L.B., Angert E.R., Setlow P.;
"Septal localization of penicillin-binding protein 1 in Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIM: THE N-TERMINUS IS BLOCKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98389671; PubMed=9721295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GROWTH REQUIREMENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subtilis."
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TRANSGLYCOSYLASE FAMILY. SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE TRANSPEPTIDASE FAMILY.

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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            810 DDEKTODDTOTDDSOKDDGOTDQDQTDDSTNDQDKKQDNTNTNPSDNNNQDQSNDNDNDN 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 SEEDFILPVYKGELEKGYQFDGWEISGFEGKKDA--GYVINLSKDTFIKPVFKKIEEKKE 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDINDE-92331925; MEDINDE-92331925; PubMed=1628825; Amberg D.C., Goldstein A.L., Cole C.N., "Isolation and characterization of RATI: an essential gene of Saccharomyces cerevisiae required for the efficient nucleocytoplasmic
                                                                                                                                                                                                                                                                                            Peptidoglycan synthesis; Cell wall; Transferase; Glycosyltransferase;
Hydrolase; Multifunctional enzyme; Transmembrane; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FIBRONECTIN TYPE-III.
ACYLATED BY PENICILLIN (BY SIMILARITY)
6978E33DFE2423E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exoribonuclease)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----PTFDVSKKKDNPQVNHSQLN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50; Indels
                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 870 SNNQDTSDGDSNSGKNDSTG--SDTNKNKTDTSNKTQTNS 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92 SHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNN 131
                                                                                                                                                                                                                                                                                                                            Antibiotic resistance; Complete protecome.

DOMAIN
1 37 CYTOPLASMIC (POTENTIAL)
TRANSMEM 38 58 SIGNAL-ANCHOR (TYPE II I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93109318; PubMed=8417335;
Kenna M., Stevens A., McCammon M., Douglas M.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND EXORIBONUCLEASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                TRANSGLYCOSYLASE.
TRANSPEPTIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-SCP-2003 (Rel. 42, Last annotation update)
Ribonucleic acid trafficking protein 1 (5'-3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.6%; Score 80.5; Dl
22.5%; Pred. No. 56;
ive 31; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
                                                                EMBL; U11883; AAA64947.1; -.
EMBL; 147838; AAB38459.1; -.
EMBL; 299115; CAB14148.1; -.
PIR; 140529; 140529.
Subtilist; BG10954; ponA.
InterPro; IPR001361; FN_III.
InterPro; IPR001264; Glyco trans_51.
InterPro; IPR001264; Glyco trans_51.
                                                                                                                                                                                                                      Pfam; PF00912; Transglycosyl; 1.
Pfam; PF00905; Transpeptidase; 1.
ProDom; PD001895; Glyco_trans_51; 1.
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RATI OR HKEI OR TAPI OR YOR048C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99562 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 EENK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 22.5%
Matches 36, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                              SMART; SM00060; FN3; 1
                                                                                                                                                                                                        Pfam; PF00041; fn3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      914 AA;
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Q02792;
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                                                                                                             RESULT 33
LIP_STAEP
                                                                                                                                                        셤
                                             용
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 FI----KPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQ------LNESH 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                683 (683 Y->H: IN ALLELE TAP1-1; ACTIVATES TRANSCRIPTION OF THE PROMOTER-DEFECTIVE YEAST SUP4 TRNA(TYR) ALLELE SUP4A53T61.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Valens M.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May function in the processing and/or trafficking of nuclear mRNA. May be involved in general transcription as well.
Possesses 5.->1 exoribonuclease activity degrading poly(A) to
"An essential yeast gene with homology to the exonuclease-encoding XRN1/KEW1 gene also encodes a protein with exoribonuclease activity.",
                                                                                                                               SEQUENCE FROM N.A.

MEDLINE=93268292; PubMed=8497260;
Aldrich T.L., di Segni G., McConaughy B.L., Keen N.J., Whelen S.,
Hall B.D.;
"Structure of the yeast TAP1 protein: dependence of transcription activation on the DNA context of the target gene.";
Mol. Cell. Biol. 13:3434-3444(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONTAINS 2 X SRYD, 2 X NNNY, AND 2 X YSGN REPEATS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 1006;
                                                                                                                                                                                                                                                                                                                                                                                                                   Bohn C., Bolotin-Fukuhara M., Daignan-Fornier B., Dang D.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nuclear protein; Hydrolase; Nuclease; Exonuclease; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005634; C:nucleus; IDA.
GO; GO:0004534; F:5'-3' exoribonuclease activity; IDA.
GO; GO:0006365; P:35S primary transcript processing; IMP.
GO; GO:0006396; P:RNA processing; IMP.
InterPro; IPRO04859; Put_53exo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44; Indels
                                                                                                                                                                                                                                                                                                                                    Landt O., Hiesel R., Unseld M.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Belongs to the 5'-3' exonuclease family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.6%; Score 80.5; Illarity 20.0%; Pred. No. 62; Conservative 37; Mismatches
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POLY-ASN.
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EMBL; Z74956; CAA99240.1; -.
PIR; S20126; S20126.
SGD; S0005574; RATI.
                                                                                    Mol. Cell. Biol. 13:341-350(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COFACTOR: Requires magnesium.
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EMBL; M95626; AAA34960.1; -.
EMBL; L06011; AAA16950.1; -.
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nes 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF03159; XRN_
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 EDFILPVYKGELEKGYQFDGWEISGFE-GKKDAGYVINLSKDTFIKPVFKKIE-EKKEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50; Indels 20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93171870; PubMed=8436947;
Farrell A.M., Foster T.J., Holland K.T.;
"Molecular analysis and expression of the lipase of Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fatty acid anion.
--- SUBGELLULAR LOCATION: Secreted.
--- MISCELLANEOUS: THE EXPRESSION OF STAPHYLOCOCCUS LIPASE IS
NEGATIVELY REGULATED BY BACTERIOPHAGE LYSOGENIZATION (LIPASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR005377; Gpos YSIRK.
InterPro; IPR000734; Lipase.
InterPro; IPR000739; Ser estrs site.
InterPro; IPR000739; Ser estrs site.
TIGRPAMS; TIGR01168; YSIRK signal; 1.
PROSITE; PS00120; LIPASE SER; 1.
Hydrolase; Lipid degradation; Zymongen; Signal; Complete proteome.
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(BY SIMILARITY)
| | | | | : | : | : | : | | : | | : | | RLEKONEEBEIAKDSKKVKTEKAESECDLDAEIKDEIVADVNDRENSETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 688;
                                                                                                                                                                                                                                  01-JUN-1994 (Rel. 29, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last nonotation update)
Lipase precursor (EC 3.1.1.3) (Glycerol ester hydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases
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E -> G (IN REF. 1).
6C95DB3A78AF86F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Chen Z., Wen Y.,
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CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillales; Staphylococcus.
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24; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF 303-315.
                                                                                                                                                                               688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gen. Microbiol. 139:267-277(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIPASE.
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Best Local Similarity 26.6%;
Matches 34; Conservative
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                                                                                                                                                                               STANDARD;
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120
188 AA;
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CONFLICT
SEQUENCE
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NKPTFDVSKKKDNPQV--NHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSK 126
                        197
            Yeast 18:69-80(2001).
-!- FUNCTION: FUNCTION IN GENERAL TRANSLATION INITIATION BY PROMOTING THE BINDING OF THE PORMYLMETHIONINE-TRNA TO RIBOSOMES. SEEMS TO FUNCTION ALONG WITH BIF-2 (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE IF-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Cloning and characterization of hIF2, a human homologue of bacterial translation initiation factor 2 and its interaction with HIV-1
                                                                                                                                                                                                                                                                                                                          Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; Prediction of the coding sequences of unidentified human genes. XI. The complete sequences of 100 new cDNA clones from brain which code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lee J.H., Choi S.K., Roll-Mecak A., Burley S.K., Dever T.E., "Universal conservation in translation initiation revealed by human and archaeal homologs of bacterial translation initiation factor
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUB-Cervical carcinoma;
MEDLINE=99362399; PubMed=1042305;
Wilson S.A., Sieiro-Vazquez C., Edwards N.J., Iourin O., Byles B.D.
Kotsopoulou E., Adamson C.S., Kingsman S.M., Kingsman A.J.,
Martin-Rendon E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 833-1220 FROM N.A.
MEDLINE=21064499; PubMed=11124703;
Astanchi F., Bertocco E., Toppo S., Dioguardi R., Simionati B.,
Cannata N., Zimbello R., Lanfranchi G., Valle G.,
"Characterization of 16 novel human genes showing high similarity"
                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Koehrer K., Beyer A., Mewes H.-W., Gassenhuber J., Wiemann S., Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 96:4342-4347(1999)
                                                                                                                                               060841; 095805; Q9URB1; Q9UMN7;
15-DEC-1998 (Rel. 37, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
IF2 OR KIAA0741.
                                                                                                                                      PRT; 1220 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99218282; PubMed=10200264;
                                                                                                                                                                                                                                                                                                                MEDLINE=99087487; PubMed=9872452;
                                                                                                                                                                                                                                                                                                                                                                             for large proteins in vitro.";
DNA Res. 5:277-286(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ochem. J. 342:97-103(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 89-1220 FROM N.A.
                                                 STINNPNK 134
                                                                        ATAQNOSK 205
                                                                                                                                                                                                                          Homo sapiens (Human).
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                yeast sequences."
                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                                                                                                                      HUMAN
 69
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coved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
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D-N: LOSS OF ACTIVITY; BOTH IN VIVO AND IN VITRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOSS OF ACTIVITY; BOTH IN VIVO AND
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   as its content is in
                                                                                                                                                                                                           R GO; GO:000343; F:translation initiation factor activity; NAS. GO; GO:000344; F:translation of translational initiation; NAS. GO; GO:0006446; P:regulation of translational initiation; NAS. R InterPro; IPR004161; EFTU D2.
R InterPro; IPR000178; IF2.
R InterPro; IPR000178; IF2.
R InterPro; IPR000178; IF2.
R Pfan, PF00194; GTP_EFTU; 1.
R Pfan, PF03144; GTP_EFTU; 1.
R Pfan, PF03144; GTP_EFTU; 1.
R TIGRFAMS; TIGR00231; Small GTP; 1.
R RIGRFAMS; TIGR00231; small GTP; 1.
R PROSITE; PS01176; IF2; FALSE_NEG.
R Initiation factor; Proctain biosynthesis; GTP-binding.
INP_BIND 638 645
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• W (IN REF. 3).
• K (IN REF. 2).
010CC15DE475E5B8 CRC64;
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POLY-GLU.
ASP/GLU-RICH (ACIDIC).
V-G: LOSS OF ACTIVITY
FULL ACTIVITY IN VITRO
use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See h
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83;
                                                      or send an email to license@isb-sib.ch).
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POLY-LYS.
POLY-GLU.
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IN VITRO.
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(69 G ->
138799 MW;
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24.8%; Fr. ...
                                                                                                                         EMBL; AP078035; AAD16006.1; -. EMBL; AL133563; CAB63717.1; -. EMBL; AJ006412; CAA07018.1; -.
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Q03188; Q9POM5;
01-OCT-1993 (Rel. 27, Created)
                                                                                            EMBL; AB018284; BAA34461.1; -.
                                                                                                            EMBL; AJ006776; CAB44357.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 24.8
Matches 35, Conservative
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640
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1180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      375 PSDKTVLDTSYALIDETVNNYRSTKYEMYSKNAEKPSRSKRTIKQKQRRKFMAKPAEEQ- 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 KPTFDVSKKKD-NPQVNHSQLNESHRKEDLQREEH-------SQKSDSTK 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Promoter characterization of centromere protein C reveals its participation in cell cycle regulation in late G1-phase and expression control by E2F-1, pRb, p107 and Sp-1."

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Component of the inner kinetochore plate. Required for normal kinetochore assembly.

-!- SUBUNIT: Binds to DAXX.

-!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 11.4%; Score 79.5; DB 1; Length 943; Best Local Similarity 23.1%; Pred. No. 69; Matches 36; Conservative 16; Mismatches 55; Indels 49; Gaps
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484 499 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
558 574 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
780 798 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
75 75 PHOSPHORYLATION (POTENTIAL)
732 732 PHOSPHORYLATION (POTENTIAL)
943 AA; 106925 MW; 6D80810A3E476376 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92323541; PubMed=1339310; Sairoh H., Tomkiel J., Cooke C.A., Ratrie H. III, Maurer M., Rothfield N.F., Barnshaw W.C.; "CENP-C, an autoantigen in scleroderma, is a component of the human inner kinetochore plate."; Cell 70:115-125(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 117141; -.
GO; GO:0005699; C:kinetochore; TAS.
GO; GO:0003677; F:DNA binding activity; TAS.
InterPro; IPR007113; Cupin_sup.
Chromosomal protein; Nuclear protein; DNA-binding; Phosphorylation;
                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-21 FROM N.A.
Poppe M., Botz J., Hahm B., Dobat K., Eickelbaum W., Paweletz N.,
Arand M., Knehr M.;
01-OCT-1993 (Rel. 27, Last sequence update)
28.FEB-2003 (Rel. 41, Last annotation update)
Centromere protein C (CENP-C) (Centromere autoantigen C).
CENPOT OR CENPC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D----VTATVLDKNNISSK 126
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EMBL; AF151723; AAF73191.1; -.
PIR; AA2681, AA2681.
Genew; HGNC:1854; CENPC1.
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                TISSUE=Placenta;
                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALTERNATIVE SPLICING, TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
MEDLINE=93180788; PubMed=7680094;
Barbas J.A., Galceran J., Torroja L., Prado A., Ferrus A.;
Barbas J.A., Galceran J., Torroja L., Prado A., Ferrus A.;
Barbas J.A., Galceran J., Torroja L., Prado A., Ferrus A.;
Malnogaster is caused by a splicing defect affecting selected troponin I isoforms. I.
Mol. Cell. Biol. 13:1433-1439(1993).
I. FUNCTION: Troponin I is the ATPase inhibitory subunit of Troponin in the thin filament regulatory complex. Involved in the development and maintenance of muscle and nervous system. May also be involved in the cytoskeletal apparatus.
                                                                                                                                                                                                                                                                                                          STRAIN=Berkeley; TISSUE=Head; MEDLINES-2436066; PubMed=12537569; MEDLINES-2436066; PubMed=12537569; Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M., George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H., Rubin G.M., Celniker S.E.; "A prosophila full-length CDNA resource."; Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing, Named isoforms=10;
Comment=Excon 3 is either present or absent, excon 6 has 4
mutually exclusive forms (6al, 6a2, 6b1 and 6b2) and C-terminal
exons 9 and 10 are mutually exclusive;
                                   STRAIN=Berkeley;
MEDLINE=22426069; PubMed=12537572;
Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Mista S., Crosby M.A., Maminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=P36188-8; Sequence=VSP_006626; VSP_006629, VSP_006630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=P36188-2; Sequence=VSP_006626, VSP_006627, VSP_006630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=P36188-4; Sequence=VSP_006626, VSP_006628, VSP_006630;
                                                                                                                                                                                                               Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=4; Synonyms=B;
IsoId=P36188-5; Sequence=VSP_006626, VSP_006628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=8; Synonyms=D, E;
IsoId=P36188-9; Sequence=VSP_006626, VSP_006629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=2; Synonyms=A;
IsoId=P36188-3; Sequence=VSP_006626, VSP_006627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=P36188-6; Sequence=VSP_006626, VSP_006630;
                                                                                                                                                                                                                                                     Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=P36188-7; Sequence=VSP_006626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=P36188-1; Sequence=Displayed;
                   REVISIONS, AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=6; Synonyms=C, F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=10; Synonyms=G;
                                                                                                                                                                                                                                     systematic review
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=1
                                                                                                                                                                                                 Lewis S.E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 ERMYICEGOKMDLEYEVRKKDWEIN-----DLNAQVNDLRGKFVKPALKKV---SKYEN 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACETYLATION (BY SIMILARITY).
METHYLATION (TRI-) (BY SIMILARITY).
METHYLATION (TRI-) (BY SIMILARITY).
TOPODNIN TINTERACTION (BY SIMILARITY).
ACTIN-BINDING (BY SIMILARITY).
Missing (in isoform 1, isoform 2, isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /FTId=vSP_006627.

GELQEICEETYERMYICEGGKWDLEYEVRKKDW -> DTIQ
SVCKDYHSKTIKLESEKYDFEYDVARKDY (in isoform
3 and isoform 4).

/FTId=vSP_006628.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GELOBICEENTYERMICEGOKWDLEYEVRKUM -> AELQ
TICKOYWQRVYSLEGDKFDLEHVQKVKAQ (in isoform
7 and isoform 8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GELQEICEEŸYERMYICEGQKWDLEYEVRKKDW -> DTLK
SLIKQHYDRINKLEDQKYDLEYVVKRKDV (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDWSKGKPGDAKVKEEVEAEA -> IKDAAVLNKAKK (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isoform 1, isoform 3, isoform 5, isoform 7 and isoform 9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 EEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIBEKKEEEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3, isoform 4, isoform 5, isoform 6, isoform 7 and isoform 8).
/FTIG=VSP_006626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 268;
containing exon 6b2 (isoforms 7 and 8) are weakly expembryos and larvae and at a higher level in adults. MISCELLANEOUS: TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; Actin-binding; Acetylation; Methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FlyBase; FBgn0004028; wupA.

GO; GO:0005861; C:troponin complex; NAS.

GO; GO:0003779; F:actin binding activity; NAS.

GO; GO:0007517; F:muscle development; IMP.

GO; GO:0007399; F:neurogenesis; IMP.

InterPro; IPR001978; Troponin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 and isoform 2)
/FTId=VSP 006627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY
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                                                                                                                                                                                                                                                                                                                              EMBL, AE003507; AAF48802.2; EMBL; AE003507; AAF48803.2; EMBL, AE003507; AAF48804.2; EMBL, AE003507; AAF48805.2; EMBL, AE003507; AAN09458.1; PRH2, AY122145; AAM52657.1; PIR; B38594; B38594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.4%;
                                                                                                                                                                                                                                                                                  EMBL; X5918; CAA41171.1; -. EMBL; X59376; CAA42020.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00992; Troponin; 1
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204
170
201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Muscle protein; Actin-Alternative splicing.
INIT MET 0 0 0
MOD_RES 1 1 1
MOD_RES 200 200
MOD_RES 204 204
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
34,5-cyclic-nucleotide phosphodiesterase regA (EC 3.1.4.17) (PDEase
                                                                                                                                                                                                                                                                                                                                                                                                             nucleoside 5'-phosphate.
DEVELOPMENTAL STAGE: EXPRESSED AT LOW LEVELS IN VEGETATIVE CELLS
AND AT HIGH LEVELS IN PRESPORE AND PRESTALK CELLS DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
                                                                                                                                                                                                                                                                                                                                              Kay R.R.; Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MORPHOLOGICAL SUPPRESSOR OF TAGB.
-!- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)O
                                                                                                                                                                                                                   Shaulsky G., Escalante R., Loomis W.F., "Developmental signal transduction pathways uncovered by genetic
                                                                                                                                                                                                                                                                                                                              Thomason P.A., Traynor D., Cavet G., Chang W.T., Harwood A.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.4%; Score 79; DB 1; Length 793; 24.4%; Pred. No. 63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Contains 1 response regulatory domain.
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                                                                                                Dictyostellum discoideum (Slime mold).
Bukaryota, Mycetozoa, Dictyostellida, Dictyostellum.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 93:15260-15265(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESPONSE REGULATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.4%; Pred. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PSO0126; PDEASE 1; 1.
PROSITE; PSS0110; RESPONSE_REGULATORY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dictybb; DD02055; regA.
InterPro; IRR00360; Wet phsphohydro.
InterPro; IRR002073; PDEase.
InterPro; IPR001789; Response_reg.
Pfam; PF00072; PD8ase; 1.
PRNWTS; PR0037; response_reg; 1.
PRNWTS; PR00387; PRESTERASE1.
ProDom; PD000039; Response_reg; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-ASN.
POLY-THR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-ASP.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-ASN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-SER
                                                                                                                                                                                                        MEDLINE=97140317; PubMed=8986798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ005398; CAA06513.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91175 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U60170; AAB03508.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00471; HDc; 1
SMART; SM00448; REC; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 1
770 7
793 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
ses 21; Conserv
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase; cAMP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEVELOPMENT.
                                                                                                                                                                                                                                                        suppressors.'
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 MKEQILKSKKLSIETLKORLENPYTF----INGYD------IIKSFYRNSIF---- 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 MSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIE
                                                                                                                                                                                                                                                                                                                                                   Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.3%; Score 78.5; DB 1; Length 531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                               Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE000686; AAC06652.1; -.
PIR; C70333; C70333.
Hypothetical protein; Complete proteome.
SEQUENCE 531 AA; 62830 MW; 6499DFE803C2F7CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 EKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQRE 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cylicin I (Multiple-band polypeptide I) (Fragment)
CYLCI OR CXLI OR CXL.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 ----ANNNPYKDII-KQENSKLLNSILNDIHRKEDMDYE
                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein AQ_372.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        598 AA.
                                                                                                                531 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 45;
                   85 NNTTTTTTTTTTSNNNSNNNNSNNNNN 110
DSTKDVTATVLDKNNISSKSTTNNPN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Testis;
MEDLINE=93359502; PubMed=8354692;
                                                                                                                                                                                                                                                                                                                                       MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hess H., Heid H., Franke W.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 25.3% nes 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 392:353-358(1998).
                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                    Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYL1 HUMAN
P35663;
                                                                                                                AQUAE
108
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                                                                                                                              066695;
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Matches
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33 TSLKSMISGIENLAVHSKGNDN------KANNNNNNNNNNNNEKQKDIVSLENNSSS 52 TFIXPVFKKIE----EKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKS

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                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 VFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHS---QKSDSTKDV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 STIVSEE----DFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLS----KDTFIKP 56
                     the sperm head cytoskeleton.";
J. Cell Biol. 122:1043-1052(1993).
-!- FUNCTION: POSSTBLE ARCHITECTURAL ROLE DURING SPERMATOGENESIS. MAY
BE INVOLVED IN SPERMATID DIFFERENTIATION.
-!- SUBCELLULAR LOCATION: CALYX; SPERM HEAD CYTOSKELETAL STRUCTURE.
-!- TISSUE SPECIFICITY: Testis.
-!- DEVELOPMENTAL STAGE: SPECIFIC TO LATE SPERMATOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 NAKKSSDAESEDSK----DAKKDSKKVK-KNVKKDDKKKDVKKDTESTDAESGDSKDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
  "Molecular characterization of mammalian cylicin, a basic protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'GO:0005856; C:cytoskeleton, NAS.
GO:0005198; F:structural molecule activity; NAS.
GO:0007283; P:spermatogenesis; NAS.
oskeleton; Structural protein; Repeat; Sperm; Spermatogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA ligase (EC 6.5.1.1) (Polydeoxyribonucleotide synthase [ATP]).
LIG-1 OR C29A12.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.3%; Score 78.5; DB 1; Length 598; 22.7%; Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPROXIMATE TANDEM REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       062BA2E2D2AB61F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90;
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRO-RICH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68034 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z22780; CAA80457.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 22.7°
Matches 32; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; B40713; B40713.
Genew; HGNC:2582; CYLC1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          548
598 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytoskeleton;
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CAEEL
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 -SKDTFIKPVFKKIEEKKEEENKPTFDVSKKK--DNPQVNHSQLNESHRKEDLQREEHSQ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00697; DNA_LIGASE_A1; 1.
PROSITE; PS00333; DNA_LIGASE_A2; 1.
PROSITE; PS050160; DNA_LIGASE_A3; 1.
DNA_repair; DNA_replication; DNA_recombination; Cell division; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 EMSSTIVSEEDFILPVYKGE-----LEKGYQFDGWEISGFEGKKDAGYVINL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27;
FUNCTION: THIS PROTEIN SEALS DURING DNA REPLICATION, DNA RECOMBINATION AND DNA REPAIR NICKS IN DOUBLE-STRANDED DNA. CATALYTIC ACTIVITY: ATP + {deoxyribonuclectide} (N) + {deoxyribonuclectide} (N) = AMP + diphosphate + {deoxyribonuclectide} (N+M).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363 363 AMP (BY SIMILARITY).
847 AA; 94501 MW; A32B7D279F91002F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.3%; Score 78.5; Di
25.2%; Pred. No. 74;
ive 24; Mismatches
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                                                                                                                                                                                                                                                                                                             license agreement
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Pfam; PF01068; DNA ligase; 1.
Pfam; PF04679; DNA ligase A C; 1.
Pfam; PF04675; DNA ligase A C; 1.
Pfam; PF04475; DNA ligase A N; 1.
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Matches 37; Conserv
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	Description	Q9aht5 streptococc	Q97ry6 streptococc	Q9s4m8 streptococc	Q8dqp7 streptococc	Q95pi5 plasmodium	Q9u0g0 plasmodium	Q25705 plasmodium	Q81436 plasmodium	077355 plasmodium	Q90784 gallus gall	Q25995 plasmodium	Q8ij55 plasmodium	Q8i5f3 plasmodium	Q9u6c4 plasmodium	Q26019 plasmodium	Q25706 plasmodium
SUMMARIES	£	Q9AHT5	Q97RY6	Q9S4M8	Q8DQP7	Q95PI5 .	050060	Q25705	Q81436	077355	090784	Q25995	Q81J55	Q815F3	Q9U6C4	Q26019	Q25706
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## ALIGNMENTS

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Infect. Immun. 69:1593-1598(2001).
-!- SUBCELLULAR LOCATION. ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY ARABIS BOND (BY SIMILARITY).
HSSP; P00782; 2SBT.
                                                                                                                                                                                                                                                  MEDLINE=21116976; PubMed=11179332; Wizemann T.M., Heinrichs J.H., Adamou J.E., Erwin A.L., Kunsch C., Choi G.H., Barash S.C., Rosen C.A., Masure H.R., Tuomanen E., Gayle A., Brewah Y.A., Walsh W., Barren P., Lathigra R., Hanson M., Langermann S., Johnson S., Koenig S.; Wenig S., Lathigra R., Adhole Genome Approach To Identify Vaccine Molecules Affording Protection against Streptococcus pneumoniae Infection.";
                                                                                                                                           Streptococcus pneumoniae.
Bacteria; Firmicutes; Lactobacillales; Strèptococcaceae;
                                                                           Last sequence update)
Last annotation update)
                             PRT; 2119 AA
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TIGRFAMB; TIGR01167; LPXTG_anchor; 1.
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nterPro; IPR001680; WD40.
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Pfam; PF02225; PA; 1.
Pfam; PF00082; Peptidase S8; 2.
                                                         01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                            Serine protease (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR006192; LPXTG.
                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR003137;
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                         NCBI_TaxID=1313;
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RESULT 1
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1973 KEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKK 2032
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R InterPro; IPR003137; PA.
R InterPro; IPR003137; PA.
R InterPro; IPR000209; Peptidase_S8.
R InterPro; IPR000209; Peptidase_S8.
R InterPro; IPR001600; Peptidase_S8.
R Pfam; PF00746; Gram_pos_anchor; 1.
R Pfam; PF00723; SUBTILISIN.
R PRINTS; PR00723; SUBTILISIN.
R PROSITE; PS50040; PA; I.
R PROSITE; PS0040; PA; I.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00137; SUBTILASE_SER; 1.
DR PROSITE; PS00137; SUBTILASE_SER; 1.
DR PROSITE; PS00137; SUBTILASE_SER; 1.
DR PROSITE; PS00137; SUBTILASE_SER; 1.
DR PROSITE; PS00147; SUBTILASE_SER; 1.
DR PROSITE; PS00173; SUBTILASE_SER; 1.
DR PROSITE; PS00174; SUBTILASE_SER; 1.
DR PROSITE; PS00175; SUBTILASE_SER; 1.
DR PROSITE; PS00175; SUBTILASE_SER; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 693; DB 2; Length 2144; Pred. No. 2.4e-45; 1; Mismatches 0; Indels (
                                                                       Length
                                                                                                                                              Indels
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2140 AA; 240426 MW; FA44AD8E2938B334 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
011-MAR-2003 (TrEMBLrel. 23, Last annotation update)
011-MAR-2001 (TrEMBLrel. 28,
                                         100.0%; Score 696; DB 16;
ilarity 100.0%; Pred. No. 1.4e-45;
Conservative 0; Mismatchic
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InterPro; IPR006192; LPXTG.
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                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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100.0%; Pred. No. 1.4e-45;
ive 0; Mismatches 0; Indels 0;
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Serine protease, subtilase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 2140 AA
           PROSITE; PS50840; PA; 1.
PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00138; SUBTILASE SER; 1.
PROSITE; PS00678; WD REPEATS 1; 1.
Cell wall; Pepildoglycan-anchor; Protease.
NON_TER
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Pfam; PF00225; PA; 1.
Pfam; PF00022; PA; 1.
Pfam; PF00002; Peptidase SB; 2.
PRINTS; PR00723; SUBTILISIN.
TIGREAMS; TIGRO1167; LPXTG anchor; 1.
PROSITE; PSSO847; GRAM POS_ANCHORING; 1.
PROSITE; PSSO840; PA; 1.
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EMBL; AE007373; AAK74791.1; -.
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InterPro; IPR003137; PA.
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Matches 134; Conservative
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TIGR; SP0641; -.
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NCBI_TaxID=1313;
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IEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDK 120
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Hisaeda H., Saul A., Long C.A., Miller L.H., Stowers A.W.;
"Merozoite Surface Protein 3 and Protection Against Malaria in Aotus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glass J.I.;
"Genome of the bacterium Streptococcus pneumoniae strain R6.";
J. Bacteriol. 183:5709-5717(2001).
EMBL; AE008434; AAK99365.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.6%; Score 693; DB 16; Length 2144; 99.3%; Pred. No. 2.4e-45; ive 1; Mismatches 0; Indels 0;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Merozoite surface protein 3 (Fragment).
Blasmodium falciparum.
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Cell Wall-associated serine proteinase PrtA (EC 3.4.21.-).
PRTA OR SPR0561.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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SEQUENCE 2144 AA; 240436 M
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Matches 133; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATV-----LDKN 121
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                                                                                                                                                                                                                                                                                                                                                                          16.1%; Score 112; DB 5; Length 361; 23.9%; Pred. No. 0.41; tive 28; Mismatches 48; Indels
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NCBI_TaxID=5854;
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15.8%; Score 110; DB 5; Length 346;
Best Local Similarity 26.2%; Pred. No. 0.56;
Matches 34; Conservative 26; Mismatches 54; Indels
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY044180; AAK94780.1; -.
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361 AA; 41163 MW; 6127A3041587BA74 CRC64;
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Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
A Buckee C.O., Burrows C., Cherevach I., Chillingworth T.,
Chillingworth T., Christodoulu Z., Clark L., Clark R.,
Crolin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
Crolin A., Davies P., Davis P., Dear P., Dearden F., Doggett J.,
A Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
A Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
A Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
Line A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,
A line X., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,
A laylor K., Ormond D., Price C., Quall M.A., Rabbinowitsch E.,
A Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
Seeger K., Sharp S., Smith R., Squares S., Stevens K.,
A Sulston J. B., Craig A., Newlold C., Barrell B.G,
T. Mcquare C. Plasmodium falciparum chromosomes 1, 3-9 and 13.";
                                                                                                                                                                                                                                                                                 -----FD---GWEISGF--EGKKDAG----YVI 46
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                                                                                                                  "Conservation of structural motifs and antigenic diversity in the Plasmodium falciparum merozoite surface protein-3 (MSP-3)."; Mol. Biochem. Parasitol. 90:21-31(1997).
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Devlin K., Baker S., Davies P., Mungal K., Berriman M., Pain
Hall N., Bowman S., Churcher C., Quail M., Barrell B.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                  15.8%; Score 110; DB 5; Length 379; 23.4%; Pred. No. 0.62; ive 30; Mismatches 41; Indels
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Pypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                        94 RKEDLOREEHSOKSDSTKDVTATVLDKNNISSKSTTNN 131
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                                                                                                           McColl D.J., Anders R.F.;
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   Plasmodium falciparum.
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Length 3008;

DB 5;

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Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bowman S., Lawson D., Basham D., Brown D., Chillingworth T., Churcher C.M., Craig A., Davies R.M, Devlin K., Feltwell T., Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T., Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S., Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A., Kutter S., Skellon J., Squares R., Squares S., Sulston J.E., Whichead S., Woodward J.R., Newbold C., Barrell B.G., "The complete nucleotide sequence of chromosome 3 of Plasmodium
                                                                                     44 YVINLSK----DTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQ----LNESHRKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 INSEEDFILPVY----KGELEKGYQFDGWEISGFEGKK----DAGYVINLSKDTFIKPV
                                          Gaps
                                                                                                                                                                                                           2367 ENKKEENKKEENKKEENKKEVNKNEENKNEVNKKEENKKEENKNEENK 2414
                                                                                                                                                                               97 DLOREEH----SOKSDSTKDVTATVLDKNNISSK-----STTNNPNK 134
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
                                          31; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.6%; Score 108.5; D
29.3%; Pred. No. 1.3;
cive 22; Mismatches
                  Pred. No. 6.4;; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        Created)
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MEDLINE=99376085; PubMed=10448855;
32.4%; FIL. 22; )
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01-OCT-2000 (TrEMBLrel. 15, Las
01-OCT-2002 (TrEMBLrel. 22, Las
Hypothetical 71.7 kDa protein.
PFC0465C, MAL3P4.20.
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EMBL, AL008970, CAA15610.2;
InterPro; IPR002483; PWI.
Ffam; PF01480; PWI; 1.
FVART; SM00311; PWI; 1.
HYPOTHETICAL PROTEIN.
SEQUENCE 600 AA; 71663 MW;
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                                          35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=36329
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01-NOV-1996
01-OCT-2002
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Q90784;
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354 AA.
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                                                                                                                                                                   01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last seq
01-WAR-2003 (TrEMBLrel. 23, Last ann
Merozoite surface protein 3.
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                                                                                                                                             PRT;
                                                                                                                                                                                                                                Plasmodium falciparum (isolate 3D7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 419:498-511(2002).
                                                                                                                                             PRELIMINARY;
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           54 IKPVFKKIEEKKEE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                  1 KEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGF--EGKKDAG-----YVINLSKDTF 53
                                                                                                                                                                                                                                                                                                                    1 KEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFK-
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          Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                Burg M.A., Cole G.J.;
"Claustrin, an antiadhesive neural keratan sulfate proteoglycan, is structurally related to MAP1B.";
Bructurally related to MAP1B.";
W. Neurobiol. 25:1-22 (1994).
EMBL; X67778; CAA47988.1; -.
SEQUENCE 1038 AA; 117112 MW; 213D694A5B510927 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95198774; PubMed=7891748;
McColl D.J., Silva A., Foley M., Kun J.F., Favaloro J.M.,
Thompson J.K., Marshall V.M., Coppel R.L., Kemp D.J., Anders R.F.;
"Molecular variation in a novel polymorphic antigen associated with
Plasmodium falciparum merzotites.";
Mol. Biochem. Parasitol. 68:53-67(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McColl D.J., Anders R.F.;
"Conservation of structural motifs and antigenic diversity in the Plasmodium falciparum merozoite surface protein-3 (MSP-3).";
Mol. Biochem. Parasitol. 90.21-31(1997).
EMBL; L28825; AAC09377.1; -.
SEQUENCE 354 AA, 40119 MW; 3A7256152F48B527 CRC64;
                                                                                                                                                                                                                                                                     DB 13; Length 1038;
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                                                                                                             Cole G.J.;
Submitted (OCT-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                            43;
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23.8%; Pred. No. 0.98;
tive 28; Mismatches
                                                                                                                                                                                                                                                                 15.6%; Score 108.5; D. 28.6%; Pred. No. 2.3; tive 25; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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MEDLINE=98156743; PubMed=9497029;
                                                                                                                                                                     MEDLINE=94157526; PubMed=7906711;
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                                                                                                                                            SEQUENCE OF 1-451 FROM N.A.
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Matches 36; Conservative
                                                                                                                                                                                                                                                                              Local Similarity 28.6 tes 34; Conservative
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Plasmodium falciparum
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                                                        NCBI_TaxID=9031;
                                                                                                TISSUE=Brain;
Cole G.J.;
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01-OCT-2002
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Q25995;
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Q25995
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--ENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQR 100
                                            185 KEASS-----YDYIL------GWEPGGGVPEHKKEENMLSHLYVSSKDKENI 225
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Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.
Bisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
Fraser C.M., Barrell B.;
"Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium NCBI_TaxID=36329;
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SEQUENCE 354 AA; 40119 MW; 3A7256152F48B527 CRC64;
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Last annotation update)
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                   286 EQSNENNDOKKDMEA----QNLISKNONNN 311
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01-NOV-1996
                                                                  01-NOV-1996
01-OCT-2002
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01-NOV-1996
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SEQUENCE 1
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SIGNAL
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Q26019;
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                                                                                                                                                                                                                                                                                                          66 EEENKPT-------FDVSKKKDN-PQVNHSQLNESH-RKEDLQREEHSQKSDS 109
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MEDLINE=22255705; PubMed=12368864;
Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roso D.S., Ralph S.A.,
Worfadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
Fraser C.M., Barrell B.;
                                                                                                                                                                                                                                                                                                                                                             6 TIVSEEDFILPVYKGELEKGYQPDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKK
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Li X.R., Yu X.B., Luo S.H., Shan Z.X., Fang J.M., Xu J.;
"Sequence of Plasmodium falciparum secreted polymorphic antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                      Length 829;
                                                                                                                                      "Genome sequence of the human malaria parasite Plasmodium
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Submirded (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF188190; AAF04099.1; -.
SEQUENCE 379 AA; 43316 MW; C152A54E1F9D5F25 CRC64;
                                                                                                                                                                              EMBL, AE014848; AAN36341.1; -.
Hypothetical protein.
SEQUENCE 829 AA; 98816 MW; EF2675E301B2CE93 CRC64;
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Last annotation update)
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Best Local Similarity 25.2%;
Matches 38; Conservative
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                                                                                                                                                                   Nature 419:498-511 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymorphic antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=5833;
                                                                                                                                                       falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                619
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Q9U6C4
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54 IKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLN-------ESHRKEDLQR 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           253 SKENDDVLDE-KEEEARETEEEELEEKNBESTESEISBDEBEEEKEEENKKKEQEK 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGF--EGKKDAG-----YVINLSKDTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212 KEASS-----YDYIL------GWEFGGGVPEHKKEENMLSHLYVSSKDKENI
                                                                                                                                                                                        MEDLINE-95198774; PubMed=7891748; McColl D.J., Silva A., Foley M., Kun J.F., Favaloro J.M., Thompson J.K., Marshall V.M., Coppel R.L., Kemp D.J., Anders R.F.; "Molecular variation in a novel polymorphic antigen associated with Plasmodium falciparum merozoites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Conservation of structural motifs and antigenic diversity in the Plasmodium falciparum merozoite surface protein-3 (MSP-3)."; Mol. Biochem. Parasitol. 90:21-31(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Polymorphic antigen.
Plasmodium falciparum.
Elkaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                          Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 25 POTENTIAL.
26 380 POLYMORPHIC ANTIGEN.
380 AA, 43290 MW, 0986CA1393094CA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
              (TrEMBLrel. 01, Last sequence update) (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.9%; Score 103.5; DB 5; 25.2%; Pred. No. 2; tive 27; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 EEHSQKSDSTKDVTATVLDKNNISSKSTTNN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     379 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         312 EQSNENNDQKKDMEA----QNLISKNQNNN
                                                                                                                                                                                                                                                                                     Mol. Biochem. Parasitol. 68:53-67(1994).
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Created)
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                                                                                                                                                                                                                                                                                                                                                 STRAIN=FC27;
MEDLINE=98156743; PubMed=9497029;
                                                      Polymorphic antigen precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 01, C
(TrEMBLrel. 01, I
(TrEMBLrel. 22, I
                                                                                                                                                                                                                                                                                                                                                                                       McColl D.J., Anders R.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                          Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                             [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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AMAINTEMERTERY N. W. Calniker S. E., Holf R. A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S. E., Holf R. A., Evans C.A., Gocayne J.D., RA Gams M.D., Celniker S. E., Lii P. W., Hoskins R. A., Galle R.F., Galler R.F., George R.A., Lewis S.E., Eli P. W., Hoskins R. A., Galle R.F., Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Randon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfelifer B.D., RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfelifer B.D., RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfelifer B.D., RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfelifer B.D., RA Brandon R.C., Backer E.G., Helf G., Nelson C.R., Mikloo G.L.G., RA Ballew R.M., Benso P.V., Bernell J., Borkstein P., Benaley E.M., Bandari D., Bolshakov S., Borkova D.A., Butler H., Cadleu B., Center A., Chandra I., Burkis K.C., Busam D.A., Butler H., Cadleu B., Center A., Chandra I., RA Beblos B. Delcher A., Deng Z., Mays A.D., Davies P., Dones M., Duzhla K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Beblos B., Delcher A., Deng Z., Mays A.D., Davies P., Andreis M., Gabrielian A.E., Gasty N.S., Gabrielian A.E., Gasty N.S., Gabrielian A.E., Gasty N.S., Chun P., Herrandez J.R., Hostin D., Houston K.A., Howland T.J., Werim W., Garsel M., Markei B., Kodirac C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Leviesky A.A., Li J., Li Z., Liang Y., Lin X., Lasko P., Lei Y., Leviesky A.A., Li J., Li Z., Liang Y., Lin X., Lasko P., Lei Y., McThtobh T.C., McLeod M.P., McThtobh T.C., McLeod M.P., McThtobh T.C., McLeod M.P., Moshrefi A., Wand K.A., Nixon K.A., Nixon K., Nixoskern D., Puri, V., Martei B., McThtobh T.C., McLeod M.P., Partman G.S., Pan S., Pollard J., Puris K., Palenco K., Saulders R., Vellar S., Pan S., Pollard J., Puris S., Wang A.H., Wang A.H., Wang A.H., Wang A.H., Wang A.H., Wang A.H., Wang A.H., Wang A.H., Wang A.H., Wang A.H., Wang C.Y., Wasaarman D.A., Walley K.C., Wu D., Yang G., Santh H., Walley K., Zhou K., Zhong K., Zhou K., Zhong K., Zhong K
                                                                                                                                                                                          211 KEASS----YDYIL------GWEFGGGVPEHKKEENMLSHLYVSSKDKENI 251
                                                                                                                                                                                                                                                                                                54 IKPVPKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLN-----ESHRKEDLQR 100
                                                                                                                                                                                                                                                                                                                                          252 SKENDDVLDE-KEEEABETEEEELEEKNBEETESEISEDEEBEBEEKEEENDKKKEQEK 310
                                                                                                                                            1 KEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGF--EGKKDAG----YVINLSKDTF
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
DB 5; Length 379;
                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9V7J0; Q9GQ81;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
CG8421 protein (Aspartyl beta-hydroxylase variant 2)
ASPH OR CG8421 OR CG18658
                                                                         41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 EEHSQKSDSTKDVTATVLDKNNISSKSTTNN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  311 EQSNENNDOKKDMEA----QNLISKNONNN 336
                                      4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    382 AA
                                                                      27; Mismatches
14.7%; Score 102.5; 25.2%; Pred. No. 2.4
                               Best Local Similarity 25.2
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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Query Match
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Q9V7J0
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| | | | : : | | | | | | | EDLDTPLSESRFSK--VFDGWVDEHRDGHDCHDVQEPSGEALDDHDCHDDHEDEDEE 135
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EROURCE FROM N.A.

Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
Celniker S.E., Adams M.D., Annatides P.G., Brandon R.C., Rogers Y.,
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Appleton M., Strong R., Svirskas R., Tector C., Tyler D.,
Williams S.M., Zaveri J.S., Smith H.O., Venter. J.C., Rubin G.M.;
Sequencing of Drosophila melanogaster genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                  Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Berman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kromiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith B., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=20564328; PubMed=10956665; Dinchuk J.E., Henderson N.L., Burn T.C., Huber R., Ho S.P., Link J., O'Neil K.T., Focht R.J., Scully M.S., Hollis J.M., Hollis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Aspartyl beta -Hydroxylase (Asph) and an Evolutionarily Conserved
Isoform of Asph Missing the Catalytic Domain Share Exons with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
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EMBL; AF289494; AAG40807.1; -.
FYBase; FBGH0034075; ASP1.
SEQUENCE 382.AA; 43287 MW; 60E5C03AEBFC6EBB CRC64;
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J. Biol. Chem. 275:39543-39554 (2000).
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Matches
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Q9V719; 01-MAY-2000 (TrEMBLrel. 13, Created)

PRELIMINARY;

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READLINE-STRONG PLANKE=10731132,

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,

George R.A., Heir S.E., Richards S., Ashburner M., Henderson S.N.,

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Ra Brandon R.C., Rogers Y.H.C., Blazel F.G., Champe M., Peleifers B.D.,

Ran Enadon R.C., Rogers Y.H.C., Blazel F.G., Champe M., Peleifers B.D.,

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Butris K.C., Busam D.A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

Autris K.C., Busam D.A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

Acherry J.M., Cawley S., Dallike C., Davensport L.B., Davise P.,

Ra Ballew R. Doup LE. Downes M., Dugan-Rochs S., Dunkov B.C., Dunn P.,

Durbin K.J., Barogelista C.C., Ferrac C., Ferrac S., Fleischmann W.,

Rosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

Ran Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Alali M., Kalush F., Zarrpen G.H., Ke Z., Gann P., Harris M.,

Alali M., Kalush F., Zarrpen G.H., Ke Z., Kannison J.A., Rocherson D.,

Ran Herulov G., Milahina N.V., Mozbary C., Morrisc J., Moshrefi A.,

Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Natole D.L,

Ran Berrulov G., Milahina N.V., Mozbary C., Morrisc J., Moshrefi A.,

Ran B.N., Nelson K.A., Nixon K., Nusskern D.R., Pall R., Pall R., Pallazzolo M., Studer E., Shradling A.C., Stendeler R., Santh T.,

Spier E., Spradling A.C., Stender E., Shran H.,

Rander R., Spradling A.C., Stender E., Wang A., Wang Z., Yang S., Yao Q.A.,

Rander R., Morrisch R., Rubinstock G.M., Waissenbach J.,

Rander R., Morrisch R., Rubinstock G.M., Waissenb
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Banson J., An H., Baldwin D., Banson J., Beeson K.Y., Busam D.A.,

Carlson J., An H., Baldwin D., Banson J., Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A Carlson J.W., Center B., Galle R.F., Garg N.S., George R.A.,

A Gonzalez M., Houck J. Hoskins R.A., Hostin D., Howland T.J.,

Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Scheeler F.,

Killiams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

Sequencing of Drosophila melanogaster genome.";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                             Drosophila melanogaster (Fruit fly).

Eukaryota, Metazoa, Arthropoda, Hexapoda; Insecta, Pterygota,

Neoptera, Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea, Drosophilidae, Drosophila.
01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                           ASPH OR CG8421 OR CG18658
                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                           CG8421 protein.
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Miëra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,

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56 PVFKKIEEKKEEENKPT----FDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |: :::||: ||| :|| :|| :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | 
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Isoform of Asph Missing the Catalytic Domain Share Exons with
Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; "Annotation of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25;
                                                                                                                                                                                                                                                                                                                                                               Rubin G.M., Venter C.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.6%; Score 101.5; DB 5; Length 556; 24.5%; Pred. No. 4.2; ive 29; Mismatches 51; Indels 25;
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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Ephydroidea; Drosophilidae; Drosophila
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FlyBase; FBgn0034075; Asph.
SEQUENCE 556 AA; 63144 MW; B420980CBD6C357A CRC64;
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1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Aspartyl beta-hydroxylase variant 1 (CG8421-PA).
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MEDLINE=20564328; PubMed=10956665;
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Cherry A. Cabrelley S. Dabler C. Davenport L.B. Davies P., R. Cherry A. Colleter A. Cherry A. Deng Z. MAY B. Davies W. Deng Z. MAY B. Davies W. Deng Z. MAY B. D. Davies W. Deng Z. MAY B. D. Davies W. Deng D. E. Downes W. Deng Z. MAY B. D. Davies W. Deng D. E. Downes W. Deng Z. MAY B. Deng S. Davies W. Deng D. E. Downes W. Deng Z. MAY B. Deng S. Davies W. Deng D. E. Downes W. Deng Z. MAY B. Deng S. MAY B. Deng D. E. Downes W. Deng Z. MAY B. Deng S. MAY B. Deng D. E. Downes W. Deng D. E. Downes W. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng D. E. Deng
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14.6%; Score 101.5; DB 5; Length 785;

Query Match

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56 PVFKKIEEKKEEENKPT-----FDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDS 109
                                                                                                                                   175 KEASS-----YDYIL------GWEFGGGVPEHKKEENMLSHLYVSSKDKENI 215
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                                                    11 EDFILPVYKGELEKGYQFDGW-----EISGFEGKKDAGYVI-----NLSKDTFIK 55
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                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40; Gaps
                       25;
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"Allelic lineages of the merozoite surface protein 3 gene in Plasmodium reichenowi and Plasmodium falciparum.";
Mol. Biochem. Parasitol. 109:185-188 (2000).
EMBL; AJ252287; CAB85901.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBL_TaxID=57266;
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Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.4%; Score 100; DB 5; Length 329; 26.0%; Pred. No. 3.2; tive 24; Mismatches 44; Indels
                     Indels
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329 AA; 36916 MW; C5B045DB5E21A159 CRC64;
                                                                                                                                                                                                                                                                                                                     01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                       51;
24.5%; Pred. No. tive 29; Mismatches
                                                                                                                                                                                                                                                                                          329 AA
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01-MAR-2003 (TrEMBLrel. 23, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum (isolate 7G8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20416497; PubMed=10960178;
                                                                                                                                                                              110 TKDVTATVLDKNNISSKST 128
                                                                                                                                                                                                 194 EGTVEATVEATTEAT 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 26.0%
Matches 38; Conservative
                     34; Conservative
                                                                                                                                                                                                                                                                                         PRELIMINARY;
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      Best Local Similarity
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STRAIN=3D7;
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NON TER
SEQUENCE
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                     Matches
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69 EGEKKDGEKKSEKKDGKKEEEKKDGEKKDDKKDDKKDEKKDEDKKDEKKDADEKKDE 128
                                                                                                                                                                                                                   Hypothetical protein.
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                                                                                                                                                                                                                                                                                                        34 SGFEGKKDAGYV--INLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNE
                                                                                                                                                                                                                                                                             14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                92 SHRKEDLOREEHSOKS-----DSTKDVTATVLDKN-NISSKSTTNNPNK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                  DB 5; Length 1130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.2%; Score 99; DB 5; Length 211; 29.4%; Pred. No. 2.4;
                                                                                                                                                "Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                             53; Indels
                                                                                                                                                                                        EMBL; AE014829; AAN35244.1; -.
Hypothetical protein.
SEQUENCE 1130 AA; 131697 WW; FE6AAFE08C4CCDB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Maggi L., Le T.;
"The sequence of C. elegans cosmid T23B3.";
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-WAY-1997 (TrEMBLrel. 03, Last sequence update) 01-WAR-2003 (TrEMBLrel. 23, Last annotation update) Hypothetical 24.0 kDa protein.
                                                                                                                                                                                                                                               Query Match 14.4%; Score 100; DB Sest Local Similarity 26.1%; Pred. No. 12; Matches 30; Conservative 18; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
     MEDLINE=22255705; PubMed=12368864;
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STRAIN-Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T23B3.5.
Caenorhabditis elegans
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Best Local Similarity
Matches 30; Conserv
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                                                                                                                                                                falciparum.
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37 EGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNH----SQLNES 92

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MEDLINE=22255708; PubMed=12368867;
MEDLINE=222555708; PubMed=12368867;
MINGBALL A., Berriman M., Churcher C., Harris B., Harris D.,
MINGBALL K., Bowman S., Arkin R., Baker S., Barron A., Brooks K.,
MINGBALL Y., Christodoulou Z., Clark L., Clark R., Corton C.,
Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
Cronin A., Davies R., Davis P., Dear P., Dear P., Dearden F., Doggett J.,
Cronin A., Davies R., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
Oliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch E.,
A sajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
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                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                            PF07_0016.
Plasmodium falciparum (isolate 3D7).
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5; Length 1859;
                        93 HRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 134
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(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 DSTKDVTATVLDKNNISSKSTTNNPN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      333 NKRND-----HNKNNELEQVYYNNPN 353
                                                                                                                                                                                             Created)
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(TrEMBLrel. 23, I
(TrEMBLrel. 23, I
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RESULT 26
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Adams M.D., Celniker S.E., Hilp R.A., Boans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
Adams M.D., Celniker S.E., Richards S., Asbhurner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Tandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
AM N. K.H., Doyle C., Baxers E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkon C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkon C.R., Miklos G.L.G.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Deleise P.,
Borkova D., Boctchan M.R., Boutler H., Cadieu E., Center A., Chandra I.,
Burtis K.C., Eusam D.A., Buller H., Cadieu E., Center A., Chandra I.,
Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
Burtis K.C., Eusam D.A., Dahlke C., Davenport L.B., Davies P.,
Borkova D., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Burtis K.J., Evangelista C.C., Ferraz C., Ferraz C., Erraz C., Bodor I., Heiman T.J., Hernandez J., Harris M.,
Barris N.L., Harvey D., Heiman T.J., Hernandez J., Harris M.,
Barris N.L., Harvey D., Heiman T.J., Weim M.-H., Ibeywam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Barris D. Lei Y., Leviteky A.A., Li J., Li Z., Liang Y., Lin X.,
Barrishian M., Murphy B., Murphy L., Muzny D.M., Nelson D.K.,
Balazzolo M., Pittman G.S., Pan S., Pollar C., Scheeler F., Shen H.,
Band Z.-Y., Wassaman D.A., Weinstook G.M., Weissenbach J.,
Barrishian S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
                                                                                                                                                                                                                                                                                                                                                                                   20 GELEKGYQFDG-WEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKK 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 KD----NPQVNHSQLNESHRKEDLQREE-HSQKSDSTKDVTATVLDKNNISSKSTTNNPN 133
                                                                                                                                                                                                                                                                                                      Gaps
     Stevens K.
Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens Faylor K., Tivey A., Unwin L., Whitehead S., Woodward J., Sulston J.E., Craig A., Newbold C., Barrell B.G;
"Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-Mmr.zv.z
CG31958 protein.
CG31958 OR CG10022.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Prhvdroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                         14.2%; Score 99; DB 5; Length 2563; 29.4%; Pred. No. 32; cive 18; Mismatches 60; Indels
                                                                                                                                                                                         2563 AA; 298805 MW; 3F9613243D26F8F1 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 AA
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MEDLINE=20196006; Pubmed=10731132;
                                                                                                   Nature 419:527-531(2002).
EMBL; AL929355; CAD51734.1; -.
Hydrolase.
                                                                                                                                                                                                                                                                                                35; Conservative
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Best Local Similarity
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1D Q9VQVV
AC AC Q9VQVV
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Celniker S.E., Adams M.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon O., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Andeson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
A. Ferriers S., Frise E., Garle R.F., Gargo R.A.,
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Scheeler F.,
A. Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
Williams S.M., Zaveri J. S., Smith H.O., Venter J.C., Rubin G.M.;
Sequencing of Drosophila melanogaster genome.",
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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   Zheng L.,
Smith H.O.
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PROSITE; PS00018; EF HAND; 1.
Calcium, Calcium-binding
SEQUENCE 157 AA; 18263 MW; 543F0480E11D9EC1 CRC64;
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HSSP; P02593; 1CTR.
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les 34; Conserv
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MEDLINE=22255705; PubMed=12368864;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42;
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NCBI _TaxID=36329;
                                                               (isolate 3D7).
Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome sequence of the human malaria parasite Plasmodium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 951 AA; 112486 MW; AC8D889358A84F4F CRC64;
01-MAY-1999 (TrEMBLrel. 10, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
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Plasmodium falciparum (isolate 3D7).
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EMBL; AE001410; AAC71925.2; -.
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                                                               Plasmodium falciparum
Eukaryota; Alveolata;
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56 PVFKKIEEKKKEEENKPT-----FDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDS 109
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Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Pertea M., Allen J., Selalom S.J., Haft D., Mather M.W., Vaidya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Vencci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B., "Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 KELLKTILKEK--ILIIYNEQQNEEKKKKKKKPPQSD---ISEKKEKSKADLQKSESKNNN
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chawez C., Dorsett V., Farfan D., Frise B., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY060905, AAL28453.1;
FlyBase; FR900034075; Asph.
SEQUENCE 556 AA, 63089 MW; 95D82EAC57D11FE8 CRC64;
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                              449 AA; 52812 MW; 85B62272D6257C68 CRC64;
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EMBL; AE014842; AAN35996.1;
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01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2002 (TrEMBLrel. 22,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 449 AA; 5
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Local Similarity
les 28; Conserv
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  falciparum.";
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01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 Q-KITDNISSKEDEKNKNPKDNENSNNNSSDQKONDELQKONSDKLNDNVQDEKANKENSN 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENKPTFDVSKKKD----NPQVNHSQLNES--HRKEDLQREEHSQKSDSTKDVTATVLDKN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 VSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson
Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
Blanchard A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence of the murine respiratory pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24;
                                                                                                                                                                                                                                                    MYPU 4650.
Mycoplasma pulmonis.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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Blasmodium falciparum (isolate 3D7).
Bukaryotan Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 622;
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SEQUENCE 622 AA; 73762 MW; 42BD88930861960D CRC64;
                                                                                                                                                                                 Last sequence update)
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Last annotation update)
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25.4%; Pred. No. 15;
tive 26; Mismatches 50;
                                                                                                                 622 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycoplasma pulmonis.";
Nucleic Acids Res. 29:2145-2153(2001).
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  194 EGTVEATVEATTEATTEAT 212
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188 SNDSKEKNDENTNK 201
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                                                                                                               PRELIMINARY;
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Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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0980A1;
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Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,

Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,

Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,

Chan M.-S., Nene V., Shallon S.J., Suh B., Peterson J., Angiuoli S.,

Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,

Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,

McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,

Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
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NCBI_TaxID=36329;
                                                                                                                                               13.6%; Score 95; DB 5; Length 3026; 30.2%; Pred. No. 79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36; Indels
Nature 419:498-511(2002).
EMBL; AE014818; AAN36777.1; -.
Hypothetical protein.
SEQUENCE 3026 AA; 357633 MW; 9ECAED915C3C25CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypochetical protein.
SEQUENCE 3193 AA; 377923 MW; 46E6B21F921C5307 CRC64;
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Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            294 IHNTVKITKEVYSSNSFSSNSDTTLSYESVNNKKNK 329
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llarity 28.3%; Pred. No. 83;
Conservative 21; Mismatches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 3193 AA
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                                                                                                                                                                                                             15; Mismatches
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EMBL; AE014849; AAN36406.1; -.
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                                                                                                                                                                           Local Similarity 30.2% tes 29; Conservative
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NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47 NLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38 ISSDDILRRRFKKKTPNKFLEELDEEYESKHTKKSNIYLKED---LINVKLEEKQSLAKK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tungaal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.; "Sequence and Analysis of Chromosome 2 of Dictyostelium."; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AC116032; AAL93046.1; -
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Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Ouail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni
reveals hypervariable sequences.";
Mature 403:665-668(2000).

Mature 403:665-668(2000).
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Campylobacter jejuni.
Bacteria, Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Campylobacteracae; Campylobacter.
NCBI_TaxID=197;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.6%; Score 94.5; DB 16; Length 312; 25.7%; Pred. No. 8; ive 30; Mismatches 55; Indels 25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              312 AA; 37221 MW; 0004FA7836A741E8 CRC64;
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614 AA; 71591 MW; 85520D7AF08530F5 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical 71.6 Kba protein.
Dictyostellum discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyostellida, Dictyostellum.
NCBI_TAXID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43;
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Best Local Similarity
Matches 38; Conserva
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Matches 21; Conserv
                                                                                                                       SEQUENCE FROM N.A. STRAIN=NCTC 11168;
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., John M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
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Rhabditidae, Peloderinae, Caenorhabditis.
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Rhabditidae, Peloderinae, Caenorhabditis.
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Nelson, J, Wohldmann, P, Sansone J.;
Nelson, J, Wohldmann, P, Sansone J.;
"The sequence of C. elegans cosmid E03H12.";
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF000299; AAC47980.1; -.
Wormbep; E03H12.5; CE09144.
SEQUENCE 210 Aa; 23703 MW; 641B64BCF7AC983B CRC64;
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                                                                                                                                              Last sequence update)
Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 60.3 kDa protein.
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28.6%; Pred. No. 5.8;
tive 18; Mismatches
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     PRT;
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MEDLINE=99069613; PubMed=9851916;
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MEDLINE=94150718; PubMed=7906398;
                                                                                         (TrEMBLrel. 04, C
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
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Caenorhabditis elegans.
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Matches 22; Conserv
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Q52006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 SSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKOTFIKPVFKKIEE 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     56;
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Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
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                                                                                                                                                                                                                                                                                                                                                                                       13.5%; Score 94; DB 5; Length 535; 23.4%; Pred. No. 15; ive 26; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Mismatches 34; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1434 AA; 168278 MW; CB95FD0E270B1712 CRC64;
                                                                                                                                                                                                                                  "Direct Submission.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; U49945; ABC47924.1; -.
Woxmbp; CO2H7.1; CE06757.
Hypothetical protein.
                                                                               Leimbac D., Minx M., "The sequence of C. elegans cosmid C02H7."; Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                               03B2D8EBE43DFFB6 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22255705; PubMed=12368864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE014832; AAN35411.1; -.
                                                                                                                                                                                                                                                                                                                            ll protein.
535 AA; 60303 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 23.4
Matches 33; Conservative
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Best Local Similarity
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STRAIN=3D7;
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Gardner M.J. Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Gardner M.J., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
Petrea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
Martin D.M.A., Fairlamb A.H. Fraunholz M.J., Roos D.S., Ralph S.A.,
McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
"Genome sequence of the human malaria parasite Plasmodium
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Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3455;
104 SQKSDSTKDVTATVLDKNNISSKSTTN-------NPN 133
                                     13.5%; Score 94; DB 5; Length 345
28.6%; Pred. No. 1.1e+02;
ative 19; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 419:498-511(2002).
EMBL; AE014825; AAN37165.1; -.
Hypothetical protein.
SEQUENCE 3455 AA; 419390 MW; AEDDB8B999CEDBEE CRC64;
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
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Guanylyl cyclase (EC 4.6.1.2)
GC-BETA.
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                                                                                                                                                                                                                                                                                                    302 SDKKIIQSLYKQGETEKIEALDLPGSDYLADFKKILAYDNSTDIEYLVQTSTDTTI--VE 359
                                                                                                                                                                                                                                                                                                                                    59 KKIEEKKEEENKPT-----FDVSKKK----DNPQVNHSQLNESHRKEDLQR--EEHSQK 106
                                                                                                                                                                                                                                                                         9 SEEDFILPVYK-GELEK-----GYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVF 58
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                                                                    Schwarz F.V., Perreten V., Teuber M.; "Sequence of the 50-kb conjugative multiresistance plasmid pRE25 from Enterococcus faecalis RE25.";
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                                                                                                                                                                                                           Query Match 13.4%; Score 93; DB 2; Length 450; Best Local Similarity 26.0%; Pred. No. 15; Matches 39; Conservative 28; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5; Length 455;
16;
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                                                                                                                                EMBL; L39769; AAA99471.1; -.
EMBL; X92945; CAC29184.1; -.
Hypothetical protein; Plasmid.
SEQUENCE 450 AA; 52755 MW; F3CA5C827CFF30CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.

Dictyostelium discoideum (Slime mold).

Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.

NCBI_TAXID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Last annotation update)
                         SEQUENCE FROM N.A.
SPECIES=E.faecalis; STRAIN=RE25; PLASMID=pRE25;
PubMed=11735367;
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OSIDAO;
01-MAR-2003 (TEMBLFEL 23,
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01-MAR-2003 (TEMBLFEL 23,
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                                                                                                                   Plasmid 46:170-187(2001)
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2059 -KKIEKKEKKEKKENNNNFLYNDDYSSYSSPKYGDNENNFVIKYIRERKDFQKKFDHPNF 2117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NHSQL------NESHRK---EDLQREEHSQKSDSTKD-VTATVLDKNNISSKSTTNNP 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------ BVSKKKDNPQV 84
                                                                                                                                                                      Harris B., Lennard N., Clark L., Line A., Barron A., Corton C.,
Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J.,
Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL844509; CAD52725.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISG---FEGKKDAGYVINLSKDTFIKPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
Plasmodium falciparum (isolate 3D7).
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                        Length 3127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58; Indels
                                                                                                                                                                                                                                                                                                                                                3127 AA; 370597 MW; F0375C72B9007560 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        13.4%; Score 93; DB 5;
24.7%; Pred. No. 1.2e+02;
ive 29; Mismatches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 FKKIEEKKEEENK---------PTF---
                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 24.79
Matches 45, Conservative
                                                                                                                       [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2178 NE 2179
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Search completed: February 10, 2004, 10:57:04 Job time: 24.725 secs

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February 10, 2004, 10:57:15; Search time 27.9011 Seconds (without alignments) 1230.730 Million cell updates/sec
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848
1 TTVKEFILNKDTGEVŠELKP......ATVLDKANISSKSTTNNPNK 164
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| cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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| cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US106_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US106_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  801455
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          801455 segs, 209382283 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                            - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                            Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                            OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
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                                                                                                                                                                                                                Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	-
		de				
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
	848	100.0	773	14	US-10-067-385-8	Sequence 8, Appli
7	848	100.0		12	US-09-769-744A-28	Sequence 28, Appl
٣	615	72.5		6	US-09-765-272-68	Sequence 68, Appl
4	106	12.5	999	11	US-09-820-843A-107	Sequence 107, App
S	96.5	11.4		12	US-10-381-596A-2	Sequence 2, Appli
9	93.5	11.0		12	US-10-172-502-10	Sequence 10, Appl
7	. 92	10.8		12	US-10-369-493-22285	Sequence 22285, A
80	90.5	10.7		12	US-10-032-585-7046	Sequence 7046, Ap
σ	90.5	10.7		15	US-10-171-311-188	Sequence 188, App
10	90.5	10.7		9	US-09-925-299-859	Sequence 859, App
11	90.5	10.7		11	US-09-925-299-859	Sequence 859, App
12	89.5	10.6	402	10	US-09-827-664-4	Sequence 4, Appli
13	89.5	10.6		12	US-10-289-762-509	Sequence 509, App
14	89.5	10.6	516	12	US-10-032-585-7407	Sequence 7407, Ap
15	89.5	10.6		10	US-09-827-664-2	Sequence 2, Appli

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8 8 8

121 ESHRKEDLOREEHSOKSDSTKDVTATVLDKNNISSKSTTNNPNK 164

Sequence 7829, Ap Sequence 106, App Sequence 2016, App Sequence 2016, App Sequence 2016, App Sequence 2013, Ap Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 18189, A Sequence 181, App Sequence 181, App Sequence 2272, Ap Sequence 2272, Ap Sequence 22102, A Sequence 22102, A Sequence 22102, A Sequence 22102, A Sequence 22102, A Sequence 22102, A Sequence 22102, A Sequence 22102, A Sequence 22102, A Sequence 22102, A Sequence 5200, Ap Sequence 5200, Ap Sequence 5200, Ap Sequence 5200, Ap Sequence 5200, Ap Sequence 5309, Ap Sequence 57146, Ap Sequence 57146, Ap Sequence 57146, Ap Sequence 57146, Ap Sequence 57146, Ap Sequence 57146, Ap Sequence 57146, Ap Sequence 57146, Ap Sequence 57146, Ap Sequence 57146, Ap Sequence 57146, Ap Sequence 57146, Ap Sequence 57146, Ap Sequence 57146, Ap	ns and Vaccines	Length 773; Indels 0; Gaps 0; EDFILEVYKGELEKGYQFDG 60
12 US-10-032-585-7829 12 US-10-144-1944-106 12 US-10-144-1944-106 12 US-10-369-493-2016 9 US-09-815-242-5898 12 US-10-032-542-13137 12 US-10-032-542-13137 13 US-10-032-543-5013 14 US-10-080-505-5 15 US-10-369-493-5013 16 US-09-815-242-14032 17 US-10-369-493-5013 18 US-09-815-242-14032 19 US-09-815-242-14032 10 US-09-914-91-10918 10 US-09-914-1227 12 US-10-369-493-22375 12 US-10-369-493-22375 13 US-10-369-493-22375 14 US-09-815-242-1313 15 US-10-369-493-22375 16 US-09-116-140-047-2272 17 US-10-369-493-22375 18 US-09-116-140-047-2272 19 US-09-116-242-1313 10 US-09-116-242-1319 10 US-09-815-242-13008 10 US-09-815-242-1343 10 US-09-815-242-5838 10 US-09-815-242-5838 10 US-09-815-242-5838 10 US-09-815-242-5838 10 US-09-815-242-5838 10 US-09-815-242-5838	ALIGNMENTS 10067385 62A1 ccoccus Pneumoniae Proteins 1. US/10/067,385 1-02-05 US/60/138,453 1-10 0	100.0%; Score 848; DB 14; Length 773; imilarity 100.0%; Pred. No. 2.9e-68; ; Conservative 0; Mismatches 0; Indels 0; Gaps TTVKEPILNKDTGEVSELKPHRYTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYOPDG
225 3051 3051 1349 9 11349 9 11349 9 11349 9 11349 9 11402 115 1202 15 1203 15 1203 16 1203 16	n US/ 01105 01105 hn 11-588 11-588 00-06 00-06 8BER: r. 2.	100.0%; larity 100.0%; Conservative  KEFILNKDTGEVSEL!
444mmmmmmmuuuuuuuuuuu	385-8  10 Application US/ ion No. US200201105 INFORMATION: INT Adamou, John NT: Choi, Gil F INVENTION: Strept FERENCE: 469201-589 APPLICATION NUMBER: FILING DATE: 2002 PPLICATION NUMBER: ILING DATE: 1999-06 PPLICATION NUMBER: ILING DATE: 1999-06 PPLICATION NUMBER: ILING DATE: 1999-06 PPLICATION NUMBER: ILING DATE: 1999-06 PPLICATION NUMBER: ILING DATE: 1999-06 PRESEQ ID NOS: 8 E: Patentin Ver: 2. 773 E: 773 ERT	Similarity 4; Conser TTVKEFILN
9999	SULT 1 -10-067-385-8 Sequence 8, Applicatio Sequence 9, Applicatio SEREAL INFORMATION: APPLICANT: Adamou, Jo APPLICANT: Choi, Gil TITLE OF INVENTION: S FILE REFERENCE: 46820 CURRENT APPLICATION NUM FRIOR APPLICATION NUM PRIOR APPLICATION NUM PRIOR FILING DATE: 19 PRIOR PLING PRIOR NUM PRIOR FILING DATE: 19 PRIOR PRIOR PRIOR NUM PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRI	itch 3al 8 164 1
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ATTORNEY/AGENT INFORMATION

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1922 TTVKEFILNKDTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDG 1981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TTVKEFILLNKDTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDG
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HV Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 848; DB 12; Best Local Similarity 100.0%; Pred. No. 1e-67; Matches 164; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                                                             APPLICANT: Wells, Jereny M
APPLICANT: Hanniffy, Sean B
APPLICANT: Hanniffy, Sean B
APPLICANT: Hanniffy, Sean B
TILE OF INVENTION: Proceeins
FILE REFERENCE: PWC/P21122WO
CURRENT APPLICATION WUMBER: US/09/769,744A
CURRENT APPLICATION NUMBER: PCT/GB99/02452
PRIOR APPLICATION NUMBER: PCT/GB99/02452
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: GB 9816336.3
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: US 60/125329
PRIOR APPLICATION NUMBER: US 60/125329
PRIOR SED ID NOS: 196
NUMBER OF SEO ID NOS: 196
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FILING DATE: 22-Jan-2001
CLASSIFICATION: <Unknown>
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APPLICATION NUMBER: 08/961,083
FILING DATE: <Unknown>
Sequence 28, Application US/09769744A Publication No. US20030134407A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Streptococcus pneumoniae US-09-769-744A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 68, Application US/09765272 Patent No. US20020061545A1 GENERAL INFORMATION:
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                                                                                            APPLICANT: Le Page, Richard WF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
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Sequence 107, Application US/09820843A
Publication No. US20030039963A1
GENERAL INFORMATION:
APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI
TITLE OF INVENTION: USFRUL A ANTI-INFECTIVES
FILE REFERENCE: Q63915
CURRENT APPLICATION UMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                  48 YKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 EEKNKINKSDLHRQNELNLQSGK-----NEQDI-----NKNEKGKQ----DISNSNA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 EGKKDAGYVINLSKDTFIKPVFKKIEEKKE-----EENKPTFD----VSKKKDNP 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 BNKKD-------VKEGVKELEEKKKEEKISDDHKVEENKKSDDHKVEENKKSDDH 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 KKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 YKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 KDTGEVSELKPHRVT-VTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEI--SGF
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                                                                                                                                                                                                                                                                                                                                                Score 615; DB 9; ]
Pred. No. 3.2e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.5%; Score 106; DB 11; 24.3%; Pred. No. 0.33;
                                                                                                                                                                                                                                                                                                                                 72.5%; Sco...
100.0%; Pred. No....
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative 35; Mismatches
                                                                                                                          INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 68:
US-09-765-272-68
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature;
CTHER INFORMATION: hypothetical protein;
NAME/KEY: misc_feature;
CTHER INFORMATION: gi|3845248
US-09-820-843A-107
                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                              Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 42; Conservi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 4
US-09-820-843A-107
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LENGTH: 665
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US-10-381-596A-2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 DAGYVINLSKDTFIKPVFKKIEE-----KKEEENKPTFDVSKKKDNPQVNHSQLNESH 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  336 SAITEPONVOPTNEKMIDLODIKYVVYESVENNESMMDTFVKH-----PIKTGMLNGKKY 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           391 MVMETTNDDYWKDFMVEGQRVRIISKDAKNNTRTIIFPYVEGKTLYDAIVKVHVKTIDYD 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         451 GOYHVRIVDKEAFTKANTDKSNKKEOQDNSAKKEATPATPSKPTPSPVEKESOKODSOKD 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 EVSELKPHRVTVTIQ-NGKEMSSTIVSEEDFILPVYKGELEKGYQFDG--WEISGFEGKK 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: FOSTER, Timothy et al.

TITLE OF INVENTION: CROSS-REACTIVE MONOCLONAL AND POLYCLONAL ANTIBODIES.

FILE REPERBENCE: P0726310301/BAS

CURRENT APPLICATION NUMBER: 2002-06-17

PRIOR APPLICATION NUMBER: US 60/298,098

PRIOR APPLICATION NUMBER: US 60/298,098

PRIOR APPLICATION NUMBER: US 60/298,098

SOFTWARE: Patentin version 3.1

SEQ ID NOS: 29

SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Sequence 2, Application US/10381596A
Publication No. US20040014178A1
GENERAL INFORMATION:
TITLE OF INVENTION: von Willebrand factor-binding proteins from TITLE OF INVENTION: Staphylococci
CURRENT APPLICATION NUMBER: US/10/381,596A
CURRENT APPLICATION NUMBER: B 003573-3
PRIOR PLING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 11.4%; Score 96.5; DB 12; Length 2060; l Similarity 25.7%; Pred. No. 10; 39; Conservative 25; Mismatches 49; Indels 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 11.0%; Score 93.5; DB 12; Length 654; Best Local Similarity 21.9%; Pred. No. 4.3; Matches 49; Conservative 34; Mismatches 74; Indels 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 EDLQ----REEHSQKSDSTKDVT-ATVLDKNNISSKSTTNNPNK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2007 VKEORSIEKSEHTDMHVSELPETGETANKUGL 2038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 RKE--DLQREEHSQKSDSTKDVTATVLDKNNI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 QF-----DGWEISGFEGKK------
                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Staphylococcus lugdunensis
US-10-381-596A-2
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Publication No. US20030185833A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                LENGTH: 2060
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Gac, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPESSION OF MICROBIAL PROPERTIES
FILE REFERBNCE: 38-10(52052) B
CURRENT FILING NATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PLILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 22285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bo. Jiang
APPLICANT: Charles, Boone
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INTENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 DGWEISGFEGKKDA-----KEEENK 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 PTFDVSKKKDNPQVNHSQLNESHR-KEDL---QREEHSQKSDSTKDVTA-----TVLDKN 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 ILNKDIGEVSELKPHRVIVIIQNGKEMSSTIVSEEDF----ILPVYKGE---LEKGYQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.8%; Score 92; DB 12; Length 1875; 25.0%; Pred. No. 23;
S11 DNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT--PTK 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36; Mismatches
                                                                                                                                                 Sequence 22285, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7046, Application US/10032585 Publication to US20030180953A1 GENERAL INFORMATION: APPLICANT: Terry, Roemer D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Saccharomyces cerevisiae US-10-369-493-22285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48; Conservative
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US-10-032-585-7046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 NISSKSTTNNPN 163
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Best Local Similarity
Matches 48; Conserv
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NAME/KEY: SITE
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LENGTH: 758
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APPLICANT: Gannavarapu, Manjula
APPLICANT: Gannavarapu, Manjula
APPLICANT: Hoersh, Sebastian
TITILE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: OF CERVICAL CANCER
FILE REFERENCE: MR.-035
CURRENT APPLICATION NUMBER: US/10/171,311
CURRENT APPLICATION NUMBER: US 60/298,159
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 238
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 188
LENGTH: 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                 64 YTANKE--KMKKFKPSPWTRMPFTPKQGIELNHWVKGSKELIEQQEF----EEDGTPKPY 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  281 EARPRR-----QSMKEKEHQVVRNEEHKAEQEEGKVAQREEELVETGNQHNDVEIEEAGE 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 EGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 ELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGE-----LEKGYQFDGWEI--SGF
6 FILNKDTGEVSELKPH---RVTVTIQNGKEM-----SSTIVSEEDFILPVYKGELEKGY
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                                                                                                                                                                        110 DNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTN 160
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Patent No. US20020055627A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           379 DSQPEEVMDVLEMVENVKHVIADQEVMETNRVESVEPSEN 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 DLQREEHS---QKSDSTKDVTA--TVLDKNNISSKSTTNN 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51;
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                                                                                                                                                                                                                                                                                     Sequence 188, Application US/10171311
Publication No. US20030087270A1
                                                                                                                                                                                                                                                                                                                                                              Chen, Yan
Zhao, Xumei
Monahan, John
Kamatkar, Shubhangi
Glatt, Karen
                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 23.8<sup>1</sup>
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-311-188
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; LOCATION: (590)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-859
                                                                                                                                                                                                                                                                                                                                          ) LOCATION: (590)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-299-859
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 758;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT APPLICATION NUMBER: PCT/US00/05883
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR PLING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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28.1%; Pred. No. >...
17; Mismatches roPII
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ilarity 28.1%; Pred. No. 9.8;
Conservative 17; Migmathul-
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION WUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
PRIOR FLING DATE: 1999-03-12
NUMBER OF SQ ID NOS: 1556
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 859, Application US/09925299; Publication No. US20030040617A9; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 10.7%
Best Local Similarity 28.1%
Matches 47; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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GENERAL INFORMATION:
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502 KEFVRHKEKIKQAKEA-VKENLKKFSDSVKSTFRHFKDTTKNIFDE 547
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STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                            Sequence 4, Application US/09827664
Patent No. US20020150956A1
GENERAL INFORMATION: Blizabeth J.
TITLE OF INVENTION: No. US20020150956A1e1 tig
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FILING DATE: 06-Apr-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,795
REFERENCE/DOCKET NUMBER: GM10085
TELECOMMUNICATION INFORMATION:
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US-09-827-664-4
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Publication No. US20040006218A1
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TELEFAX: 215-994-2222
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STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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in particular for the diagnosis, preve
APPLICANT: Griffals, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides,
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnos
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/10/289,762
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 6849
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APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jiang
APPLICANT: Charle, Boone
APPLICANT: Charle, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REPRENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
SUFRARE: Patentin version 3.1
SEQ ID NO 7407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----VSKKKDNPQVNHSQLNESHRK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          369 KAKGRISRYLANKCSIASRIDNYSEEPTTAFGE-----ILKKQVEDRLKFYDTGSAPMK 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                    Length 511;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 KDTGEVSELKPHRVTVT--IQNGKEMSSTIVSEEDFILPVYKGELEKGYQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  480 DKKEKKDKKEKKDKK--DKKRKSDDGEETPKKKKKKSKD 516
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TITLE OF INVENTION: No. US20020150956A1el tig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58;
                                                                                                                                                                                                                                                                                                                                                                                       DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 EDLQREEHSQKSDSTKDVTATVLDKNNISSKSTT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
10.6%; Score 89.5; Di
Best Local Similarity 23.3%; Pred. No. 7.4;
Matches 37; Conservative 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 10.6%; Score 89.5; D 24.5%; Pred. No. 7.3; ive 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 7407, Application US/10032585; Publication No. US20030180953A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 IKPVFKKIEEKKEEENKPTFD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09827664; Patent No. US20020150956A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     ; ORGANISM: Chlamydia pneumoniae US-10-289-762-509
                                                                                                                                                                                                                                                                                                                                                                                                                                           23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Candida albicans
US-10-032-585-7407
                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-032-585-7407
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Best Local
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DB 12; Length 3051;
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SOFTWARE: Patentin version 3.0
SEQ ID NO 62
                                  TYPE: PRT
; ORGANISM: Candida albicans
US-10-032-585-7829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45; Conservative
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ORGANISM: Homo sapiens
US-10-144-194A-106
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 45; Conserv
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US-10-144-194A-106
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SEQ ID NO 7829
                    225
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Publication No. US20030180953A1
GENERAL INFORMATION:
APPLICANT: Terry, Roemer D.
APPLICANT: Terry, Roemer D.
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT APPLICATION NUMBER: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 AIDHSLGHLAEMVVKEDGVVENGDTVNIDFSG-SVDGEEFEGGQAEGYDLEIGSGSFI-P 198
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10.6%; Score 89.5; DB 10; Length 529;
Best Local Similarity 22.1%; Pred. No. 7.6;
Matches 50; Conservative 33; Mismatches 60; Indels 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 -----SHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTN 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
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                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/827,664
FILING DATE: 06-Apr-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Falk, Stephen T
REGISTRATION NUMBER: 36, 795
REFERENCE/DOCKET NUMBER: GM10085
                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA: APPLICATION NUMBER: 09/464,483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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TELEPHONE: 215-994-2488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 529 amino acids TYPE: amino acid
                                                                                                                                     ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO: 2:
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US-10-032-585-7829
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944 KPSG-IAELOREPLLVNESLNVENSGFRTNEEIHSESYNKGEISSGRKDNAEAISGHSVE 1002
                                                                                                            56 YQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKK----IEEKKEEENKPTFDVSKKK-- 109
                                                                                                                                             80 YDDDDDFFEGFESSNGAAKELNLSESQAIKEWKQRRDLEIEEREKLNSKKKEBIIEKAKS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 KDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKK-------DNPQVNHSQ 118
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                                                          Gaps
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                                                       12;
                                                                                                                                                                                                                  110 -- DNPOVNHSQLNESHRKEDLQREEH--SQKSDSTKDVTATVLDKNN 152
                                                                                                                                                                                                                                                      DB 12; Length 1298;
                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence 106, Application US/10144194A
; Publication No. US20030215809A1
; GENERAL INFORMATION:
; APPLICANT: OriGene Technologies Inc
; TITLE OF INVENTION: Regulated Breast Cancer Genes
; FILE REFERENCE: 3U 103 R1
; CURRENT APPLICATION NUMBER: US/10/144,194A
; CURRENT FILING DATE: 2002-06-12
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patentin version 3.0
                                                       43;
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Sequence 62, Application US/10144194A

Publication No. US20030215809A1

GENERAL INFORMATION:

APPLICANT: OriGene Technologies Inc

TITLE OF INVENTION:

FILE REFERENCE: 3U 103 R1

CURRENT APPLICATION NUMBER: US/10/144,194A
Query Match 10.4%; Score 88; DB 12; Best Local Similarity 28.0%; Pred. No. 3.5; Matches 30; Conservative 22; Mismatches 43;
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Ohlsen, Kari L.
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APPLICANT:
APPLICANT:
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APPLICANT: Chen, Xianteng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10(52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
                                                                                                   2697 KPSG-IAELQREPLLVNESLNVENSGFRTNEEIHSESYNKGEISSGRKDNAEAISGHSVE 2755
                                                                                                                                                                                                             ------KEVEE--EERHMPK---RKRKOHYLSSEDEPDDNPDVLDSR 2794
                                                                                                                                                               70 KDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKK------DNPQVNHSQ 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209 YIINKRINSIK----RSVSRILRKGK-----TDSILPVYQSELKPFRRPSDDDYKF 255
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256 TNIEDNKVREEGR-----VHVSKESTADSQTKQLGKKEQKVIQSHLRRHDNNSTFRPHR 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 DGWEISGF--EGKKDAGYVINLSKDTFIKPVFKKIEEKKEE------ENKPTFDVSK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 FILINKDIGEVSELKPHRVIVIIQNGKEMSSTIVSEEDFILPVYKGEL-----EKGYQF 58
                                                                      10 KOTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39; Gaps
                          46; Gaps
                                                                                                                                                                                                                                                                                      119 LNESHR-----KEDLQR--EEHSQKSDSTKDVTATVL-DKNNISSKSTT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.3%; Score 87.5; DB 12; Length 655; 20.5%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 KKDNPQV--NHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKN 151
                          60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57; Indels
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APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
TILE OF INVENTION: Identification of Essential Genes in ITLE OF INVENTION: Prokarvotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36; Mismatches
25.9%; Pred. No. 96; tive 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2016, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
                        45, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34; Conservative
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  Best Local Similarity
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LENGTH: 655
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854 VEFETPSGYTPT-----QVGSGTDEGIDSNGTSTTGVIKDKDNDTIDSGFYKPTYNL 905
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 NKDTGEVSELKP-HRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGF- 66
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APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: EITRA.011A
CURRENT APPLICATION UNMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 9;
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PRIOR DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
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PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION WUMBER: 60/207, 727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Staphylococcus aureus
US-09-815-242-5898
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Wall, Daniel
Trawick, John D.
Carr, Grant J.
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CORRESPONDENCE ADDRESS:
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APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
PILE REFERENCE: 10182-005-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 FEGKKDAGYVINLSKDT-----FIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             804 NKDGKQDSTEKGISGVTVTLKN-----ENGEVLQTTKTDKDGKYQFTGLENGTYK 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 -EGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         854 VEFETPSGYTPT-----QVGSGTDEGIDSNGTSTTGVIKDKDNDTIDSGFYKPTYNL 905
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 NKDTGEVSELKP-HRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGF-
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Publication No. US20030009010A1
GENERAL INFORMATION:
APPLICANT: St. Geme III, Joseph W.
Falkow, Stanley
TITLE OF INVENTION: Haemophilus Adherence and Penetration
                                                                                                                                                                                                                                                                                                                                                                              Query Match 10.3%; Score 87.5; DB 9; Length 1349; Best Local Similarity 25.0%; Pred. No. 38; Matches 41; Conservative 23; Mismatches 73; Indels 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  906 GDYVWEDTINKNGVQDKDEKGISGVTVTLKDENDKVLKTVTTDEN 949
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NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13137
LENGTH: 1349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/032,585 CURRENT FILING DATE: 2001-12-20
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Sequence 7800, Application US/10032585

; Publication No. US20030180953A1

; GENERAL INFORMATION:
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NUMBER OF SEQUENCES: 9
                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-13137
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Best Local Similarity 25.09
Matches 41; Conservative
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US-09-839-996-5
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1296 INTGSATALTETAEKSDKPQTETAASTEDASQHKANTVADNSVANNSESSEPKSRRRSI 1355
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; Publication No. US20030073166A1
; Publication No. US20030073166A1
; Publication No. US20030073166A1
; Publication St. Geme, Joseph W.
TITLE OF INVENTION: HARMOPHILUS ADHERENCE AND PENETRATION PROTIENS
; PILE REFERENCE: A-59941-1/RFT/DCF/DHR
; CURRENT FILING DATE: 1020-02-22
; PRIOR APPLICATION NUMBER: US 08/296,791
; PRIOR PELING DATE: 1094-10-25
; PRIOR APPLICATION NUMBER: US 09/839,996
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
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Э
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
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                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/839,996
FILING DATE: 20-Apr-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/296,791
FILING DATE: 25-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-59941/RFT/RMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 -- OKSDSTKDVTATVLDKNNISSKSTTNNPNK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Fred. No. 51;
14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 87.5;
Pred. No. 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 87.5;
Pred. No. 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (415) 781-1989
                                                                   STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION TELEPHONE: (415) 781-198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRGANISM: Haemophilus influenzae US-10-080-505-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 27.2%;
Matches 25, Conservative 14
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Best Local Similarity 27.2%;
Matches 25; Conservative 14
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater. Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPESSION OF MICROBIAL PROFERIES
FILE REFERENCE: 38-10(52052)B
CURRENT PELLING DATE: 2003-02-28
PRIOR PAPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 5013
LENGTH: 6642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1182 DGQEGARVTRDESTVDGASILTIDTATYYSEVNHLTISVVAENTLGAEETGAQLTIEPKK 1241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 DGWE---ISGFEGKKDAGYVINLSKDTFIKPV----FKKIEEKK--EEENKPTFDVSKKK 109
                                                                                                                                                                                                                                                                                                                                                     139 QSQVYSSIIADTLIHRSNEVANANTKDNSNSDDEEHSSKKRKTKKKSITDFFKKQKKNED 198
                                                                                                                                                                                                                                                                                                                          56 YQFDGWEISGFEGKKDAGYVINLSKDTFIKPVPKKIEEKKEEENKPTFDVSKKKDNPQVN 115
                                                                                                                                                                                                                                                                                                                                                                                                                       16 HSQLNES-----HRKEDLQR----EHSQKSDSTKDVTATVLDKNNISSKS 157
                                                                                                                                                                                                                             4 KEFILNKDTGEVSELKPHRVTVTIQNGKEMSST-----IVSEEDFILPVYKGELEKG 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TTVKEFILNKDTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDF--ILPVYKGELEKGYQF
                                                                                                                                                                                                                                                           110 DNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTT 159
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                                                                                                                                      Length 778;
                                                                                                                                                                                    Indels
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illarity 21.8%; Pred. No. 3.2e+02;
Conservative 33; Mismatches 80;
                                                                                                                                      DB 12;
                                                                                                                                                                                    26; Mismatches
                                                                                                                                      10.3%; Score 87; 24.2%; Pred. No.
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Patent No. US20020061569A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5013, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
                        ; LENGTH: 778
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-21889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Caenorhabditis elegans US-10-369-493-5013
                                                                                                                                                           Best Local Similarity 24.2%
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 37; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TT 159
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SEQ ID NO 21889
LENGTH: 778
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                                                                                                                                          Query Match
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US-10-369-493-16456

i Sequence 16456, Application US/10369493

j Sequence 16456, Application No. US20030233675A1

i GENERAL INFORMATION:
    APPLICANT: Chor, Yongwei
    APPLICANT: Slater, Steven C.
    APPLICANT: Gldman, Barry S.
    APPLICANT: Gldman, Barry S.
    TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
    TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: UNMBER: US/10/369, 493
    CURRENT APPLICATION NUMBER: US 60/360,039
    PRIOR APPLICATION NUMBER: US 60/360,039
    PRIOR APPLICATION NUMBER: US 60/360,039
    NUMBER OF SEQ ID NOS: 47374
    SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gao, Yongwei
APPLICANT: Gao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                                                     1296 INTGSATAITETAEKSDKPQTETAASTEDASQHKANTVADNSVANNSESSEPKSRRRSI 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87 VFKKIEEKKEEENKPTFDVSKKKDNPOVNHSQLNESHRK-EDLOREEHSOKSDSTKDVTA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222 LINKINEIKQSKQTVSDDLSKKKQDLDIKINDFKHTEKKIDDKLAELHTKQNVDNKINE 281
                          76 INLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHS- 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 VKEFILNKDTGEVSELKPHRVTV--TIQNGKEMSSTIVSEEDFILPVYK-----GELEK 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 10.3%; Score 87; DB 12; Length 323; Best Local Similarity 22.1%; Pred. No. 6.9; Matches 44; Conservative 33; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 GYQFDGWEISGF------EGKKDAGYVINLSKDTFI-----
                                                                                                                                               135 -- QKSDSTKDVTATVLDKNNISSKSTTNNPNK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-369-493-21889
; Sequence 21889, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     282 VSQSKQTQADNGTKNNNAK 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-369-493-16456
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66 F-EGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHR 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F-EGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHR 124
                                                                                                                                                                                                                                                                                                                                6 FILNKDTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 FILINKOTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISG
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                                                                                                                                                                                                                                       Length 732;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 KEDLOREEHSOKSD----STKDVTATVLDKNNISSKST--TNNPN 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259 -EDVGSDEEDEKKDGDKKKKKKIKEKYIDKEELNKTKPIWTRNPD 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 KEDLOREEHSOKSD----STKDVTATVLDKNNISSKST--TNNPN 163
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TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                       DB 9;
                                                                                                                                                                                                                                  10.2%; Score 86.5; DI
23.6%; Pred. No. 22;
tive 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.2%; Score 86.5; D: 23.6%; Pred. No. 22; Live 29; Mismatches
CURRENT APPLICATION NUMBER: US/09/874,923
CURRENT FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 122
SSCTWARE: FastSEQ for Windows Version 4.0
EEQ ID NO 18
LENGTH: 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 137
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 732
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CURRENT APPLICATION NUMBER: US/09/991,496
CURRENT FILING DATE: 2001-11-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18, Application US/09991496
Patent No. US20020169285A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dillon, Davin C.
Skeiky, Yasir A.W.
                                                                                                                                                                                                                                                          Best Local Similarity 23.6%
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 23.64
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bhatia, Ajay
APPLICANT: Coler, Rhea
APPLICANT: Probst, Peter
                                                                                                                                                                    ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapien
US-09-991-496-18
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US-10-369-493-5292
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 KEEE-----NKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTAT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----EDFILPVYKGELEKGYQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 SRFTPSLRTHTIMNLTELKNTPVSELITLGESMGLENLARMRKQDIIFAILKQHAKSGED 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 F-----DGWEISGFEGKKDAGYVINLSKDTFIKP-------VFKKIEEK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Reed, John R.
APPLICANT: Webb, John R.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Coler, Rhea
APPLICANT: Probst, Peter
APPLICANT: Brannon, Mark
TITLE OF INVENTION: LEISHWANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHWANIASIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                         Essential Genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 9;
                                                                                                                             APPLICANT: Call, Usuano C. APPLICANT: Call, Usuano C. APPLICANT: Call, Usuano C. APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essenti
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-01-023
PRIOR PELING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/245,578
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR FILING DATE: 2000-12-22
PRIOR PRILING DATE: 2000-12-22
PRIOR PRILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 10.2%; Score 86.5; D
Best Local Similarity 23.5%; Pred. No. 11;
Matches 43; Conservative 21; Mismatches
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Patent No. US20020081320A1
GENERAL INFORMATION:
                                                                                      Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
                   Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 VLD 149
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G. TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
  716
                                                                                 62 ---EISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQ 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 PVEEIKNY--TKEHNNLILLINKDV------QQESSEQKNKST-DKGEKK--PDSNEKG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                   111 NPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNI-----SSKSTTNNPN
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146 ERKKEKKEKTEKKFDHSKKSEDTQKVKDEKQAKEKEVESLKLPSEKNSNKAKT 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 12; Length 204;
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TITLE OF INVENTION: NO. US20030236392Ale1 full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2272
LENGTH: 734
671 SAMHQYDGIDEQAGNIESRYKSAYQENIKMKTLVDSYTERIEETEE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION: MAP TO ACO06445.10
INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6
INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.8
INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
INFORMATION: EXPRESSED IN LIVER, SIGNAL = 1.5
INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
INFORMATION: SWISSPROT HIT: P41891, EVALUE 1.00e-03
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CURRENT APPLICATION NUMBER: US/10/029,386 ·
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SEQ ID NO 32082
LENGTH: 204
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                                                                                                                                                                                                                                                                                                                                         Sequence 32082, Application US/10029386 Publication No. US20030194704A1
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Publication No. US20030236392A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 LNESHRKEDLORE-EHSOKSDST
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Best Local Similarity 26.0%
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: OTHER INFORMATION:
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                                                              APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPERSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10(52052)B
CURRENT FILING NATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 5292
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 10918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 YVINLSKDTFIKPVFKKIEEKKEEENKPTFD----VSKKKDNPQVNHSQLNESHRKEDL 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 ELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYOFD---GWEISGFEGKKDAG 73
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10.2%; Score 86.5; DB 12; Length
Best Local Similarity 20.4%; Pred. No. 28;
Matches 37; Conservative 37; Mismatches 64; Indels
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Publication No. US20030233675A1
Sequence 5292, Application US/10369493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: Caenorhabditis elegans US-10-369-493-5292
                           US20030233675A1
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180 EKENRKIKEEDDED 193
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Matches 32; Conservative
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Length 884;

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APPLICANT: Cao, Yongwei
APPLICANT: HinkLe, Gregory J.
APPLICANT: HinkLe, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT PILING DATE: 2003-02-28
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 22275
                                                                                                                                                                                                                                                                                                                             64 SGFEGKKDAGYVINLSKDTFIKPVFKKIE---EKKEEENKPTFDVSK--KKDNPQVNHSQ 118
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Publication No. US20030054436A1
GENERAL IMPORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVEXTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 DTGEVSELKPHRVTVTIQNGKEMSSTI-----VSEEDFILPVYKGELEKGYQFDGWEIS 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 KEDLOREEHSOKSDSTKDVTATVLD-----KNNISSKSTTNN 161
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                                                                                                                                                                                                                                   Score 85.5; 1
Pred. No. 34;
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Pred. No. 40
CURRENT APPLICATION NUMBER: US/10/032,585 CURRENT FILING DATE: 2001-12-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Saccharomyces cerevisiae US-10-369-493-22375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.1%;
21.0%;
                   CURRENT FILING DATE: 2001-12-2
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: Patentin version 3.1
SEQ ID NO 7122
LENGTH: 884
                                                                                                                                                                                                                                   10.1%;
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Best Local Similarity
Matches 34; Conserv
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Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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US-08-781-986A-5200
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APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF FILE PERERRICE: 38-10(52052)8
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                æ
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Publication No. US20030180953A1
GENERAL INFORMATION:
APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
                                                                                                                                                                                                                                                                                                                 280 TIDTAISSSN---NHEKDSGYGRIDESLRNDESSEQENBAREDPNSTSLKSKRDLGQSQDT 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 GELEKGYQFDGWEISGFEGKKDAGYVINLSKDTF-----IKPVFKKIEE-KKBEENKP 101
                                                                                                                                                                                                                                                                                                                                                                                102 TFDVSKKKDNPQVNHSQLNESHR-KEDLQREEHSQKSDSTKDVTATVL-DKNNISSKSTT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 ----GWEI---SGFEGKKDAGYVINLSKDTFIKPVFKK------IEEKKEEENKPTFD 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 ILDSSDDEKVEAKK---TTKKRKGKN-NKKKVSEGDNLDEDVHEDLDAGFKFDLDADDTT 81
                                                                                                                                                                                          -TIQNGKEMSSTIVSEE--DFILPVYK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 ILNKDTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 752;
                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.1%; Score 85.5; DB 12; 21.8%; Pred. No. 27;
                                                                                            Query Match 10.1%; Score 85.5; DB 12; Best Local Similarity 21.7%; Pred. No. 27; Matches 39; Conservative 42; Mismatches 58;
                                                                                                               ; Pred. No. 27;
42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 35
US-10-369-493-22302
; Sequence 22302, Application US/10369493
; Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                          10 KDTG-EVSELKPHRVTV--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 21.8
Matches 38; Conservative
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-369-493-22302
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LENGTH: 752
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LOCATION: (255)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 EAVLNTTCKKCGCKGHFAKDCFMQPGGTKYSLIPDEEEEKEEAKSAEFE----KPDFTRN 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 EGKKDAGYVINLSKDTFIKPVFKK----IEEKKEE-ENKPTFDVSKKKDNPQVNHSQLN- 120
                                                                                                 , LOCATION: (259)
, OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 EGK----KDAGYVINLSKDTFIKPVFKKI-----EEKKEEENKPTFDVSKKKDNPQVN 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 ILNKDTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDPILPVYKGELEKGYQFDGWEISGF
                                                                                                                                                                                                                                                                                                                                                                               17 BLKPHRVTVTIQ-----NGKEM--SSTIVSEEDFILPVYKGELEKGYQ-FDGWEISGF
                                                                                                                                                                                                                                                                                                          Indels 34;
                                                                                                                                                                                                                                  10.0%; Score 85; DB 10; Length 259; ilarity 23.8%; Pred. No. 7.9; Conservative 30; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 636;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Trawick, John D.
APPLICANT: Garr, Grant J.
APPLICANT: Garr, Grant J.
APPLICANT: Xu, H. Howard
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.0%; Score 85; DB 9; 22.0%; Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 HSQLNESHRKEDLQREEHSQKSDSTKDVTAT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 PSRKRKKEKKKKKHRDRKSSDSDSSDSESDT 230
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5838, Application US/09815242
Patent No. US2002061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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US-09-815-242-5838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
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Best Local Similarity 22.0%
Matches 35; Conservative
                                                                                                                                                                                                             Query Match
Best Local Similarity
Trans 36; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-815-242-5838
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
10.0%; Score 85; DB 8; Length 208;
Best Local Similarity 21.7%; Pred. No. 6;
Matches 38; Conservative 22; Mismatches 89; Indels
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                                                                                                                                                                     ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
COMPUTER: HP Vectra 486/33
COPTAME: ASCII Text
SOCTAME: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
TILE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
       ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 KKDAGYVINLSKDTFIKP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1313, Application US/09764864
Patent No. US20020132753A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5200:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
                                STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
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ORGANISM: Homo sapiens
                                                                    CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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LENGTH: 259
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Search completed: February 10, 2004, 11:23:56 Job time : 28.9011 secs

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GenCore version 5.1.6
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February 10, 2004, 10:48:45; Search time 11.1197 Seconds (without alignments) 1331.870 Million cell updates/sec Run on:

US-10-067-385-8_COPY_620_773
799
1 DTGEVSELKPHRVTVTIQNG......ATVLDKNNISSKSTTNNPNK 154 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:* Database :

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

÷ .	Description	serine proteinase,	metalloproteinase	hypothetical prote		hypothetical prote	hypothetical prote	-	_	hypothetical prote	_	_	_	_		hypothetical prote	ᆸ		lipoprotein (impor			hypothetical prote		hypothetical prote	_	hypothetical prote	7	hypothetical prote	hypothetical prote	probable transcrip
SUMMARIES	ID	F95074	A97942	T18467	JC5497	B71609	T18283	G81339	T25911	A84152	S46817	T20410	T14188	D86432	T37189	G71609	T47835	137271	A90570	T10466	T18427	T28771	T05612	B72291	T32879	G96542	T28391	T27136	T27135	841552
	DB	7	~	~	~	7	~	~	~	~	~	~	~	~	~	~	~	~	7	7	N	~	~	~	7	~	7	N	7	7
	Query Match Length	2140	2144	558	1038	665	325	312	211	614	1345	385	988	540	535	2500	644	348	622	1397	3724	210	456	219	253	629	670	867	871	1332
<b>a</b> to	Query Match	100.0	9.66	13.8	13.6	13.1	13.0	12.5	12.4	12.2	12.2	12.1	12.1	12.1	12.0	12.0	12.0	11.9	11.9	11.9	11.8	11.8	11.7	11.6	11.4	11.3	11.3	11.3	11.3	11.3
	Score	799	196	110	108.5	105	103.5	100	66	97.5	97.5	97	97	96.5	96	96	95.5	95	. 95	95	94.5	94	93.5	93	91	90.5	90.5	90.5	90.5	90.5
i	Result No.	П	7	m	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

rhoptry protein -	conserved hypothet	probable DNA-direc	trigger factor [im	hypothetical prote	hypothetical prote	hypothetical prote	probable membrane	ankyrin related pr	unknown protein F2	hypothetical prote	hypothetical prote	hypothetical prote	serine-type D-Ala-	protein T04A8.13 [	hypothetical prote
T28676	E89883	805362	A89951	B81594	C72074	E86549	867610	T19006	E96795	T39009	T33068	A71683	S66040	G88436	T24435
7	N	Н	~	~	7	7	~	~	~	~	N	~	~	~	0
2401	645	1202	433	508	508	508	700	1016	528	1888	301	371	443	762	791
11.3	11.3	11.3	11.2	11.2	11.2	11.2	11.2	11.2	11.1	11.1	11.1	11.1	11.1	11.1	11.1
90.5	90	90	89.5	89.5	89.5	89.5	89.5	89.5	83	68	88.5	88.5	88.5	88.5	88.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 RESULT 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Settlu 1 Set	umoniae (strain TIGR4) -Aug-2001 D.; Peterson, S.; Heid dune, D.; Holtzapple, herty; B.A.; Morrison, coccus pneumoniae.
Query Match         100.0%;         Score 799;         DB 2;         Length 2140;           Best Local Similarity         100.0%;         Pred. No. 7.2e-52;         Additional constraints         0;         Mismatches         0;         Indels         0;         Gaps           Qy         1         DTGEVSELKPHRVTVIQNGKEMSSTIVSEEDFILPVXKGELEKGYQFDGWEISGFEGKK         0         Indels         0;         Gaps           Db         1953         DTGEVSELKPHRVTVIQNGKEMSSTIVSEEDFILPVXKGELEKGYQFDGWEISGFEGKK         0         0         Indels         0         0         0         Indels         0         0         0         0         Indels         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0	; Gaps 0; ISGFECKK 60 ISGFECKK 2012 ISGFECKK 2012 HRKEDLOR 120 HRKEDLOR 2072

metalloproteinase (EC 3.4.21.-) A [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Date: 2.2-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C;Accession: A97942
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E
Y; P.; Sun, P.M.; Winkler, M.E.
J; Bacteriol. 183, 5709-5717, 2001
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234

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hypothetical protein C0465c - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Species: 15-Oct-1999 #text_change 11-Jan-2002
C;Accession: T18467
R;Lawson, D; Bowman, S.; Barrell, B.
R;Lawson, D; Bowman, S.; Barrell, B.
R;Lawson, D; Bowman, S.; Barrell, B.
A;Reference number: 218937
A;Reference number: 218937
A;Reference number: T18467
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-558 «LAM»
A;Residues: 1-558 «LAM»
A;Cross-references: EMBL:AL008970; NID:e1407852; PIDN:CAA15610.1
C;Genetics:
A;Map position: 3
A;Introns: 84/1; 160/1
A;Note: C0465c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---DLQREEH-----SQKSDSTK----DVTATVLDKNNISSKSTTN 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Cross-references: GB:AE007317; PIDN:AAK99365.1; PID:g15458138; GSPDB:GN00174 C,Genetics:
C,Genetics:
A;Gene: pttA
C;Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FKKI--EEKKEE-----SNKPTFDVSK-KKDNPQVNHSQLNE-----SHRK 115
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NiAlternate names: keratan sulfate proteoglycan
C;Species: Gallus gallus (chicken)
C;Date: 07-Jul.1997 #sequence revision 12-Sep-1997 #text_change 21-Jul-2000
C;Accession: JC5497; PC4334; §37561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---DAGYVINLSKDTFIKPV
                                                                                                                                                                                                                                                                                                                                  DAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQR
                                                                                                                                                                                                                                                    DIGEVSELKPHRVIVILONGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEKK
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                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                              ;
                                                                                                                                                                         Length 2144;
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                                                                                                                                                                                                              Indels
                                                                                                                                                                     Score 796; DB 2; Lk
Pred. No. 1.2e-51;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    EEHSQKSDSTKDVTATVLDKNNISSKSTINNPNK 154
                                                                                                                                                                         Query Match 99.6%;
Best Local Similarity 99.4%;
Matches 153; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54; Conservative
                                A; Molecule type: DNA
A; Residues: 1-2144 <KUR>
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Best Local Similarity
Matches 54; Conserv
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                    A;Status: preliminary
A; Accession: A97942
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R;Burg, M.A.; Cole, G.J.
J. Neurobiol. 25, 1-22, 1994
A;Title: Claustrin, an antiadhesive neural keratan sulfate proteoglycan, is structurally, A;Reference number: JC5497; MUID:94157526; PMID:7906711
A;Accession: JC5497
A;Accession: JC5497
A;Molecule type: mRNA
A;Residues: 1-1038 - BURL>
A;Cross-references: EMBL:X67778; NID:9406318; PIDN:CAA47988.1; PID:9406319
A;Accession: PC4334
A;Accession: PC4334
                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 79-813,299-412,485-502 cBUR2>
A; Residues: 79-813,299-412,1485-502 cBUR2>
A; Experimental source: brain
C; Comment: This protein inhibits neural cell adhesion and neurite outgrowth in the nervo C; Keywords: chondroitin sulfate proteoglycan; glycoprotein; keratan sulfate
C; Keywords: chondroitin sulfate proteoglycan; glycoprotein; keratan sulfate
F; 120,786; 130,000 Region: cell attachment (R-GD) motif F; 112,213,490,191,820,191 site: carbohydrate (Rsn) (covalent) #status predict
F; 112,213,490,410,793,820/Binding site: chondroitin sulfate (Ser) (covalent) #status predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE001410; GB:AE001362; NID:g3845245; PIDN:AAC71925.1; PID:g384524
A;Experimental source: clone 3D7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein PFB0680w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Bate: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C;Accession: B71609
R;Gardner, M.J; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743; PMID:9804551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 GKKDAGYVINLSKDTFIKPVFKKIEEKKE------EENKPTFD----VSKKKDNPQ 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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C;Species: Dictyostelium discoideum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Length 665;
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Pred. No. 2;
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Best Local Similarity 24.4%
Matches 42; Conservative
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A; Residues: 1-665 <GAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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C;Accession: A84152
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Rutcleic Acids Res. 28, 4317-431, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: A84152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-614 <STO>
A;Cross-references: GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BAB07736.1; GSPDB:GN00
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 ЕĞЕККDĞEKKSEKKDGDKKEEEKKDEEKKDGDKKEDDKKDEKKDEDKKDEKKDADEKKDE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 FECKKDAGYVINLSKDTFIKPVFKKIEEKK--EEENKPTFDVSKKK----DNPQVNHSQL 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               436 FAGRNIASQL------GKIEEEKLQDKYNNYTFDFFKKEVVNVQSPIKSTSAL 482
                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:U88309; PIDN:AAB42334.1; GSPDB:GN00019; CESP:T23B3.5 A;Experimental source: strain Bristol N2; clone T23B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein YHR080c - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 19-Apr-2002
                        C.Species: Caenorhabditis elegans
C.Spacies: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein BH4017 [imported] - Bacillus halodurans (strain C-125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 EGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNH----SQLNES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 SELKPHRVTVTIQNGKEMSSTIVSE-----EDFILPVYKGELEKGYQFDGW----EISG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 211;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 154
                                                                           C,Accession: T25911
R;Maggi, L.; Le, T.
submitted to the EMBL Data Library, February 1997
A;Description: The sequence of C. elegans cosmid T23B3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.
  - Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 99; DB;
; Pred. No. 1.5;
17; Mismatches
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Best Local Similarity 29.4*
Matches 30; Conservative
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     hypothetical protein T23B3.5
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A; Introns: 30/2; 200/3
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                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: CESP:T23B3.5
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable membrane protein Cj0692c [imported] - Campylobacter jejuni (strain NCTC 11168)
C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Species: Ja.Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C;Accession: G81339
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: G81339
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-312 < PAR>A;Residues: 1-312 < PAR>A;Residues: 1-312 < PAR>A;Experimental source: serotype O2, strain NCTC 11168
C;Accession: T18283
R;Rieben Jr., W.K.; Gonzales, C.M.; Gonzales, S.T.; Pilkington, K.J.; Kiyosawa, H.; Hugh Genetics 148, 117-1125, 1998
Genetics 148, 117-1125, 1998
A;Title: Dictyostelium discoideum nuclear plasmid Ddp5 is a chimera related to the Ddp1
A;Reference number: Z14684; MUID:98198836; PMID:9539429
A;Accession: T18283
A;Accession: T18283
A;Accession: T18283
A;Accession: T18283
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-325 <RIE>
A;Residues: 1-325 <RIE>
A;Cross-references: EMBL:U00796; NID:g2702254; PID:g2702258; PIDN:AAC18634.1
C;Genetics:
A;Introns: 85/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 NHIKOSGYYATNEEIEIFLESCTLCKEITAQTKRNSYKKRNIINKLPEEEEEEEEEEEE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --IEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKE-----DLQREEHSQKSDSTK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----- 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 INGGKPLDDDLRDEISSDDILRRRFKKKTPNKFLEELDEEYESKHTKKSNIYLKED---L 00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 IQNGKEMSSTI---VSEEDFILPVYK-----GELEKGYQFDGWEISGFEGKKDAGYV 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                11 HRVTVTIQNGKEMSSTIVSEEDFILPVYK-GEL--EKGYQFDGWEISGFEGK-----
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                                                                                                                                                                                                                                                                                                                                                                                               63;
                                                                                                                                                                                                                                                                                                                                            Length 325;
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Best Local Similarity 25.3%; Pred. No. 2;
Matches 41; Conservative 32; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                             50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 ---KDAGYV-----INLSKDTFIKPV-----FKK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 TTQTKQEKKELTNSIEKIQKTETKIQKPLIIEKKLDVKNQPN 182
                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                          13.0%; Score 103.5; D
23.8%; Pred. No. 1.2;
:ive 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               43; Conservative
                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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36; Conservative
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Best Local Similarity
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                      Rifavello, T.

Submitted to the EMBL Data Library, June 1994
A; Bescription: The sequence of S. cerevisiae cosmid 9205.
A; Reference number: 846795
A; Accession: 846795
A; Accession: 846317
A; Accession: 846317
A; Residues: 1-1345 < FAV>
A; Residues: 1-1345 < FAV>
A; Residues: 1-1345 < FAV>
A; Residues: BMBL:U10556; NID:g500825; PIDN:AAB68895.1; PID:g500838; MIPS:YHR080c, C, Genetics:
A; Cross-references: SGD:S0001122
A; Map position: 8R
C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1150 SHDKHRPFHSKVE-----QKSSESRKSDDNKDILTHILDFVQNNFSSEIFMNKLLSP 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
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Cipacie: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
Cipacesion: T20410
R;Thomas, K.
Bilmitted to the EMBL Data Library, October 1996
A;Reference number: Z19271
A;Reference number: Z19271
A;Reference number: Z19271
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A;Reference number
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 KKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 KGELEKGYQFDGWEISGFEGKK-DAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DTGEVSELKPHRVTVTIQ--NGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein B02A10.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 5
A;Introns: 32/1; 72/1; 85/1; 122/1; 133/1; 220/3
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12.1%; Score 97; DB
Best Local Similarity 29.6%; Pred. No. 4.3;
Matches 42; Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.2%; Score 97.5; 1
27.0%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 QREEHSQKSDSTXDVTATVLDK 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  350 KKEEEEKKEDEVEEKSEKUEEK 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          311 KKDE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153 NK 154
C, Accession: S46817
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hypothetical protein T28D5.30 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 28-Jul-2000

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M.A.; Barrell, B.G.; Bancro
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Anture 408, 816-820, 200
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Ayauthors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                A; Introns: 162/3; 201/3; 416/3; 438/3; 460/3; 482/3; 504/3; 519/3; 534/3; 559/3; 579/3; C; Superfamily: Arabidopsis thaliana hypothetical protein T21C14.40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 IKPVFKKIEEKKE-----EENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  442 VEPVGDDVRSSGDMSPNPSAANNVREGPATFDIMESEDNPGRDNVAPMEDHIRSEVQLSP 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 YVINLSKDTFIKPVFKK---IEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Cross-references: GB:AE005172; NID:94587525; PIDN:AAD25756.1; GSPDB:GN00141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein T518.14 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 NGKEMSSTIVSEEDFILPVYKGELEKGY----QFDGWEISGFEGKKDAGYVINLSKDTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 12.1%; Score 97; DB 2; Length 988; Best Local Similarity 22.1%; Pred. No. 12; Matches 34; Conservative 31; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
C;Accession: T14188
R;Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, submitted to the Protein Sequence Database, August 1999
A;Reference number: Z17931
A;Accession: T14188
A;Molecule type: DNA
                                                                                                                                                                                                        A;Residues: 1-988 <BEV>
A;Cross-references: EMBL:AL109819
A;Cross-references: EMBL:AL109819
C;Genetics:
A;Gene: ATSP:T28D5.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HVL---GAKDVTDVSDPTDKVGVNDVTDASDPTE 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 HSQKSDSTKDVT--ATVLDKNNISSKSTTNNPNK 154
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bovine and human sperm heads: the
                                                                                                                                   hypochetical protein T209.90 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47835
R;Nyakatura, G;.Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.; submitted to the Protein Sequence Database, February 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cylicin II - human
Cyspecies: Homo sapiens (man)
Cyspecies: Homo sapiens (man)
Cyspecies: Homo sapiens (section 12-Aug-1996 #text_change 21-Jul-2000
Cyspecies: Marg-1996 #section 137271; Section R.; Franke, W.W.
Ryhess, H.; Heid, H.; Zimbelmann, R.; Franke, W.W.
Exp. Cell Res. 218, 174-182, 1995
A;Title: The protein complexity of the cytoskeleton of bovine and human spen
A;Reference number: 137271; MUID:95255491; PMID:7737358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 QNGKEMSSTIVSEE----DFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 IKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDS----
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A;Residues: 1-348 <HES>
A;Cross-references: EMBL:246788; NID:9758586; PIDN:CAA86752.1; PID:9758587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 644;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
2281 LEEEE---KSDDKRD-----DKKNDNTREKNNLDNK 2308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:AL138658
A;Experimental source: cultivar Columbia; BAC clone T209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.0%; Score 95.5; DB 2;
ilarity 23.4%; Pred. No. 10;
Conservative 22; Mismatches 58;
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Best Local Similarity
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A,Introns: 158/2; 329/3
A,Note: T209.90
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-644 <NYA>
                                                                                                                                                                                                                                                                                                                                                         A,Accession: T47835
A,Status: preliminary
A,Molecule type: DNA
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G71609
hypotherical protein PPB0650w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C;Accession: G71609
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
Ferrea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743; PMID:9804551
A;Accession: G71609
A;Accession: G71609
A;Residues: 1-2500 <GAR>
A;Roblecule type: DNA
A;Residues: 1-2500 <GAR>
A;Cross-references: GB:AE001408; GB:AE001362; NID:93845238; PIDN:AAC71919.1; PID:9384524
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
                                                                                                       C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 18-Feb-2000
C.Accession: T37189
R.Lelimbac, D.; Minx, M.
Submitted to the EMBi Data Library, February 1996
A.Description: The sequence of C. elegans cosmid C02H7.
A.Reference number: Z20523
A.Reference number: Z20523
A.Residues: T37189
A.Residues: 1-535 < LEI>
A.Residues: 1-535 < LEI>
A.Cross-references: EMBI:U49945; PIDN:AAC47924.1; GSPDB:GN00029; CESP:CO2H7.1
A.Residues: 1-535 < LEI>
A.Cross-references: EMBI:U49945; PIDN:AAC47924.1; GSPDB:GN00029; CESP:CO2H7.1
A.Resperimental source: strain Bristol N2; clone C02H7
C.Genetics:
A.Gene: CESP:CO2H7.1
A.Map position: X
A.Introns: 47/3; 100/3; 149/3; 304/2; 347/3; 458/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 -----SKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNE----SHRKED 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 12.0%; Score 96; DB 2; Length 535; Best Local Similarity 21.3%; Pred. No. 7.4; Matches 35; Conservative 28; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEHSQKSDSTK-----DVTATVLDKNNISSKSTTNNPNK 154
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                                                                                       - Caenorhabditis elegans
                                                                                    hypothetical protein C02H7.1
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A;Residues: 1-210 <NEL>
A;Cross-references: EMBL:AF000299; PIDN:AAC47980.1; GSPDB:GN00022; CESP:E03H12.5
A;Experimental source: strain Bristol N2; clone E03H12
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hypothetical protein C033Sc - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000 C;Accession: T18427 R;Lawson, D.; Bowman, S.; Barrell, B. Bubmitted to the EMBL Data Library, August 1997 A;Reference number: Z18935 A;Reference number: Z18935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: EMBL: 298547; NID: e1325376; PID: e1325379; PIDN: CAB11104.1 C; Genetics:
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Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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submitted to the EMBL Data Library, June 1997
A;Description: The sequence of C. elegans cosmid E03H12.
A;Reference number: Z20520
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A,Molecule type: DNA
A,Residues: 1-3724 <LAW>
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A,Molecule type: DNA
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11.8%; Score 94; DB 3
Best Local Similarity 28.6%; Pred. No. 3.6;
Matches 28; Conservative 18; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Introns: 307/1; 1545/2
A;Note: C0335c
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A; Introns: 30/2; 201/3
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C;Superfamily: eukaryotic type II DNA topoisomerase; phage T4 DNA topoisomerase (ATP-hyd
C;Keywords: ATP; DNA binding; isomerase; nucleus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : | | :: | |: | | : | | : | | : | | : | | : | | : | | 129 Q-KITDNISSKEDEKAKNPKDNENSNNNSSDQKNDELQKNNSDKLNDNVQDEKANKENSN 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENKPTFDVSKKKD----NPQVNHSQLNES--HRKEDLQREEHSQKSDSTKDVTATVLDKN 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 VSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEE 87
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;Species: Plasmodium falciparum
;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
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poprotein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
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A,Accession: T10466
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1397 «CHE»
A;Cross-references: EMBL:X79345; NID:g994807
A;Gene: Topol1
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S.J. S.J. S.J. S.J. S.J. S.J. Submitted to the EMBL Data Library, September 1995
A,Reference number: Z17031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 -NISSKSTTNNPNK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 SNDSKEKNDENTNK 201
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GB: AE005173; NID: g11054631; PIDN: AAG27876.1; GSPDB: GN00141
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C,Species: Caenorhabditis elegans
C,Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F17J6.14 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33; Indels
                                                                                                                                                      Rigattung, S.; Scheet, P. submitted to the EMBL Data Library, January 1998 A;Description: The sequence of C. elegans cosmid C17F3. A;Reference number: Z21240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99
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                                                                                                                                                                                                                                                                                                         A,Accession: T32879
A,Status: preliminary; translated from GB/EMBL/DDBJ
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Fred. No. 7.6;
7; Mismatches
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19.5%; Pred. No. 23;
iive 37; Mismatches
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32.6%;
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Best Local Similarity 32.6'
Matches 31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-253 <GAT>
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A; Status: preliminary
A; Molecule type: DNA
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                                                                                                                           Accession: T32879
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
C;Accession: T05612
R;Bevan, M.; Wedler, H.; Wedler, B.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F. submitted to the Protein Sequence Database, February 1999
A;Reference number: Z15419
A;Reference number: Z15419
A;Residues: T05612
A;Molecule type: DNA
A;Residues: 1-456 < BEV>
A;Coss-references: EMBL:AL035394
A;Experimental source: cultivar Columbia; BAC clone F9D16
C;Genetics:
A;Map position: 4
A;Introns: 110/3; 247/2; 282/3; 304/3; 361/3; 390/2; 418/3
A;Note: F9D16.270
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Vypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: B72291
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
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A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq A;Reference number: A72200; MUD:99287316; PMID:10360571

A;Accession: B72291

A;Actus: preliminary

A;Molecule type: DNA

A;Residues: 1-219 cARN>

A;Residues: 1-219 cARN>

A;Croas-references: GB:AE001771; GB:AE000512; NID:g4981678; PIDN:AAD36218.1; PID:g498168

A;Experimental source: strain MSB8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249 EKDPLKPKHPVSAFLVYANERRAALREENKSVVEVAK-----ITGEEWKNLSDKKKA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GY--VINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 PYEKVAKKNYETYLO-AMEEYKRTKEEE----ALSOKKE----EEELLKLHKOEALQM 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIPNFVFVELYATDEKTTLFAKE-----VLGEESVSYRDLFAGFGVRGTPTFFFFKGK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 KDAGYVIN-LSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKED- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 EVSELKP-HRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 LKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQ--FDGWEISG-----FEGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.7%; Score 93.5; DB 2; Length 456; 25.0%; Pred. No. 9.5; tive 28; Mismatches 58; Indels 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---LQREEHSQKSDS-----TKDVTATVLDK 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      350 LKKKEKTDN-----LIKKEKATKKKNENVDPNK 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 EEHSQKSDSTKDVTATVLDKNNISSKSTTNN--PNK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.6%; Score 93; DB 2 26.2%; Pred. No. 4.5; tive 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 25.03
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 42; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63
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RESULT 29
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submitted to the EMBL Data Library, September 1997
A;Reference number: Z20316
A;Accession: T27136
A;Accession: T27136
A;Accession: T27136
A;Accession: T27136
A;Molecule type: DNA
A;Residues: 1-867 <WIL>
A;Access-references: EMBL:Z99278; PIDN:CAB16493.1; GSPDB:GN00020; CESP:Y53C12B.3a
A;Experimental source: clone Y53C12B
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
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                                                                                                                Cydcession: T28391
RyAccession: T28391
RyAccession: T28391
RyAccession: T28391
RyAccession: T28391
A) Virol. 73, 533-552, 1939
A) Virol. 73, 533-552, 1939
A) Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A) Reference number: Z20484; MUID:99102612; PMID:9847359
A) Rocession: T28391
A) Rocession: T28391
A) Rocession: T28391
A) Rocession: Rocession: RAPO
A) Rocession: RAPO
A) Rocession: CAPO
A) Coss-references: EMBL:AF063866; NID:g4049647; PIDN:AAC97713.1; PID:g4049753
C) Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KDAGYVINLSKDTFIKPVFKKIE----EKKEEENKPTFDVSKKKDNPQVNHSQLNESHRK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 EGKKDAGYVINLSKDTFIKPVFKKIE-EKKEEENKPTFDVSKKKDNPQVNHSQL-NESHR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 DSDSDSGVNIDESQNSDSKVNINKLENESQNSDSKVNIDESQNSDS-KVNINKLENESQN 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -- QFDGWEISGF 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | | : | : | | : | | : | | 33 VNFEEKKQIISTLLKFNNFDKTEMCGVSVEKFVQLINNKSASEKYSDVDSSIDESQNSDS 92
                                          F MSV230 hypothetical protein - Melanoplus sanguinipes entomopoxvirus Species: Melanoplus sanguinipes entomopoxvirus Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein Y53C12B.3a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 EVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELE----KGYQFDGWEISGFEGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.3%; Score 90.5; DB 2; Length 670; 22.5%; Pred. No. 25; ive 34; Mismatches 69; Indels 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -VSEEDFILPVYKGELEKGY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 KEDLOREEHSOKSDSTKDVTATVLDKNNISSKSTTNNPNK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 367 PIDPQEISDDQDDTVPDVPDQIVEQDNQSHKSRHNSENR 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 EDLOREEHSOKSDSTKDVTATVLDKNNISSKSTTNNPNK 154
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A;Map position: 2
A;Introns: 100/3; 177/3; 218/1; 423/3; 714/2; 864/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
11.3%; Score 90.5; DE
Best Local Similarity 26.4%; Pred. No. 33;
Matches 42; Conservative 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 22.5$
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 VTIQNGKEMSSTI-
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A, Note: MSV230
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RESULT 26
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1332 <STE>
A; Residues: 1-1332 <STE>
A; Cross-references: EMBL: 235950; NID: 9536341; DIDN: CAA85026.1; DID: 9536342; MIDS: YBR081c
R; Andre, B.; Cziepluch, C.; Hein, C.; Jauniaux, J.C.; Urrestarazu, A.; Vissers, S.
Bubmitted to the Protein Sequence Database, August 1994
A; Reference number: 845893
A; Accession: 845948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-835 cAND.
A; Residues: 1-835 cAND.
A; Residues: 1-835 cAND.
A; Cross-references: EMBL: 325950; MIPS:YBR081c
R; Haynes, S.R.; Dollard, C.; Winston, F.; Beck, S.; Trowsdale, J.; Dawid, I.B.
R; Haynes, S.R.; Dollard, C.; Winston, F.; Beck, S.; Trowsdale, J.; Dawid, I.B.
A; Haynes, S.R.; Dollard, C.; Winston, F.; Beck, S.; Trowsdale, J.; Dawid, I.B.
A; Haynes, S.R.; Dollard, C.; Winston, F.; Beck, S.; Trowsdale, J.; Dawid, I.B.
A; Reference number: S40800; MUID: 92285152; PMID: 1350857
A; A; Accession: S40800
A; Status: nucleic acid sequence not shown
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-871 <WIL>
A;Cross-references: EMBL:Z99278; PIDN:CAB16492.1; GSPDB:GN00020; CESP:Y53Cl2B.3b
A;Experimental source: clone Y53Cl2B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                720 KDNG-----DLWCEHM-KKIKCGHCEATGEOGHHPLICPKKKEEERVAKSR--ESSOK 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59
   C.Species: Canonhabditis elegans
C.Species: Genorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C.Accession: T27135
R.Kershaw, J.; Lennard, N.
submitted to the EMBL Data Library, September 1997
A.Reference number: Z20316
A.Accession: T27135
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Moclecule type: DMA
A.Moclecule type: DMA
A.Moclecule type: DMA
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N;Alternate names: protein YBR0739; protein YBR081c
C;Species: Saccharomyces cerevisiae
C;Date: 28-Jan-1994 #sequence revision 09-Sep-1994 #text change 20-Sep-1999
C;Accession: S41552; S45946; S45948; S40800; S45478; S54985; S59716
R;Gansheroff, L.; Dollard, C.; Tan, P.; Winston, F.
a;Reference number: S41552
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A,Residues: 1-1332 <GAN>
A,Cross-references: EMBL:L22537; NID:g349189; PIDN:AAC37424.1; PID:g349190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 EVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELE----KGYQFDGWEISGFEGK
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submitted to the Protein Sequence Database, August 1994
A;Reference number: S45932
A;Accession: S45946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 2
A;Introns: 100/3; 177/3; 218/1; 423/3; 717/2; 867/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.3%; Score 90.5; D. 26.4%; Pred. No. 33; ive 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 26.4%
The 42; Conservative
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conserved hypothetical protein SA0976 [imported] - Staphylococcus aureus (strain N315) C;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001 C;Accession: E89883 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguci ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - fungus (Ascobolus immersus) mitochon-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       983 IY--NILKLNKIKKIIDKVKEYTDEIEK----NNKKINAELSNSEKIITQLKENSSLKE 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 GYVINLSKDTFIKPVFKKIEEKKEBENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:BA000018; PID:g13700929; PIDN:BAB42225.1; GSPDB:GN00149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            341 KMTDLQDTKYVVXSSVENNESMMDTFVKH-----PIKTGMLNGKKYMVMETTNDDYWKDF 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                396 MVEGORVRIISKDAKNNTRIIIFPYVEGKTLYDAIVKVHVKTIDYDGOYHVRIVDKEAFT 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 KPVFKKIEEKKEEENKPTFDV----SKKKDNPQVNHSQLNESHRKEDLQ----REEHSQ 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: E89883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable DNA-directed DNA polymerase (EC 2.7.7.7) - fungus (Ascobolus immers C; Species: mitochondrion Ascobolus immersus C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000 C; Accession: S0536; Meinhardt, F.; Esser, K. RiKempken, F.; Meinhardt, F.; Esser, K. Mol. Gen. Genet. 218, 523-530, 1989
                                                                                                                                                                                                                                                                                                                                                                                              16 TIQNGKEMSSTI------VSEEDFILPVYKGELEKGY---QFDGWEISGFEGKKDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --DAGYVINL-SKDTFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 EVSELKPHRVTV--TIQNGKEMSSTIVSEEDFILPVYKGELE-KGYQF-----DGWEIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                     Length 2401;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1036 CQSKIKSTIDDNYVSECIKNITNLKTYIVNEKNNINT 1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 HSQKSDSTKD------VTATVLDKNNISS 145
                                                                                                                                                                                                                                 11.3%; Score 90.5; DB 2; 27.4%; Pred. No. 1e+02; tive 26; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67;
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26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.3%; Score 90;
larity 21.4%; Pred. No.
Conservative 32; Mismatcl
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                                                                                                                                                                                                                                     Query Match
Best Local Similarity 27.4*
Matches 43; Conservative
                                      A;Status: preliminary
A;Molecule type: DM
A;Residues: 2260-2401 <KEE>
A;Cross-references: GB:M34281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 45; Conserv
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A; Residues: 1-645 < KUR>
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A:Accession: A45521
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                 A; Cross-references: EMBL:M87651; NID:q172683; PIDN:AAA35087.1; PID:q172684

R; van der Aart, Q.J.M.; Barthe, C.; Doignon, F.; Aigle, M.; Crouzet, M.; Steensma, H.Y.

R; van der Aart, Q.J.M.; Barthe, C.; Doignon, F.; Aigle, M.; Crouzet, M.; Steensma, H.Y.

R; van der Aart, Q.J.M.; Barthe, C.; Doignon, F.; Aigle, M.; Crouzet, M.; Steensma, H.Y.

A; Reference analysis of a 31 kb DNA fragment from the right arm of Saccharomyces of A; Reference number: 845478

A; Reference number: 845478

A; Status: nucleic acid sequence not shown; translation not shown

A; Reatives: nucleic acid sequence not shown; translation not shown

A; Reatives: L-624, LRGKKRKI', 633-1332 < VAN>

A; Cross-references: EMBL:X76294

A; Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1993

A; Cross-references: EMBL:X76294

A; Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1993

A; Reference number: 854985; MUID:95229044; PMID:7713415

A; Reference number: 854985; MUID:95229044; PMID:7713415

A; Reterence number: S64985

A; Status: nucleic acid sequence not shown

A; Molecule type: DNA

A; Reaidues: 1-1332 < GAWN

A; Reaidues: 1-1332 < GAWN

A; Reaidues: L-1332 < GAWN

A; Cross-references: EMBL:L22537; NID:9349189; PIDN:AAC3742.1; PID:9349190

R; van der Aart, Q.J.M.

B; Deference number: Scaton
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C;Species: Plasmodium yoelii
C;Species: Plasmodium yoelii
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 01-Dec-2000
C;Accession: T28676; A45521
R;Sinha, K.A.; Keen, J.K.; Ogun, S.A.; Holder, A.A.
Mol. Biochem. Parasitol. 76, 329-332, 1996
A;Title: Comparison of two members of a multigene family coding for high-molecular mass A;Reference number: Z20507; MUD: 97077455; PMID: 8920022
A;Acteris: preliminary; translated from GB/EMBL/DDBJ
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Retus: preliminary
A;Ross-references: EMBL: U36927; NID: 91041784; PID: 91041785; PIDN: AAB41263.1
R;Keen, J; Holder, A.; Playfair, J; Lockyer, M.; Lewis, A.
Mol. Biochem: Parasitol. 42, 241-246, 1990
A;Title: Identification of the gene for a Plasmodium yoelii rhoptry protein. Multiple cc
A;Reference number: A45521; MUD: 91101660; PMID: 2270106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: S59702
A;Accession: S59716
A;Accession: S59716
A;Accession: S59716
A;Accession: S59716
A;Accession: S59716
A;Coss-references: EMBL:X76294; NID:g974203; PIDN:CAA53940.1; PID:e264674; PID:g558360
A;Experimental source: strain S288C
C;Genetics: A;Genetics:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----NPQVNHSQLNESH 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Superfamily: unassigned bromodomain proteins; bromodomain homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37;
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24.5%; Pred. No. 54;
tive 26; Mismatches
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C;Superfamily: unassigned bromodomain proteins
C;Keywords: nucleus; transcription regulation
F;Ke6-521/Domain: bromodomain homology <BRO>
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Matches 39; Conservative
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Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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A; Molecule type: DNA
A; Residues: 1-508 <ARN>
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K.;
A,Title: In organello replication and viral affinity of linear, extrachromosomal DNA of A,Reference number: S05362; MUID:90066356; PMID:2573821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: A89951
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; C;Kuroda, M.; Ohta, T.; Uchiyama, I.; Sawano, T.; Inoue, R.; Katco, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-433 «KUR»
A;Cross-references: GB:BA000018; PID:g13701472; PIDN:BAB42766.1; GSPDB:GN00149
A;Cross-references: strain N315
C;Genetics:
A;Gene tig
C;Superfamily: trigger factor; BKBP-type peptidylprolyl isomerase homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       trigger factor [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 VNHSQLNESHRKEDLOREEHSOKSDSTKDVTATVLDKNNI-----SSKSTTNNPN 153
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                                       A;Accession: S05362
A;Molecule type: DNA
A;Molecule type: DNA
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A;Molecule type: DNA
A;Molecule type: DNA
A;Genetics: 1-1202 <KEM>
A;Cross-references: EMBL:X15982; NID:g2933; PIDN:CAA34106.1; PID:g1370212
C;Genetics:
A;Genome: mitochondrion
A;Genome: code: SGC3
C;Superfamily: Ascolobus probable DNA-directed DNA polymerase
C;Keywords: DNA binding; mitochondrion; nucleotidyltransferase
                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                       11.3%; Score 90; DB 1; Length 1202; ilarity 22.6%; Pred. No. 52; Conservative 35; Mismatches 74; Indels
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11.2%; Score 89.5; D:
Best Local Similarity 22.1%; Pred. No. 18;
Matches 50; Conservative 33; Mismatches
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Best Local Similarity
Matches 40; Consern
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RESULT

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C,Accession: BB1594
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, T.ILe: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: AB1500; MUID:20150255; PMID:10684935
A;Accession: BB1594
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C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
C;Accession: C72074
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
Nature Genet. 22, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
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A;Experimental source: strain CWL029
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C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C;Accession: E86549
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
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pneumoniae (strain AR39)
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       hypothetical protein CP0281 [imported] - Chlamydophila pneumoniae (strain Al
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
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Pred. No. 21;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDLDRVGHDSNEDSTEDSRS---EGGEPSSKSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.2%; Score 89.5; DE 24.5%; Pred. No. 21; ive 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 IKPVEKKIEEKKEEENKPTFD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 IKPVFKKIEEKKEEENKPTFD----
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24.5%;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                A, Experimental source: clone C06C3
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Best Local Similarity 21.6*
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 24.3'
Matches 35; Conservative
                                                                                                                                                                                                                                                                                    A; Residues: 1-1016 <WI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-528 <STO>
                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: CESP: C06C3.1
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                                                                                                                                                                                                                                                                                                                                                               C:Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probable membrane protein YDL074c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein D2483
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Beccharomyces cerevisiae
C;Bate: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
C;Accession: S67610
R;Wambutt, R:; Wedler, H:; Wedler, E.; Scharfe, M.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67608
A;Accession: S67610
A;Molecule type: DNA
A;Residues: 1-700 <a href="https://documents.org/">https://documents.org/</a>
A;Residues: 1-700 <a href="https://documents.org/">https://documents.org/</a>
A;Residues: 1-700 <a href="https://documents.org/">https://documents.org/</a>
A;Cross-references: EMBL: Z74122; NID:g1431087; PID:e253213; PID:g1431088; GSPDB:GN00004;
A;Experies: 1-700 <a href="https://documents.org/">https://documents.org/</a>
A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Map position: L;
C;Keywords: transmembrane #status predicted <TWM>
F;69-85/Domain: transmembrane #status predicted <TWM>
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                                                                                                                                                                                                                                                                                                                                                               ----VSKKKDNPQVNHSQLNESHRK 115
                                                                                                                                                                                                                                                                                                                                                                                           | : ||| :| : || 30 NDTKSSST----QDALIKEIQ-DLEKGFR----BLSDLTHKKYSEIINHESVISKLTVEK 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   481 TKADQKYFAAMRSKDSILIEIKTLSKSLSKSNEL-----ILQLKDSDRLLQQKIGNLH 533
                                   A;Accession: E86549
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-508 <STO>
A;Cross-references: GB:BA000008; NID:g8978843; PIDN:BAA98679.1; GSPDB:GN00142
A;Cross-references: etrain J138
C;Genetics: A;Gene: CPj0473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ---DAGYVINL-SKDTF---IKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 NGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKK---------
                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                              21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41;
                                                                                                                                                                                                                                                                   Length 508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 700;
                                                                                                                                                                                                                                                                                                              33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ankyrin related protein C06C3.1 - Caenorhabditis elegans N;Contains: myosin-light-chain-phosphatase (EC 3.1.3.53) C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_C;Accession: T19006; T22086 R;Berks, M. R;Berks, M. R;Rercore number: Z19058 A;Reference number: Z19058 A;Accession: T19006
A;Reference number: A86491; MUID:20330349; PMID:10871362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 EDLQREEHSQKSDSTKDVTATVLDKNNISSKSTT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152 GDLDRVGHDSNEDSTEDSRS---EGGEPSSKSSS 182
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                                                                                                                                                                                                                                                                                                              17; Mismatches
                                                                                                                                                                                                                                                                                       21;
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                                                                                                                                                                                                                                                             Score 89.5;
Pred. No. 21
                                                                                                                                                                                                                                                                                                                                                               74 IKPVFKKIEEKKEEENKPTFD---
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11.2%;
1 Similarity 24.5%;
23; Conservative 1
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nes 36; Conservative
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 23; Conserv
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A;Map position: 2
A;Introns: 27/3; 94/3; 279/3; 352/2; 462/2; 523/3; 569/2; 657/2; 718/3; 766/3; 833/3; 89
C;Keywords: phosphoric monoester hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown protein F28016.8 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: E96795
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., ansen, N.F.; Hughes, B.; Hujzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A.; Liu, Y.; Liu, X.; Liu, Z.A.; Liu, Z.A.; Liu, Z.A.; Liu, Z.A.; Liu, Z.A.; Liu, Z.A.; Maiti, R.; Marziali, Rizzo, M.; Roomey, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: E96795
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 KKEEENKPIFDVSKKK--DNPQVNHSQLNESHRKEDLQREEH-----SQKSDSTKD- 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83
A;Molecule type: DNA
A;Residues: 1-1016 <WIL>
A;Cross-references: EMBL:Z36719; PIDN:CAA85318.1; GSPDB:GN00020; CESP:C06C3.1
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A;Experimental source: clone F42A8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: GB: AE005173; NID: g6143888; PIDN: AAF04434.1; GSPDB: GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 ELEKGYQFDGW------EISGFEGKKDAG----YVINLSKDTFIKPVFKKIEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 VTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule Type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          358 HSHPSTASVGSTTSSNTNTTTTTVIGENDISA 390
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                                                                                                                           R;Matthews, P. submitted to the EMBL Data Library, January 1995 A;Reference number: 219510 A;Accession: T22086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.2%; Score 89.5; DE 21.6%; Pred. No. 47; Live 33; Mismatches
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A;Accession: T39009
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1888 AGRN>
A;Residues: L-1888 AGRN>
A;Cross-references: EMBL:Z98531; PIDN:CABI1064.1; GSPDB:GN00066; SPDB:SPAC6B12.02c
A;Experimental source: strain 972h-; cosmid c6B12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       449 FLRVFARSSSHIP--KMIRRKRQMDSKKYFSFDKESDRQVIDQVLSDWYSGKHELVQQSH 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 YVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEH 123
257 RYSVDKIPVYDSAEDELTSEPSKNGESNTNEEKEKDISTENHLESTALNIQQQSDSTPTP 316
                                                                                                                                                                                                                   hypothetical protein SPAC6B12.02c - fission yeast (Schizosaccharomyces pombe); Species: Schizosaccharomyces pombe; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000; Accession: T39009 ...
; Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V. ubmitted to the EMBL Data Library, August 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C,Genetics:
A,Gene: SPDB:SPAC6B12.02c
A,Rap position: 1
C,Superfamily: Schizosaccharomyces hypothetical protein SPAC6B12.02c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 11.1%; Score 89; DB 2; Length 1888; Best Local Similarity 23.9%; Pred. No. 1e+02; Matches 37; Conservative 29; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 SQKSDS-TKDVTATVLDKN-----NISSKSTTNN 151
                                                                                             317 MEEDVVTETVKTETSEDMKLLSQN 340
                                                  133 ----VTATVLDKNNISSKSTTNN 151
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Search completed: February 10, 2004, 10:58:34 Job time : 12.1197 secs

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OM protein - protein search, using sw model

February 10, 2004, 10:48:44; Search time 7.15925 Seconds (without alignments) 1011:574 Million cell updates/sec Run on:

US-10-067-385-8_COPY_620_773
799
1 DIGEVSELKPHRVIVIIQNG......AIVLDKNNISSKSTINNPNK 154 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P38800 saccharomyc		P41001 plasmodium			. P22374 ascobolus i															P44969 haemophilus		Q15695 homo sapien					m	4		P37899 pyrenomonas	P15205 rattus norv	P49957 saccharomyc
SUMMARIES	. di	YHOO YEAST	CYL2 HUMAN	TOP2 PLAFK	MAPB HUMAN	SPT7_YEAST	DPOM_ASCIM	TIG STAAM	YDTZ SCHPO	DACA_BACSU		GYRA_STAEP	MAPB MOUSE	RAT1_YEAST	MLP1_YEAST	GLNA_PYRKO	MDN1_HUMAN	PBPA_BACSU	RGA1_YEAST	IF2 STAEP	UN89 CAEEL	IGAO_HAEIN	YFK8_YEAST	U2R1_HUMAN	ARS2_DROME	IF31 HUMAN	TONB_HAEIN	LIP STAEP	- 1			1		YMB4_YEAST
	Length DB			398			1202 1			443 1				1006 1	1875 1	443 1	5596 1	914 1			632	1694 1	Н		Н	-1			715 1		439 1	649 1	2459 1	279 1
d	Query Match 1	12.2		11.9	11.6	11.3	11.3	11.2	11.1	11.1	11.0	10.9	10.9	10.8	10.8	10.8	10.8	10.7	10.7	10.6	10.6	10.6	10.5	10.5	10.5	10.4	10.4	10.4	10.4	10.4	10.3	10.3	•	•
	Score	i	95	95	92.5	90.5	96	89.5	89	88.5	87.5	87	87	86.5	86.5	98	98	85.5	85.5	85	85	84.5	84	83.5	83.5	83	83	83	83	83	82.5	82.5	82.5	82
	Result No.	-	7	m	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	. 33

39 KGELEKGYQFDGWEISGFEGKK-DAGYVINLSKDTFIKPVFKKIEEKKEBENKPTFDVSK

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Query Match 12.2%; Score 97.5; DB 1; Length 1345; Best Local Similarity 27.0%; Pred. No. 7.9; Matches 33; Conservative 18; Mismatches 38; Indels 33;

98 KKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLD--KNNISSKSTTN---NP 152

9

Gaps

P36046 saccharomyc Q05907 pyrococcus P36687 pyrococcus Q03188 homo sapien Q9znef helicobacte Q00799 plasmodium Q04151 arabidopsis P2562 mycoplasma Q12224 saccharomyc P32892 saccharomyc Q9pqb5 ureaplasma			) intergenic region.	a; Saccharomycetes; romyces.		Dover J.	, Menezes S., Mouser L., evaskis E., Vaughan K., i R., Wilson R.,	Vaudin M.; "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome VIII."; Science 265:2077-2082(1994). -!- SIMILARITY: TO YEAST YFL042C.	duced through a collaboration is and the EMBL outstation :	use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	64C2 CRC64;
1 YKT5 YEAST 1 GLNA PYRFU 1 GLNA PYRFU 1 CENC_HUMAN 1 IPZ HELDJ 1 RBPZ PELDJ 1 LMDL HUMAN 1 LMDL HUMAN 1 YO40_MYCPN 1 RLMI YEAST 1 DRS1_YEAST 1 DRS1_YEAST	ALIGNMENTS	PRT; 1345 AA.	ed) sequence update) annotation update ein in IREI-KSP1	YHR080C. Saccharonyces cerevisiae (Baker's yeast). Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes Saccharomycetales; Saccharomycetaceae; Saccharomyces.	-8091929.	Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., I Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirste Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,	, Macri C., Mardis E. s L., St Peter H., Tr ohldman P., Waterston	uence of Saccharomyce 94). YFL042C.	copyright. It is pro tute of Bioinformatic	titutions as long as ent is not removed. nse agreement (See ht nse@isb-sib.ch).	5.1; C. GRAM_dom. 1. Transmembrane. 8 POTENTIAL. 149679 MW; 2FDAB94A686564C2
10.3 427 10.3 439 10.3 439 10.3 943 10.3 1251 10.2 675 10.2 675 10.2 676 10.2 676		STANDARD;	Rel. 3 Rel. 3 Rel. 3	s cerevisiae ungi; Ascomyo tales; Saccho 932;	M N.A. / AB972; 8003. PubMed	Andrews S., lo A., Fultor illier L., J.	, Louis E.J., kin L., Riles Wilcox L., Wo	<pre>lin M.; iplete nucleotide sequence of i; snce 265:2077-2082(1994). SIMILARITY: TO YEAST YFL042C.</pre>	ROT entry is Swiss Instit	-profit instruction this statement uires a licer mail to licer	EMBL; U10556; AAB68995.1; PIR; S46817; S46817. SGD; S0001122; YHR080C. InterPro; IPR004182; GRAM_dom. Pfam; PF02893; GRAM; 1. Hypothetical protein; Transmembrane TRANSMEM 1198 1218 POTENT: SEQUENCE 1345 AA; 149679 MW; 2F1
34 82 35 82 37 82 37 82 33 82 41 81.5 42 81.5 44 81.5 44 81.5	i 1	YEAST YHOO YEAST P38800;	995 995 995 ical	YHR080C. Saccharomyce Eukaryota; F Saccharomyce NCBI_TaxID=4	SEQUENCE FROM N.A STRAIN=S288c / AB	Johnston M., Du Z., Favel Kucaba T., H	Latreille P. Nhan M., Rif Vignati D.,	Vaudin M.; "Complete nu VIII."; Science 265: -!- SIMILARI	This SWISS-P between the	use by non modified and entities requested or send an e	EMBL; U10556 EMBL; U10555 SGD; S000112 InterPro; IP Pfam; Pf0289 SMART; SM005 Hypothetical TRANSMEM 1 SEQUENCE 1
ता ता ता ता ता ता <b>ता च च च च च च</b>	RESULT 1	8		88888	2 2 2 2 2 2 2 3 3	888	<b>888</b> 8	8 E E E E E	8888	88888	%1₹₽₽₽₽₽₽

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01-FEB-1995 (
01-FEB-1995 (
30-MAY-2000 (
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NP_BIND
ACT_SITE
                    PLAFK
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                                     P41001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lb-sib.ch)
SK--KKDNPQVNHSQLN-----ESHRKEDLQREEHSQKSDSTKD---VTATVLDKNNI 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTF---DV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hess H., Heid H., Zimbelmann R., Franke W.W.;
"The protein complexity of the cytoskeleton of bovine and human sperm heads: the identification and characterization of cylicin II.";
Exp. Cell Res. 218:174-182(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE INVOLVED IN SPERWATID DIFFERENTIATION.
-!- SUBCELLULAR LOCATION: CALYX; SPERM HEAD CYTOSKELETAL STRUCTURE.
-!- TISSUE SPECIFICITY: Testis.
                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Structural protein; Repeat; Sperm; Spermatogenesis.

347 31 X 3 AA REPEATS OF K-K-X.

240 3 X APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.9%; Score 95; DB 1; Length 348; llarity 30.9%; Pred. No. 2.8; Conservative 20; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D86766599C1809E7 CRC64;
                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEBS-2003 (Rel. 41, Last annotation update)
CYLC2 OR CYLZ.
                                                                                                                                                                                                        348 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95255491; PubMed=7737358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39079 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; 246788; CAA86752.1; -.
                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genew; HGNC:2583; CYLC2.
                  1150 SHDKHRPFHSKVE-
                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; 137271; 137271.
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348 AA;
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Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                      QK 1203
                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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                                                            153 NK 154
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                                                                                                                                                                                                        HUMAN
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REPEAT
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CYL2_HUMAN
                                                                                                                                                                                                                     Q140<u>9</u>3
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RESULT 3

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 NGKEMSSTIVSEEDFIL--PVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKP 76
                                                                                                                                                                                                                                                                                                                                                                                                                                               "The gene encoding topoisomerase II from Plasmodium falciparum.";
Nucleic Acids Res. 22:2547-2551(1994).
-!- FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY TRANSIENT
BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPOISOMERASE II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAKES DOUBLE-STRAND BREAKS.
CATALYTIC ACTIVITY: AFP-dependent breakage, passage and rejoining
of double-stranded DNA.
SUBUNIT: Homodimer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Topoisomerase; DNA-bInding; ATP-binding; Nuclear protein. 144 149 ATP (POTENTIAL). 830 DNA CLEAVAGE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- SUBUNIT: Homodimer (By similarity).
-:- SUBCELLULAR LOCATION: Nuclear.
-:- MISCELLANEOUS: EUKARYOTIC TOPOISOMERASE I AND II CAN RELAX BOY
NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS PROKARYOTIC ENZYMES
RELAX ONLY NEGATIVE SUPERCOILS.
-:- SIMILARITY: Belongs to the type II topoisomerase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26;
                                                                                                                                                                                                                                    Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5839;
                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94316496; PubMed=8041616;
Cheesman S., McAleese S., Goman M., Johnson D., Horrocks P.,
Ridley R.G., Kilbey B.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1398;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1227 1234 POLY-LYS.
1398 AA; 161029 MW; BAAD7BEE88FE5BE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                    01-FEB-1995 (Rel. 31, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) DNA topoisomerase II (EC 5.99.1.3).
                                                                                                                                                                                                           / Thailand)
PRT; 1398 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 95;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003594; ATPbind ATPase.
InterPro; IPR003595; CBFA NFYB topis.
InterPro; IPR001241; DNA_CopoisoII.
InterPro; IPR002205; DNA_topoisoIV.
Pfam; PF00204; DNA_topoisoIV; I.
Pfam; PF00521; DNA_topoisoIV; I.
Pfam; PF00521; HATPase c; I.
PRINTS; PR00615; CCAATSUBUNTA.
PRINTS; PR00418; TPI2FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-ASN.
POLY-LYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00177; TOPOISOMERASE_II; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-ASN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD000742; DNA topoisolV; 1.
SMART; SM00387; HATPase c; 1.
SMART; SM00433; TOP2c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X79345; -; NOT_ANNOTATED_CDS.
HSSP; P06786; 1BGW.
                                                                                                                                                                                                           (isolate K1
                                                           Created)
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STANDARD;
                                                                                                                                                                                                              Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                    FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 VFKKIEE--
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<u>:</u>:
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SEQUENCE
                                                Query Match
DOMAIN
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SPT7_YEAST
                                                                        Matches
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1190 DIEKVEEAIEFQRNVELSNREESNK--FKVARKQ-----GPSSMKKKKKKKKLSSDEESE 1242
                                                                                                                                                                                                                                                                                TISSUB-Fetal brain;

TISSUB-Fetal brain;

MEDLINE=9104815; PubMed=7806212;

MEDLINE=95104815; PubMed=7806212;

Lien L.L., Feener C., Fischbach N., Kunkel L.M.;

"Cloning of human microtubula-associated protein 1B and the identification of a related gene on chromosome 15.";

Genomics 22:173-280(1994).

-! FUNCTION: THE FUNCTION OF BRAIN MAPS IS ESSENTIALLY UNKNOWN.

PHOSPHORYLATED MAPIB MAY PLAY A ROLE IN THE CYTOSKELETAL CHANGES THAT ACCOMPANY MEDRIAE EXTENSION. POSSIBLY MAPIB BINDS TO AT LEAST TWO TUBULIN SUBDNITS IN THE POLYMER, AND THIS BRIDGING OF SUBUNITS MIGHT BE INVOLVED IN NUCLEATING MICROTUBULE POLYMERIZATION AND IN
                                                                                                                                                                                                                                                                                                                                                                                                                      STABLIZING MCKCYUBULES.
SUBUNIT: 3 DIFFERENT LIGHT CHAINS, LC1, LC2 AND LC3, CAN ASSOCIATE WITH MAPLA AND MAPLE PROTEINS.
WITH MAPLA AND MAPLE PROTEINS.
KKEE and KKEI/V, repeated but not at fixed intervals, which is responsible for the binding of MAPLE to microtubules.
FYM: LC1 is coexpressed with MAPLE. It is a polypeptide generated from MAPLE by proteolytic processing. It is free to associate with both MAPLE (By similarity).
SIMILARITY: TO MAPLE.
                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Microtubule-associated protein 1B (MAP 1B) (Contains: MAP1 light chain
                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 157129; -.
GO; GO:0005875; C:microtubule associated complex; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR00102; MAP1B neuraxin.
PRO0414; MAP1B neuraxin, 10.
PROSITE; PS00230; MAP1B NEURAXIN; 6.
Microtubules; Repeat; Phosphorylation.
CHAIN ? 2468 MAP1 LIGHT CHAIN LC1.
REPEAT 1878 1894 MAP1B 1.
REPEAT 1895 1911 MAP1B 2.
                                    126 ---KSDSTKDVTATVLDKNNISSKSTTNNPN 153
                                                                                                            PRT; 2468 AA
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                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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1997
2014
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ID MAPB_HU
AC P46821;
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REPEAT
REPEAT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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Gansheroff L.J., Dollard C., Tan P., Winston F.;
"The Saccharomyces cerevisiae SPT7 gene encodes a very acidic protein
important for transcription in vivo.";
Genetics 139:523-536(1995).
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                                                                                                                                                                                                                                                                                                                                                      Gaps
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-!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR OF TY ELEMENTS AND POSSIBLY
LYS-RICH (HIGHLY BASIC, CONTAINS MANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=S288c;
MEDLINE=S5076715; PubMed=7985423;
van der Aart Q.J.M., Barthe C., Doignon F., Aigle M., Crouzet M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sequence analysis of a 31 kb DNA fragment from the right arm of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Andre B., Cziepluch C., Hein C., Jauniaux J.C., Urrestarazu A.,
Visbers S.;
                                                                                                                                                                                                                                                                                                                                                Indels 13;
                                                                                                                                                                                                                              DB 1; Length 2468;
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MEDLINE=92285152; PubMed=1350857;
HATHES S.R., Dollard C., Winston F., Beck S., Trowsdale J.,
Dawid I.B.;
                                                                                                            2468 AA; 270618 MW; 540839CBDF09D461 CRC64;
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                                                            KKEE AND KKEI/V REPEATS)
                                                                                                                                                                                                                              11.6%; Score 92.5; DB 1; I
31.0%; Pred. No. 35;
ive 19; Mismatches 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1332 AA.
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Yeast 10:959-964(1994).
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-!- SIMILARITY: Contains 1 bromodomain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1994 (Rel. 28, Created)
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SPT7 OR YBR081C OR YBR0739.
                                                                                                                                                                                                                                                                                    Local Similarity 31.0%
nes 22; Conservative
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690 KEEKKEPKKEV 700
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Q99TIG;
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CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
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-!- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY. STRONG, TO
DNA POLYMERASE OF OTHER FUNGAL AND PLANTS MITOCHONDRIAL PLASMIDS.
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PROSITE; PS50014; BROMODOWAIN 2; 1.
Transcription regulation; Nuclear protein; Activator; Bromodomain.
DOMAIN 458 528 BROMODOWAIN.
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Pezizales, Ascobolaceae, Ascobolus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            458 528 BROMODOMAIN.
1332 AA; 152616 MW; 083B63624669244F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kempken F., Meinhardt F., Esser K.;
"In organello replication and viral affinity of linear,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 RKEDLQR-EEHSQKSDSTKDVTATVLD-KNNISSKSTTN 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      655 KNEEQDMVEESSKTEDSSKDADAAKKDTEDGLQDKTAEN 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1202 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.3%; Score 90.5; I 24.5%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probable DNA polymerase (EC 2.7.7.7)
                                                                                                                                                                                                                                                                           InterPro; IPR001487; Bromodomain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=2/1;
MEDLINE=90066356; PubMed=2573821;
                                                                                                                                                                                                                                                 C:SAGA complex;
                                                                                                                                                                                                                                                                                                           Pfam; PF00439; bromodomain; 1.
                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00503; BROMODOMAIN.
SMART; SM00297; BROMO; 1.
                                                                                                       EMBL; M87651; AAA35087.1;
PIR; S41552; S41552.
HSSP; Q92831; 1B91.
                         EMBL; L22537; AAC37424.1;
EMBL; X76294; CAA53940.1;
                                                                                   Z35950; CAA85026.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 39; Conservat
                                                                                                                                                                                             TRANSFAC; T04835; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ascobolus immersus.
Mitochondrion.
                                                                                                                                                                                                                    SGD; S0000285; SPT7
GO; GO:0000124; C:S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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DPOM_ASCIM
                                                                                   EMBL;
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CCC DDR DDR DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR KW DDR 
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                           380 KPLKTIEGTKYANYTFPIKKDIVVKDINKKINFNGLDLPKTMDLSKWPNLKLNKDKTSGE 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              440 IRMTIKNKNNQSYDI--IGHMINDGENVITFNRAVDNSIIKIFTVTDSMGNTNDPN 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (By similarity).
-!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. TIG SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 VNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNI-----SSKSTTNNPN 153
                                                                                                                                                                                                                                                                                                                              2 TGEVSELKPHRVTVTIQNGKEMSSTI---VSEEDF--ILPVYKGELEK-----GYQFDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        !- FUNCTION: Involved in protein export. Acts as a chaperone by maintaining the newly synthesized protein in an open conformation
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=MISO / ATCC 700699, and N315;
MEDLINE=21311952; PubMed=11418146;
MEDLINE=21311952; PubMed=11418146;
MINTAIN=MISO / ATCC 700699, and NIS;
MINTAIN=MISO / ANGIN F. T. Uchiqama I., Baba T., Yuzawa H., Kobayashi I.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N. K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oguchi A.,
                                                                                                                                                                                                                                                                                     28;
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Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi J.
Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
Yamamoto K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                           Length 1202;
                                        InterPro; IPR006172; DNA_pol_B.
InterPro; IPR004868; DNA_pol_B_2.
InterPro; IPR004868; DNA_pol_B_2.
SWART; SMO0486; POLBC; T.
PROSITE; PS00116; DNA_POLYMERASE B; 1.
Transferase; DNA-directed DNA_polymerase; DNA_replication;
                                                                                                                                                                                                                                                                                   74; Indels
                                                                                                                                                                          DNA-binding; Plasmid; Mitochondrion.
SEQUENCE 1202 AA; 138279 MW; 51D41FCEBDBF2CDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trigger factor (TF).
TIG OR SAV1675 OR SA1499 OR MW1619.
Staphylococcus aureus (strain Mu50 / ATCC 700699),
Staphylococcus aureus (strain N315), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus (strain MW2).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=158878, 158879, 196620;
                                                                                                                                                                                                                                        DB 1;
25;
                                                                                                                                                                                                                           11.3%; Scc. 22.6%; Pred. No. 22.4%; Pred. No. 429, 11.4% 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       433 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
EMBL; X15982; CAA34106.1; -. PIR; S05362; S05362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lancet 357:1225-1240(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acquired MRSA.";
Lancet 359:1819-1827(2002)
                                                                                                                                                                                                                                                             Local Similarity 22.6 tes 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 AIDHSLGHLAEMVVKEDGVVENGDTVNIDFSG-SVDGEEFEGGQAEGYDLEIGSGSFI-P 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 VFK-----KIEEKKE-----EE---NKPTFDVS----KKKDNPQVNHSQLNE- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GYQFDGWEISG--FEGKKDAGYVINLSKDTFIKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21848401; PubMed=11859360; Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Squolos J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Genles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., Stutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
                                                                                                                                                                 1 DIGEVSELKPHRVTVT-IQNGKE--MSSTIVSEEDFILPVYKG-ELEK-----
                                                                                                                                                                                                                                                                                                                                                                             11.2%; Score 89.5; DB 1; Length 433; 22.1%; Pred. No. 9.1; tive 33; Mismatches 60; Indels 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----SHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTN 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
SPACGB12.02C in chromosome SPACGB12.02C.
                                                                                                                EMBL; AP003363; BAB57837.1; -. EMBL; AP003134; BAB42766.1; -. EMBL; AP004827; BAB95484.1; -.
                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 22.1
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014207;
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Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Wodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vangreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Berzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Berz P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Dominquez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P., The genome sequence of Schizosaccharomyces pombe.";

"The genome sequence of Schizosaccharomyces pombe.";

"The Genome sequence of Schizosaccharomyces pombe.";

"I subure 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      390 SSSLTSENPFQLNVAANAVSTIPVYRTTKTKMKKN-RFKYVEVEKLPDLILESYGKKAPK 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 YVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEH 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : :: : : | | | | :: :: | | | :: :: | 449 FLRVPARSSSHIP--KMIRRKRQMDSKKYFSFDKESDRQVIDQVLSDWYSGKHELVQQSH 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW; 8AD3BBCE32397C29 CRC64;
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29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; Transmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPombe; SPAC6B12.02c;
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1336
1645
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Hypothetical
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(EC 3.4.16.4) (DD-

01-OCT-1994 (Rel. 30, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
D-alanyl-D-alanine carboxypeptidase precursor (i peptidase) (DD-carboxypeptidase) (CPase)

01-AUG-1988 (Rel. 08, Created)

STANDARD;

DACA BACSU P08750;

RESULT 9

443 AA

Firmicutes; Bacillales; Bacillaceae; Bacillus

Bacillus subtilis NCBI_TaxID=1423;

DACA_BACSU 1D DACA_B AC POSTO DT 01-AUG DT 28-FEB DE PEPT 28-FEB DE PEPT 28-FEB OC BACTO OC BACTO OC NCBI T RN [1] RN [1] RN [2]

Bacteria;

SEQUENCE FROM N.A. STRAIN=168;

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RA Azevedo V., Berrero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Azevedo V., Berrero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Bortiss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

RA Brouilser S., Pruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

RA Fritz C., Fujita M., Pabret C., Ferrari E., Foulger D.,

RA Guiseppi G., Guy B.J., Hage K., Haiech J., Grandi G.,

RA Guiseppi G., Guy B.J., Hage K., Haiech J., Harwood C.R., Henaut A.,

RA Hilbert H., Holaappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

RA Hilbert H., Holaappel S., Lauber J., Lazarevic V.,

RA Median N., Mellado R.P., Liu H., Masuda S., Mauel C., Medigue C.,

RA Median N., Mellado R.P., Liu H., Mosell D., Nakai S., Noback M.,

RA Prescan E., Pujic P., Purnalle B., Rapoport G., Rey M., Reynolds S.,

RA Prescan E., Pujic P., Purnalle B., Rapoport G., Rey M., Reynolds S.,

RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

RA Scrokin A., Tacconi E., Takahashi H., Takemaru K.,

RA Scrokin A., Tacconi E., Takahashi H., Takemaru K.,

RA Tosato V., Uchiyama S., Vandenbol M., Vannier P., Vassumoto K., Yata K.,

Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,

RA Tosato V., Wiphikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,

RA Haken Complete genome sequence of the Gram-positive bacterium Bacillus
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"Primary structure of the COOH-terminal membranous segment of a penicillin-sensitive enzyme purified from two Bacilli.";
J. Biol. Chem. 256:2067-2077(1981).
-!- FUNCTION: REMOYES C-TERMINAL D-ALANYL RESIDUES FROM SUGAR-PEPTIDE CELL WALL PRECURSORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Reduced heat resistance of mutant spores after cloning and mutagenesis of the Bacillus subtilis gene encoding penicillin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- CATALYTIC ACTIVITY: D-alanyl-D-alanine + H(2)O = 2 D-alanine.
-!- PATHWAY: Peptidoglycan synthesis; final stages.
-!- SUBCELLUIAR LOCATION: Membrane-associated.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SII; ALSO KNOWN AS THE D-ALANYL-D-ALANINE CARBOXYPEPTIDASE I FAMILY.
MEDLINE=96051385; PubMed=7584024; Qogasawara N., MAKai S., Yoshikawa H.; Sogasawara N., Makai S., Yoshikawa H.; Soystematic sequencing of the 180 kilobase region of the Bacillus subtilis chromosome containing the replication origin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waxman D.J., Strominger J.L.; "Sequence of active site peptides from the penicillin-sensitive alanine carboxypeptidase of Bacillus subtilis. Mechanism of penicillin action and sequence homology to beta-lactamases."; J. Biol. Chem. 255:3964-3976(1980).
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MEDLINE-86250602; PubMed=3087956;
Todd J.A., Roberts A.N., Johnstone K., Piggot P.J., Winter G.
                                                                                                                                                                                                                                                            MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=80182289; PubMed=6768745;
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MEDLINE=81117303; Pubmed=6780559;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 390:249-256(1997).
                                                                                                                                   DNA Res. 1:1-14(1994).
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SEQUENCE FROM N.A.
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SUBCELLULAR LOCATION: Secreted.

DOMAIN: THE SIGNAL PEPTIDE GUIDES THE PRECURSOR TO THE PERIPLASMIC SPACE, AND THE CARBOXY-TERMINAL HELPER DOMAIN ASSOCIATES WITH THE OUTER MEMBRANE TO FORM A PORE FOR EXCRETION OF THE PROTEASE DOMAIN. THE HELPER DOMAIN IS THEN RELEASED BY AUTOPROTEOLYSIS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Immunoglobulin Al protease precursor (EC 3.4.21.72) (IGA1 protease).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Poulsen K., Reinholdt J., Kilian M.;
Poulsen K., Reinholdt J., Kilian M.;
"A comparative genetic study of scrologically distinct Haemophilus
"Influenzae type I immunoglobulin Al proteases.";
J. Bacteriol. 174:2913-2921(1992).
-!- FUNCTION: VIRULENCE FACTOR; CLEAVES HOST IMMUNOGLOBULIN A
PRODUCING INTACT FC AND FAB FRAGMENTS.
-!- CATALYTIC ACTIVITY: Cleavage of immunoglobulin A molecules at
certain Pro-|-Xaa bonds in the hinge region. No small molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D-ALANYL-D-ALANINE CARBOXYPEPTIDASE. ACYLATED BY PENICILLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase; Carboxypeptidase; Peptidoglycan synthesis; Cell wall;
Membrane; Signal; Complete proteome.
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Pasteurellaceae, Haemophilus.
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E -> Q (IN REF. 4).
DAGCSB0307D7C117 CRC64;
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EMBL; Z99104; CAB11786.1; -.
EMBL, M13766; AAA22375.1; -.
PIR; S66040; S66040.
MEROPS; S11.001; -.
Subtilist; BG10074; dacA.
InterPro; IPR001967; Ala/AlaCBptase1.
Pfan; PP00768; Peptidase S11; 1.
PRINTS; PR00725; DADACEPTASE1.
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MEDLINE=92234949; PubMed=1373717;
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443 AA; 48636 MW;
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100
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01-NOV-1995 (
28-FEB-2003 (
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P45384;
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MAPB MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 INLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHS- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X 8 AA TANDEM REPEATS OF A-K-V-E-K-E-E-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase; Serine protease; Transmembrane; Zymogen; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92102204; PubMed=1662027; Sreedharan S., Peterson L.R., Fisher L.M.; Erecharan S., Peterson L.R., Fisher L.M.; Erecharan S., Peterson D.R., Fisher L.M.; Erecharan S., Peterson E.R., Fisher L.M.; Erecharan resistance in coagulase-positive and -negative staphylococci: role of mutations at serine 84 in the DNA gyrase A protein of Staphylococcus aureus and Staphylococcus epidermidis."; Antimicrob. Agents Chemother. 35:2151-2154(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=ATCC 12228;
Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin
Chen Z., Wen Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.0%; Score 87.5; DB 1; Length 1702; 27.2%; Pred. No. 55; Live 14; Mismatches 50; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1117 1124 2.
1702 AA; 186539 MW; 860F70D2667807A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMUNOGLOBULIN AL PROTEASE HELPER PEPTIDE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-94 FROM N.A., AND MUTAGENESIS OF SER-84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GYRA_GYAEP STANDARD; PRT; 893 AA.
P54112;
01-0CT-1996 (Rel. 34, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA gyrase subunit A (EC 5.99.1.3).
GYRA_GYRA OSE0005.
Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
                        SIMILARITY: BELONGS TO PEPTIDASE FAMILY S6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1356 SQPQETSAEETTAASTDETTIADNŠKRSKPNR 1387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 -- OKSDSTKDVTATVLDKNNISSKSTTNNPNK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FIGREAMS; TIGR01414; autotrans_barl; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROBABLE
                                                                                                                                                                                                                                                                                                                      InterPro; IPR006315; Autotransport.
InterPro; IPR00546; Autotransporter.
InterPro; IPR00710; ISA_86.
InterPro; IPR004899; Pertactin.
Pfam; PP03797; Autotransporter; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02395; IGA1; 1.
Pfam; PF03212; Pertactin; 1.
PRINTS; PR00921; IGASERPTASE.
                                                                                                                                                                                                                                                       EMBL; M87489; AAA24966.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 2/...
Loca 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1702
288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1116
                                                                                                                                                                                                                                                                               PIR; A41859; A41859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1015
                                                                                                                                                                                                                                                                                                   MEROPS; S06.001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROPEP
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
GYRA_STAEP
  셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            746 TITERNGNIVCITTVTGEEDLMVVTNAGVI---IRLDVHDISQ-NGRAAQGVRLMKLGDG 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 TFIKPVFKKIEEKKEEEN-----KPTFDVSKKKDNPQVNHSQLNESHRKEDLQREE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      802 OFVSTVAKVNEEDDNEENADEAQOSTTTETADVEEVVD----DQTPGNAIHTEGDAEMES 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 TVTIQNGKEMS-STIVSBEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGY-VINLSKD 71
                                                                                                                                              -!- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.
-!- SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS RESPONSIBLE FOR DNA BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HYDROLYSIS. THE ENZYME FORMS AN A2B2 TETRAMER.
FUNCTION: DNA GYRASE NEGATIVELY SUPERCOILS CLOSED CIRCULAR DOUBLE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                  STRANDED DNA IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES THE INTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED DNA RINGS, INCLUDING CATENANES AND KNOTTED RINGS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Swiss Webster; TISSUE=Brain; MEDLINE=90094539; PubMed=2480963; MODLE M., Lewis S.A., Cowan N.J.; Moble M., Lewis S.A., Cowan N.J.; MThe microtubule binding domain of microtubule-associated protein MAP1B contains a repeated sequence motif unrelated to that of MAP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65; Indels 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 84 S->F: RESISTANT TO CIPROFLOXACIN.
893 AA; 100113 MW; 2A6A7CD3,45A526CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1990 (Rel. 14, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Microtubule-associated protein 1B (MAP 1B) (MAP1.2) (MAP1(X))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGRFAMB; TIGR01063; gyrA; 1.
Topoisomerase; Isomerase; DNA-binding; Antibiotic resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA CLEAVAGE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.3%; Pred. No. 30; tive 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 -HSQKSDSTKDVTATVLDKNNISSKSTTNN 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        858 VESPENDDRIDIRODFMDRVNEDIESASDN 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 2464 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.9%; Score 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE016744; AA003602.1; -.
EMBL; S72603; AAB20672.1; -.
PIR; A49832; A49832.1; -.
HSSP; P09097; 1AB4.
InterPro; IPR002205; DNA_topoisoIV.
Pfan; PF03999; DNA_gyraseA_C; 6.
ProDom; P0000742; DNA_topoisoIV.
SMART; SM00434; TOP4C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and tau.";
J. Cell Biol. 109:3367-3376(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [Contains: MAP1 light chain LC1]. MAP1B OR MTAP5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1990 (Rel. 14, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 25.3$
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome.
ACT SITE 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 LSKOTFIKPVFK-KIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQRE---- 121
                                                                                          WITH MAPIA AND MAPIB PROTEINS.

BURNIT: 3 DIFFERENT LIGHT CHAINS, LC1, LC2 AND LC3, CAN ASSOCIATE MITH MAPIA AND MAPIB PROTEINS.

DOMAIN: Has a highly basic region with many copies of the sequence KKEE and KKEI/V, repeated but not at fixed intervals, which is responsible for the binding of MAPIB to microtubules.

PTM: LC1 IS COEXPRESED WITH MAPIB: IT IS A POLYPEPTIDE GENERATED FROM MAPIB BY PROTECLYIC PROCESSING: IT IS PREE TO ASSOCIATE WITH MAPIA AND MAPIB. IT INTERACTS WITH THE AMINO-TERMINAL REGION
FUNCTION: THE FUNCTION OF BRAIN MAPS IS ESSENTIALLY UNKNOWN. PHOSPHORYLATED MAPIB MAY PLAY A ROLE IN THE CYTOSKELETAL CHANGES THAT ACCOMPANY NEURITE EXTENSION. POSSIBLY MAPIB BINDS TO AT LEAST TWO TUBULIN SUBUNITS IN THE POLYMER, AND THIS BRIDGING OF SUBUNITS MIGHT BE INVOLVED IN NUCLEATING MICROTUBULE POLYMERIZATION AND IN STABILLIZING MICROTUBULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           632 VIXDKVVKKEIKTKLEEKKEE--KPKKEVVKKEDKTPL---KXDEKPRKEEVKKEIKKEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LYS-RICH (HIGHLY BASIC, CONTAINS MANY KKEE AND KKEI/V REPEATS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exoribonuclease)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 2464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FBD3DD99CFDBDA87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 -----EHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      687 KKEERKELKKEVKKETPLKDAKKEVKKEEKKEVKKEEKEPKK 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Microtubules, Repeat, Phosphorylation.
CHAIN? 2464 MAP1 LIGHT CHAIN LC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ribonucleic acid trafficking protein 1 (5'-3'
EC 3.1.11.-) (P116).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0016358; P:dendrite morphogenesis; IMP. GO; GO:0001578; P:microtubule bundling; IMP. InterPro; IPR000102; MAPIB_neuraxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1006 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Pred. No. 89;
16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAPIB 1.
MAPIB 2.
MAPIB 3.
MAPIB 4.
MAPIB 5.
MAPIB 6.
MAPIB 6.
MAPIB 7.
MAPIB 9.
MAPIB 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00230; MAPIB_NEURAXIN; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00414; MAPIB_neuraxin; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MW.
                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X51396; CAA35761.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.9%;
28.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270408
                                                                                                                                                                                                                                                                                                                                                                                                                              S07549; QRMSP1.
MGI:1306778; Mtaplb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 28.4 tes 29, Conservative
                                                                                                                                                                                                                                                SIMILARITY: TO MAPIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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1907
1924
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1958
1975
2009
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                                                                                                                                                                                                                                OF MAP1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAT1 YEAST
Q02792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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REPEAT
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REPEAT
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RAT1_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                PIR;
     SGERFINGS
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Saccharomyces cerevisiae (Baker's yeast)

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                                                                                                                                                          MEDIANE=92331925; PubMed=1628825; Amberg D.C., Goldstein A.L., Cole C.N.; "Isolation and characterization of RAT1: an essential gene of Saccharomyces cerevisiae required for the efficient nucleocytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y->H: IN ALLELE TAP1-1; ACTIVATES
TRANSCRIPTION OF THE PROMOTER-DEFECTIVE
YEAST SUP4 TRNA(TYR) ALLELE SUP4A53T61.
                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93109318; PubMed=8417335;
Kenna M., Stevens A., McCammon M., Douglas M.G.;
"An essential yeast gene with homology to the exonuclease-encoding
XRNI/KEMI. gene also encodes a protein with exoribonuclease
activity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- FUNCTION: May function in the processing and/or trafficking of nuclear mRNA. May be involved in general transcription as well. Possesses 5'->3' exoribonuclease activity degrading poly(A) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONTAINS 2 X SRYD, 2 X NNNY, AND 2 X YSGN REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [3]
MEDLINE=93268292; PubMed=8497260;
MEDLINE=93268292; PubMed=8497260;
Aldrich T.L., di Segni G., McConaughy B.L., Keen N.J., Whelen S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Structure of the yeast TAP1 protein: dependence of transcription activation on the DNA context of the target gene."; Mol. Cell. Biol. 13:3434-3444(1993).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBL_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [5]
SEQUENCE FROM N.A.
Bobnn C., Bolotin-Fukuhara M., Daignan-Fornier B., Dang D.V.,
Valens M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005634; C:nucleus; IDA.
GO; GO:0004534; F:5'-3' exoribonuclease activity; IDA.
GO; GO:0006365; P:35S primary transcript processing; IMP.
GO; GO:0006396; P:RNA processing; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; Hydrolase; Nuclease; Exonuclease; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- COFACTOR: Requires magnesium.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: Belongs to the 5'-3' exonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unseld M.; to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND EXORIBONUCLEASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
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POLY-ASN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M95626; AAA34960.1; -.
EMBL; L06011; AAA16950.1; -.
EMBL; Z11746; -; NOT ANNOTATED_CDS.
EMBL; Z74956; CAA99240.1; -.
PIR; S20126; S20126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mol. Cell. Biol. 13:341-350(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR004859; Put_53exo. Pfam; PF03159; XRN_N; 1.
                                                                                                                                                                                                                                                                                                                    Genes Dev. 6:1173-1189(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; S61567; AAB26818.1; -.
                                                                                                                                                                                                                                                                                       trafficking of mRNA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Landt O., Hiesel R.,
Submitted (JUL-1996)
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                                                                                                                                   SEQUENCE FROM N.A.
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301 301 R -> A (IN REF. 1).
1875 AA; 218455 MW; 683A0D34C9066867 CRC64;
                                                                                                                                                                                                                                  149 TNNPN 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=69014;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Phermococcus
                                                                                                                                                                                                                                                                                                                     GINA PYRKO
008467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=KOD1
   SEQUENCE
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BINDING
                                       Query Match
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                                                  8
                                                                                        ----KPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQ------LNESHRK 115
                                                                                                                                       17 IQNGKEMSSTIVSEEDFILPVY--KGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFI 74
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94205265; PubMed=8154186;
Bou G., Esteban P.F., Baladron V., Gonzalez G.A., Cantalejo J.G.,
Remacha M., Jimenez A., del Rey F., Ballesta J.P.G., Revuelta J.L.;
"The complete sequence of a 15,820 bp segment of Saccharomyces
cerevisiae chromosome XI contains the UBI2 and MPL1 genes and three
new open reading frames.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reast 9:1349-1354(1993).
-!- FUNCTION: MYOSIN-LIKE PROTEIN THAT IS PROBABLY INVOLVED IN DNA
                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Pungi, Ascomycota, Saccharomycotina, Saccharomycetes, Saccharomycetales, Saccharomycetaceae, Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Koelling R., Nguyen T., Chen E.Y., Botstein D.; "A new yeast gene with a myosin-like heptad repeat structure."; Mol. Gen. Genet. 237;359-369(1993).
                                                  49;
                          DB 1; Length 1006;
                                                                                                                                                                                      EDLQREEH-----SQKSDSTKDVTATVLDK-----NNISSKSTT 149
                                                 47; Indels
   1006 AA; 115933 MW; SDDD5B0245F3E12A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- SIMILARITY: SOME, TO THE TPR ONCOGENE.
-i- CAUTION: REF.2 MISQUOTES THE GENE NAME AS "MPL1".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COIL (POTENTIAL)
COIL (POTENTIAL)
COIL (POTENTIAL)
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EMBL; X73541; CAA51948.1; -.
EMBL; Z28320; CAA62174.1; -.
PIR; S38173; S38173.
SGD; S0001803; MLP1.
GO; GO:0005635; C:nucleor membrane; IDA.
GO; GO:0006606; P:protein-nucleus import; IDA.
Coiled coil; DNA repair.
                                                                                                                                                                                                                                                                                01-OCT-1993 (Rel. 27, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
MLP1 OR YKR095W OR YKR415.
                                                                                                                                                                                                                                                          PRT; 1875 AA
                         10.8%; Score 86.5; Di
19.0%; Pred. No. 37;
ive 40; Mismatches
                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
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COILED
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MEDLINE=93247549; PubMed=8483450;
                                                  32; Conservative
                                                                                                                                                                                                                                                            STANDARD;
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                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                          MLP1_YEAST
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                                                                                                                                                                        116
   SEQUENCE
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                                                                                                                                                                 98 KKDNPQVNHSQLNESHR-KEDL---QREEHSQKSDSTKDVTA----TVLDKNNISSKST 148
                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                 56 FEGKKDA-----GYVINLSKDTFIKPVFKKIEEK------KEEENKPTFDVSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDILINE=97316461; PubMed=9172372;
Adul Rahman R.N.Z., Jongsareejit B., Fujiwara S., Imanaka T.;
Adul Rahman R.N.Z., Jongsareejit B., Fujiwara S., Imanaka T.;
"Characterization of recombinant glutamine synthetase from the
hyperthermophilic archaeon Pyrococcus sp. strain KOD1.";
Appl. Environ. Microbiol. 63:2472-2476(1997).
-!- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate +
                                                                                                                              4 EVSELKPHRVTVTIQNGKEMSSTIVSEEDF----ILPVYKGE---LEKGYQFDGWEISG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pyrococcus kodakaraensis.
Archaea; Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase) (GS)
                                                             62; Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMP (UNDER CONDITIONS OF ABUNDANT
DB 1; Length 1875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L-glutamine.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLUTAMINE) (BY SIMILARITY 9426DCCFEEF18168 CRC64;
Query Match 10.8%; Score 86.5; DE
Best Local Similarity 24.3%; Pred. No. 72;
Matches 45; Conservative 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001637; GlnA_adenyl:
Pfam; PF00120; gln-synt; 1.
Pfam; PP03951; gln-synt.N; 1.
ProDom; PD001057; Gln synt C; 1.
TIGRFAMS; TIGR00653; GlnA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00180; GLNA_1; 1.
PROSITE; PS00181; GLNA_ATP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       443 AA; 50259 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D86222; BAA20530.1; -. HSSP; P06201; 1LGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             362
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                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          involved in in the
                                                                                                                                                                                                                                                                                                                                                                                                                          -----STKDVTATVLD 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Midasin (MIDAS-containing protein).

MDN1 OR KIAA0301.

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Garbarino J.E., Gibbons I.R.;
"Expression and genomic analysis of midasin, a novel and highly conserved AAA protein distantly related to dynein.";
BMC Genomics 3:18-18(2002).
                                                                                                    72;
                    10.8%; Score 86; DB 1; Length 443; 17.8%; Pred. No. 17; 17.8%; Pred. S5; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTION: May function as a nuclear chaperone and be assembly/disassembly of macromolecular complexes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                        75 --KPVFKKIEEKKEEEN-----KPTFDVSKKKD----
                                                                                                                                                                38 YKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9NUZ2; 015019;
28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1255-2356 AND 3550-5596 FROM N.A. TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 3550-5596 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AF503925; AAM77722.1; -. EMBL, AL096678; CAB8666.1; -. EMBL, AL096678; BAA20761.1; -. EMBL, AB002299; BAA20761.1; -.
Query Match
Best Local Similarity 17.00
Thes 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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PubMed=12102729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tracey A.;
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Genew; HGNC:18302; MDN1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 AGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQRE 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annoctation update)
Penicillin-binding protein 1A/1B (PBP1) [Includes: Penicillin-insensitive transglycosylase (EC 2.4.2.-) (Peptidoglycan TGase);
Penicillin-sensitive transpeptidase (EC 3.4.2.-) (DD-transpeptidase)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 LKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKG-----YQFDGWEISGFEGKKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Popham D.L., Setlow P.; "Cloning, uncleotide sequence, and mutagenesis of the Bacillus subtilis pond operon, which codes for penicillin-binding protein (PBP) 1 and a PBP-related factor."; J. Bacteriol. 177:326-335 (1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5596 AA; 632802 MW; 586C62616A1F96D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus. NCBI_TaxID=1423;
                  GO; GO:0016887; F:ATPase activity; NAS.
GO; GO:0003754; F:Chaperone activity; NAS.
GO; GO:0006461; P:protein complex assembly; NAS.
InterPro; IPR002593; AAA ATPase.
InterPro; IPR002035; VWFA.
Pfam; PF00004; AAA; 1.
SWART; SM00382; AAA; 7.
FROSITE; PS50234; VWA; 1.
Chaperone; ATP-binding; Repeat; Nuclear protein.
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23.4%; Pred. No. 2.5e+02;
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ATP (POTENTIAL).
ATP (POTENTIAL).
ATP (POTENTIAL).
ATP (POTENTIAL).
ATP (POTENTIAL).
POLY-GLU.
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POLY-GLU.
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MEDLINE=96349105; PubMed=8760912;
C:nucleus; NAS.
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1397
1760
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5187
5583
2312
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The serk and kdg loci cloned in a yeast artificial chromosome.";

M. Miccobiology 112.2005-2016[1956].

M. Richarles 164.

M. SERRANA-165.

M. SERRANA-165.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 VSKKKDNPQVNHSQLN------ESHRKEDLQREEHSQKSDSTKDVTATVLDKNNI 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94
SUGGESTING IT IS INVOLVED IN SEPTUM SYNTHESIS; INCREASED LEVELS OF MG(2+) OR CA(2+) ONLY PARTIALLY ELIMINATE THE SEPTATION DEFECTS.
SIMILARITY: Contains 1 fibronectin type III domain.
SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE TRANSCHYCOSTARE FAMILY.
TRANSCHYCOSTARE FAMILY.
TRANSPEPTIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DTGEVSELKPHRVTVTIQNGKEMSSTIVSBEDFILPVYKGELEKGYQFDGWEISGFEGKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptidoglycan synthesis, Cell wall; Transferase, Glycosyltransferase, Hydrolase, Multifunctional enzyme; Transmembrane; Signal-anchor; Antibictic resistance; Complete proteome.

1 CYTOPLASMIC (POTENTIAL).

TRANSMEM 38 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSPEPTIDASE.
FIBRONECTIN TYPE-III.
ACYLATED BY PENICILLIN (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL)
TRANSGLYCOSYLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6978E33DFE2423E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RGAI_YEAST STANDARD; PRT; 1007 AA. P390318; P39334; Created) 101-FEB-1995 (Rel. 31, Created) 101-FEB-1995 (Rel. 31, Last sequence update) 115-SEP-2003 (Rel. 42, Last annotation update) Rho-type GTPase-activating protein 1. Rho-type GTPase-activating protein 1. RKGAI OR DBM1 OR THEI OR YOR127W OR 03290 OR YOR3290W. Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DA--GYVINLSKDTFIKPVFKKIEEKKEEENK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.7%; Score 85.5;
                                                                                                                                                                                                                                                                                    EMBL; U11883; AAA64947.1; -...
EMBL; 147838; AAB38459.1; -...
EMBL; 299115; CAB14148.1; -...
FIR; 140529; 140529.
SubtiList; BG10954; ponA.
InterPro; IPR001964; FN III.
InterPro; IPR001264; Glyco_trans_51.
InterPro; IPR001466; Transpeptdse.
PEam; PF00041; fn3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00912; Transglycosyl; 1.
Pfam; PF00905; Transpeptidase; 1.
ProDom; PD001895; Glyco_trans_51; 1.
SWART; SM00060; FN3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            914 AA; 99562 MW;
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Matches 43; Conserv
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SEQUENCE FROM N.A.
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Ramer S.W., Elledge S.J., Davis R.W.;
Romer S.W., Elledge S.J., Davis R.W.;
Romer S.W., Elledge S.J., Davis R.W.;
Romer S.W., Elledge S.J., Davis R.W.;
Romer S.W., Elledge S.J., Davis R.W.;

a strong inducible promoter.",
Proc. Natl. Acad. Sci. U.S.A. 89:11589-11593 (1992).
-!- FUNCTION: GTPASE-ACTIVATING PROFIEIN (GAP) FOR CDC42 AND/OR RHO1.
-!- FUNCTION: GTPASE-ACTIVATING PROFIEIN (GAP) FOR CDC42 AND/OR PROFIEIN STEED PROTEIN KINASE, ACTS AT A STEP BETWEEN THE G-PROTEIN AND THE STE20 PROTEIN KINASE, OMINANT SUPPRESSOR OF BUD EMERGENCE DEFECT CAUSED BY DELETION OF IPL2/RBM2: INVOLVED IN THE CONTROL OF POLARIZED CELL GROWTH AND FROPER BUD SITE SELECTION.
-!- SIMILARITY: Contains 1 Rho-GAP domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIINE=97344368; PubMed=9200815; Voss H., Benes V., Andrade M.A., Valencia A., Rechmann S., Teodoru C., Schwager C., Paces V., Sander C., Ansorge W.; DNA sequencing and analysis of 130 kb from yeast chromosome XV."; Yeast 13:655-672(1997).
                                                                                                                                                                             Chen G.-C., Zheng L., Chan C.S.M., "The LIM domain-containing Dbmd GPPase-activating protein is required "The LIM domain-containing Dbmd GPPase-activating protein is required for normal cellular morphogenesis in Saccharomyces cerevisiae."; Mol. Cell. Biol. 16:1376-1390(1996).
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Stevenson B.J., Ferguson B., de Virgilio C., Bi E., Pringle J.R.,
Ammerer G., Sprague G.F. Jr.,
"Mutation of RGA1, which encodes a putative GTPase-activating protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for the polarity-establishment protein Cd642p, activates the pheromone-response pathway in the yeast Saccharomyces cerevisiae."; Genes Dev. 9:2949-2963(1995).
                                                                                                                                                                                                                                                                                                                                                                               Wiemann S., Rechmann S., Benes V., Voss H., Schwager C., Vlcek C., Stegemann J., Zimmermann J., Erfle H., Paces V., Ansorge W.; Stegemenn J., analysis of 51 kb on the right arm of chromosome XV from Saccharomyces cerevisiae reveals 30 open reading frames.";
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO:0005100; F:Rho GTPase activator activity; IPI. GO:0004871; F:signal transducer activity; IPI. GO:0007015; P:actin filament organization; IMP.
                                                                                                        SEQUENCE FROM N.A., AND MUTAGENESIS.
                                                                                                                                                                                                                                                                                                                                STRAIN=S288c / FY1679;
MEDLINE=97060020; PubMed=8904341;
                                                                                                                                STRAIN=S288c;
MEDLINE=96239492; PubMed=8657111;
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SGD; S0005653; RGA1.
GO; GO:0005100; F:Rh
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                                                       WCBI_TaxID=4932;
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                                                                                                               .; IGI.
GO; GO:0007118; P:apical bud growth; IPI.
GO; GO:000283; P:eetablishment of cell polarity (sensu Sacch. . .; IPI.
GO; GO:0007125; P:invasive growth; IPI.
GO; GO:0007119; P:isotropic bud growth; IPI.
GO; GO:0007129; P:psudchyphal growth; IPI.
GO; GO:000750; P:signal transduction during conjugation with. .; IGI.
GO; GO:0007564; P:small GTPase mediated signal transduction; IPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- FUNCTION: One of the essential components for the initiation of protein synthesis. Protects formylambihonyl-tRNA from spontaneous hydrolysis and promotes its binding to the 30S ribosomal subunits. Also involved in the hydrolysis of GTP during the formation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DIGEVSELKPHRVIVIIQNGKEMSSII-----VSEEDFILPVYKGELEKGYQFDGWEIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1007;
                                                                                                                                                                                                                                                                                                                                                                                            Metal-binding; Zinc;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112831 MW; C805411B57553791 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | | : : : : | | | : 455 SQDLMRDNDSHTGLDIPNSNSTSLDILVNNQKSLNYKRFTDN 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 KEDLQREEHSQKSDSTKDVTATVLD-----KNNISSKSTTNN 151
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K -> R.
S -> G.
C -> S: BIPOLAR BUDDING.
C -> S: BIPOLAR BUDDING.
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
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-> P (IN REF. 4)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34; Mismatches
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Pred. No. 44
                                                                                                                                                                                                                                                                                                                                                                                          GTPase activation; Repeat; LIM domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                       LIM 1.
LIM 2.
RHO-GAP.
                                                                                                                                                        InterPro; IPR001781; LIM.
InterPro; IPR00198; RhoGAP.
Pfam; PF00412; LIM; 1.
ProDom; PD00620; RhoGAP; 1.
ProDom; PD000094; LIM; 2.
SWART; SW00132; LIM; 2.
SWART; SW00132; LIM; 2.
PROSITE; PS00478; LIM DOWAIN 1; 1.
PROSITE; PS50238; RHOGAP; 1.
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21.0%;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 IEEKKEEEUKPTFDVSKKKD----NPQVNHSQLNESHRKEDLQREEHSQKSDSTK---D 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 LEEEQIKALDKKFKASQAKDTINKQNTQNNHQKSNNKQNSNDKEKQQSKNNSKPTKKKEQN 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Gaps
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Structural component of the muscle M-line. Myofilament
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Rhabditidae; Peloderinae; Caenorhabditis.
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Ig and signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 10.6%; Score 85; DB 1; Length 720; Best Local Similarity 28.0%; Pred. No. 34; Matches 23; Conservative 15; Mismatches 36; Indels
                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Du Z., Le T.T., Wilson R.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
STRAIN=Bristol N2;
MEDLINE=96180278; PubMed=8603916;
Benian G.M., Tinley T.L., Tang X., Borodovsky M.;
"The Caenorhabditis elegans gene unc-89, required for massembly, encodes a giant modular protein composed of transduction domains.";
J. Cell Biol. 132:835-848(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07FB5A6A59CF970C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).

    -!- SUBCELLULAR LOCATION: Cytoplasmic.
    -!- SIMILARITY: BELONGS TO THE IF-2 FAMILY.

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277 281 GTI
331 334 GTI
720 AA; 79343 MW; (
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Caenorhabditis elegans.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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  62 AGYVINLSKDTFIKPV----FKKIEEKK--EEENKPTFDVSKKKDNPQVNHSQLNESHRK 115
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SUBSCELULAR LOCATION: SECRETED.
BOWAIN: THE SIGNAL PEPTIDE GUIDES THE PRECURSOR TO THE PERIPLASMIC SPACE, AND THE CARBOXY-TERMINAL HELPER DOMAIN ASSOCIATES WITH THE OUTER MEMBRANE TO FORM A PORE FOR EXCRETION OF THE PROTEASE DOMAIN. THE HELPER DOMAIN IS THEN RELEASED BY AUTOPROTEOLYSIS (BY SIMILARITY)
SIMILARITY.
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STRAINE=SGS 630; PubMed=7542800;

MEDLINE=955350630; PubMed=7542800;

Relachmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L. I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Genehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Immunoglobulin Al protease precursor (EC 3.4.21.72) (IGAl protease)
IGA OR IGAL OR H10990.
Haemophilus influenzae.
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-!- CATALYTIC ACTIVITY: Cleavage of immunoglobulin A molecules at certain Pro-|-Xaa bonds in the hinge region. No small molecule
                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellaceae, Haemophilus.
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STRALM-Serotype D;
Wright A. Fishman Y., Tai F., Plaut A.G.;
Submitted (MAY-1991) to the EMBL/GenBank/DDBJ databases.
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EMBL; U32.779; AAC22651.1; -.
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Interpro; IPR005546; Autotransport
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Interpro; IPR004899; Perfactin.
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MEROPS; S06.001; -.
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        This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics
                                                       MEDLINE=96287654; PubMed=8686381;

Eki T., Nairou M., Hagiwara H., Abe M., Ozawa M., Sasanuma M., Tsuchiya Y., Shibata T., Wtanabe K., Yamazaki M.-A., Tashiro H., Hanaoka F., Murakami Y "fifteen open reading frames in a 30.8 kb region o chromosome VI from Saccharomyces cerevisiae.";

Yeast 12:177-190(1996)
                                                                                                                           SEQUENCE FROM N.A.
STRAIN=S288c / AB972;
                                                                                                                                                                                                                STRAIN=S288c / AB972;
MEDLINE=95400292; PubMed=7670463;
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Saccharomycetales; Saccharomycetaceae;
NCBI_TaxID=4932;
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Hypothetical
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01-NOV-1995
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European
                                     SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY.
                                                SUBCELLULAR LOCATION: Nuclear (Potential)
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PF03212; Pertactin;
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(Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
1 88.7 kDa helicase in CDC26-SAP155
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Pfam; PF00176; SNF2_N; I.
SMART; SM00487; DEXDG; 1.
SMART; SM00490; HELICG; 1
                                                         mouse gene U2afbp-rs.";
Biochem. Biophys. Res. Commun. 222:171-177(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U2AF1-RS1 OR U2AFBPL.
Homo sapiens (Human).
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                                                                                           Pearsall R.S., Shibata H., Brozowska Dejong P.J., Plass C., Chapman V.M., "Absence of imprinting in UZAFBPL, a
                                                                                                                                                       MEDLINE=96212931; PubMed=8630064;
                                                                                                                                                                         SEQUENCE FROM N.A.
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SUBCELLULAR LOCATION: Nuclear SIMILARITY: Contains 1 RNA rec SIMILARITY: Contains 2 C3H1-ty
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S0001934; YFR038W.
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IPR001650; Helicase_C.
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0271; helicase_C; 1.
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T., Mitsuya K., (
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Oshimura M.,
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
B Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
B Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
B Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
B Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
B Beeson K.Y., Benos P. V., Berman B.P., Bhandari D., Bolshakov S.,
A Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
B Bottie K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dankov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
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Best Local S
Matches 26
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Pfam; PF00076; rrm; 1.
SMART; SM00360; RRM; 1.
SMART; SM00356; znf C3H1; 2.
SMART; SM00356; znf C3H1; 2.
PROSITE; PS50102; RRM; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS501030; RRM RNP 1; FALSE NEG.
Nuclear protein; RNA-Binding; Ribonucleoprotein; Zinc-finger; Nuclear protein; RNA-BINDING (RRM).
203
309
RNA-BINDING (RRM).
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SF326694BD4E7CO CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CG7843.
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InterPro; IPR000571; Znf_CCCH.
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(Rel. 41, Last sequence up
(Rel. 41, Last annotation
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F:RNA binding
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RA Harris N.L., Harvey D., Heiman T.J., Weim. H.,
RA Hostin D., Houston K.A., Howland T.J., Weim.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lia X., Mattei B., McIntosh T.C., McLeod M.P., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.
RA McIson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Spier E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassaman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassaman D.A., Weinstock G.M., Weissenbach J.,
RA Mang S.M., Moodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Milliams S.M., Moodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong R.N., Zhong M., Zhou X., Zhou X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000)
                                                                                                                                                     Matches
                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E. Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B. Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                         FlyBase; FBgn0033062; CG7843.
Pfam; PF04959; ARS2; 1.
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-!- ALTERNATIVE PRODUCTS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Berkeley;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Annotation of the Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REVISIONS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lewis S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
332 DDDDAENSAPKKELAEDSKDSDSKPEDKOLNKKKTKKRKRNSSDDDSSSSESSSSSDEEK
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                                     EISGFEGKKDAGYVINLSKDTFIKPVFKKIEE---KKEEENKPTFDVSKKKDNPQVNHSQ
                                                                         KVLDEKPKDPVVYERKAEQMQSVKEVEKTINSPKEEMSEADPVSTQRKPVRPVNSDGENW
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Missing (in isoform
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109

LNESHRKEDLOREEHSOKSDSTKD

LKEKYDVEDGLRAE - - QKTEAEKD

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A Strausberg R.D., Feligold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan R., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Sodares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Stapleton M., Sodarin R.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Hitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,

B Lakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE—CVARIAN CARCINOMA;

TISSUE—CVARIAN CARCINOMA;

IBOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

Wagateuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara |

Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

Ninomiya K., Iwayanagi T.;

"NEDO human cDNA sequencing project.";

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99041954; PubMed=9822659; Block K.L., Vornlocher H.-P., Hershe "Characterization of cDNAs encoding translation initiation factor eIF3."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Eukaryotic translation initiation factor 3 su
(eIF3 p35) (eIF3j).
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O75822; Q9BUD2; Q9H8Q2;
30-MAY-2000 (Rel. 39, C
                     modified
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                                                                                                                                                                     human and mouse cDNA sequences.";
proc. Natl. Acad. Sci. U.S.A. 99:16899-1
-!- FUNCTION: BINDS TO THE 40S RIBOSOME
METHIONYL-TRNAI AND MRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22388257; PubMed=12477932;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                               This
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                                                        European Bioinformatics Institute.
                                                                                                                                    similarity).
                                                                         SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
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requires a license
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license agreement
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GO; GO:0005852; C:eukaryotic translation:
GO; GO:0003743; F:translation initiation
GO; GO:0006446; P:regulation of translati
GO; GO:0006446; Protein biosynthesis:
                                                                                                                                                                            SEQUENCE F
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CONFLICT
SEQUENCE
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DOMAIN
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                                                                  MEDLINE-95350630; PubMed-7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.
Fleischmann R.D., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Gocayne J.D.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                      SEQUENCE TO STRAIN THI TUN106;
MEDLINE=94245357; PubMed=8188372;
MEDLINE=94245357; Sanders J.D., Cope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genew; HGNC:3270;
GK; 075822; -.
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                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gar
Pasteurellaceae; Haemophilus
                                                                                                                                                                                                                                                                                                                                                                        TonB protein.
TONB OR HI0251
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28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995
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                       Science 269:496-512(1995)
                                                            Venter J.C.
                                                                                                                                                                                                               "A functional tonB gene is required virulence expression by Haemophilus Infect. Immun. 62:2470-2477(1994).
                                                                                                                                                                                                                                                    Hansen E.J
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41,
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annotation
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                                             assembly of Haemophilus influenzae
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influenzae type b.";
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Lipase precursor (EC 3.1.1.3) (Glycerol ester hydrolase).
GEHC OR SE0281.
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DOMAIN
NCBI_TaxID=1282; [1]
                                               Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales; Staphylococcus
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EMBL; U32711; AAC21917.1; -.
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Pfam; PF03544; TonB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IGR; HI0251; -.
InterPro; IPR003538; TonB.
Tobn06260; TonB_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; F64057; F64057.
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een the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
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ane; Signal-anchor;
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-1- MISCELLANEOUS: THE EXPRESSION OF STAPHYLOCOCCUS LIPASE IS NEGATIVELY REGULATED BY BACTERIOPHAGE LYSOGENIZATION (LIPASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Triacylglycerol + H(2)0 = diacyl
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RX MEDLINE=22388257; PubMed=12477932;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altechal S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altechal S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Robask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Morley M., Steteman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

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RA Rodriguez A.C., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Schmutz J., Myers R.M.,

RA Rodr
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                                                                                    DOMAIN
DOMAIN
REPEAT
                                                                                                                                                                                                                PRINTS; PR00597; GEL;
SMART; SM00262; GEL;
Cytoskeleton; Actin-l
                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; BC021090; AAH21090.1; -.
EMBL; AC005281; AAD15423.1; -.
EMBL; AK027778; BAB55361.1; -.
HSSP; P02640; 2VIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for com
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Submitted (JUL-1998) to
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 248-715 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-527 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Placenta,
                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001974; Gelsolin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Ca(2+)-dependent actin filament-severing protein that presumed to have a regulatory function in exocytosis by affective the organization of the microfilament network underneath the plasma membrane. In vitro, also has barbed end capping and nucleating activities in the presence of Ca(2+).

SIMILARITY: BELONGS TO THE VILLIN/GELSOLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Contains 6 gelsolin-like repeats.
                                                                                                                                                                                                                                                                                                                                                PF00626; Gelsolin;
        364
27
148
265
                                                                                                                                                                                                                    Actin-binding;
                                                                                                                                                                                                                                                                                                    GELSOLIN.
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        363
715
76
188
307
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the EMBL/GenBank/DDBJ databases
Repeat, Calcium; Capping protein. ACTIN-SEVERING (POTENTIAL). CA(2+)-DEPENDENT ACTIN BINDING. GELSOLIN-LIKE 1. GELSOLIN-LIKE 2. GELSOLIN-LIKE 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99:16899-16903 (2002)
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Best Local S
Matches 34
                                 WormPep; C29A12.3; CE05328.
InterPro; IPR000977; DNA ligase; 1.
Pfam; PP01068; DNA ligase; 2.
Pfam; PP04679; DNA ligase A C; 1.
Pfam; PP04679; DNA ligase A N; 1.
IIGASEAMS; TIGR00574; dnl1; 1.
PROSITE; PS00697; DNA LIGASE A1; 1.
PROSITE; PS00333; DNA LIGASE A2; 1.
PROSITE; PS01630; DNA LIGASE A3; 1.
PROSITE; PS01630; DNA LIGASE A3; 1.
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Q27474;
Q1-NOV-1997
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                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA ligase (EC 6.5.1.1) (Polydeoxyribonucleotide synthase [ATP]).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAEEL
                                                                                                                                                                EMBL; Z73970; CAA98242.1; -. PIR; T19544; T19544.
                                                                                                                                                                                                                                                                                                                                                                                               Submitted
                                                                                                                                                                                                                                                                                                                                                                                                           Wilkinson
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIG-1 OR
          DNA repair; DNA ATP-binding.
                                                                                                                                                                                                                                                                                                                                  mitted (JŪN-1996) to the EMBL/GenBank/DDBJ databases. FUNCTION: THIS PROTEIN SEALS DURING DIA RECOMBINATION AND DNA REPAIR NICKS IN DOUBLE-STRANDED CATALYTIC ACTIVITY: ATP + {deoxyribonucleotide} (N) + {deoxyribonucleotide} (N) = AMP + diphosphate +
                                                                                                                                                                                                                                                                                                                        \{deoxyribonucleotide\} (N+M).
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715
363
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                          replication;
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b; Pred. No. 47;
30; Mismatches
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GELSOLIN-LIKE 5.
GELSOLIN-LIKE 6.
POLYPHOSPHOINOSITIDE I
                          DNA
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(BY SIMILARITY)
                          recombination; Cell division; Ligase;
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Best Local Similarity

17.8%;

Pred. No.

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Query Match
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                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
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16-OCT-2001
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                                                                                Pfam; PF03951; gln-synt_N; 1.
proDom; PD001057; Gln synt_C; 1.
TIGRPAMs; TIGRR0653; GlnA; 1.
PROSITE; PS00180; GLNA_1; 1.
PROSITE; PS00181; GLNA_ATP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                        archaeon Pyrococcus abyssi.";
mol. Microbiol. 47:1495-1512(2003).
-!- CATALYTIC ACTIVITY: AIP + L-glutamate + NH(3) =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecol
Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,
Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.;
"An integrated analysis of the genome of the hyperthermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase)
GLNA OR PYRAB16090 OR PAB1292.
                                                                                                                                                               InterPro; IPR001691; GLN synth.
InterPro; IPR004809; GlnA.
InterPro; IPR001637; GlnA adenyltn.
                             SEQUENCE
                                                                                                                                         Pfam; PF00120; gln-synt; Pfam; PF03951; gln-synt
                                                                                                                                                                                                               HSSP; P06201; 1LGR
                                                                                                                                                                                                                                         EMBL; AJ248288; CAB50513.1;
                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                   entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                 - !- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=12622808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-GE5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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SUBCELLULAR
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Pred. No.
Score 82.5;
                           AMP (UNDER CONDITIONS GLUTAMINE) (BY SIMILAR 62CCFD3970A98AF0 CRC
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56;
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Length 439;
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PRODOm; PD000089; HSp70; 1.
PROSITE; PS00297; HSP70_2; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
PROSITE; PS01036; HSP70_3; Nucleo SEQUENCE 649 AA; 72079 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PYRSA
                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The smallest known eukaryotic genomes encode a protein an understanding of nucleomorph functions."; Mol. Gen. Genet. 243:600-604(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=94268506; PubMed=8208251;
Hofmann C.J.B., Rensing S.A., Haeuber M.M., Martin W.F.,
Couch J., McFadden G.I., Igloi G.L., Maier U.-G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pyrenomonas salina.
Nucleomorph.
Eukaryota; Cryptoph
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01-OCT-1994 (Rel. 30, Last sec
28-FEB-2003 (Rel. 41, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MO1. Gen. Genet. 243:600-604(1994).
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3034;
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PF00012; HSP70; 1.
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  LQREEHSQKSDSTKDVTATVLDK 140
                                                    --GYVINLS---KOTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKED
                                                                               KSNKITITNDKGRLSKEEIERMVEEAE----KYKTEDEK
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                                                                                                                                                                                    Nucleomorph.
9 MW; B627B08FF90C9164 CRC64;
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Pred. No. 4
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                                                                                 -LDKKLEAKNS
                              -VLEFIETNED
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MEDINE-97405699; PubMed-9260743;
MEDINE-97405699; PubMed-9260743;
MEDINE-97405699; PubMed-9260743;

"Differential regulation of microctubule-associated protein 1B (MAP1B)
in rat CNS and PNS during development.";

J. Neurosci. Res. 49:319-332(1997).

-i- FUNCTION: The function of brain MAPS is essentially unknown.
Phosphorylated MAP1B may play a role in the cytoskeletal changes
that accompany neurite extension. Possibly MAP1B Binds to at least
two tubulin subunits in the polymer, and this bridging of subunits
might be involved in nucleating microtubule polymerization and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAPB_RAT STANDARD; PRT;
P15205; Q62958; Q958721; Q92W92;
01-APR-1990 (Rel. 14, Created)
16-OCT-2001 (Rel. 40, Last sequence
28-FEB-2003 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Isolation and sequencing of the 5' end of the associated protein (MAP1B)-encoding cDNA."; Gene 172:307-308(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rienitz A., Grenningloh G., Hermans-Borgmeyer I., Kirsch J., Littauer U.Z., Prior P., Gundelfinger E.D., Schmitt B., Betz H.; "Neuraxin, a novel putative structural protein of the rat central nervous system that is immunologically related to microtubule-associated protein 5."; EMBO J. 8:2879-2888(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1541-2459 FROM N.A., TISSUE=Spinal cord;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 96-2459 FROM N.A., DOMAIN, AND INDUCTION STRAIN-Sprague-Dawley; TISSUE-Brain, and Glial tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-142 FROM N.A.
STRAIN-Sprague-Dawley; TISSUE=Testis;
MEDLINE=96257242; PubMed=8666295;
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zauner W., Kratz J., Staunton J., Feick P., "Identification of two distinct microtubule recombinant rat MAP 1B.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92347374; PubMed=1639092;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        light chain LC1].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90059871; PubMed=2555150;
                              nerve levels are high early in development but decrease du postnatal development and are low in adults. In dorsal roo ganglia levels remain high throughout development. INDUCTION: By nerve growth factor. INDUCTION: By nerve growth factor. DOMAIN: Has a highly basic region with many copies of the EXEE and KKEI/V, repeated but not at fixed intervals, whice responsible for the binding of MAPIB to microtubules. PTW: LC1 is coexpressed with MAPIB. It is a polypeptide get
                                                                                                                                                                                                                 SUBUNIT: 3 different light chains, LC1, LC2 and with MAP1A and MAP1B proteins.
TISSUE SPECIFICITY: Nervous system (spinal cord, cerebellum and cerebrum). Not expressed in liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
                                                                                                                                                                                DEVELOPMENTAL STAGE: In cerebral cortex, spinal
                                                                                                                                                                                                   heart or muscle.
                                                                                                                                                                                                                                                                                           stabilizing microtubules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fischer
                   MAP1B by proteolytic processing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last annotation update)
 It interacts
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spleen, kidney,
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RESULT 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
Eukaryota; Fungi; Ascomycota; Saccharomycetales; Saccharomyc NCBI_TaxID=4932;
                                       Hypothetical 32.4 kDa
YML014W OR YM9571.04.
                                                           01-OCT-1996
15-SEP-2003
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EMBL; X60370; CAC16162.1; -.
EMBL; X16623; CAA34620.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an
                                Saccharomyces cerevisiae (Baker's yeast).
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PTM: Phosphorylated.
SIMILARITY: TO MAP1A.
CAUTION: A C-terminal fra
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lles; Repeat; Phosphorylation.
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                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformaticy Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL;
PIR; S
SGD; S
                                                                                                                                                                                                                                                                                            Guerreiro P., Rodrigues-Pousada C.; Submitted (MAR-1994) to the EMBL/GenBank/DDBJ
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Guerreiro P., Ro
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Q05907;
Q1-FEB-1994
CONFLICT
                                                                        PROSITE; PS00180; GLNA 1; 1
PROSITE; PS00181; GLNA ATP;
Ligase; Complete proteome.
BINDING 358 358
                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Vc1 / DSM 3638 / ATCC 43587 / JCM 8422; Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.; "The complete sequence of the Pyrococcus furiosus genome."; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Vc1 / DSM 3638 / ATCC 43587
MEDLINE=94365840; PubMed=7916055;
Brown J.R., Masuchi Y., Robb F.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pyrococcus turiosus.
Archaea; Euryarchaeota;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glutamine synthetase (EC 6.3.1.2) (Glutamat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
SEQUENCE 427 AA; 47416 MW;
                                                                                                                                                                                                                                          InterPro; IFR004809; GlnA.
InterPro; IFR001637; GlnA adenyltn.
InterPro; IPR001637; GlnA adenyltn.
                                                                                                                                                                                                                                                                                                                                                                           EMBL; L12410; AAA71968.1; -. EMBL; AE010168; AAL80574.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       synthetase genes.";
J. Mol. Evol. 38:566-576(1994).
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                                                                                                                                                                       ProDom; PD001057; Gln synt C; TIGRFAMs; TIGR00653; GlnA; 1.
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                                                                                                                                                                                                                                                                                                                                                      HSSP; P06201; 1LGR

    -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
    -!- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Evolutionary relationships of bacterial and archaeal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=2261;
                                                                                                                                                                                                                                                                                                                             InterPro; IPR001691; GLN_synth.
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203
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Pred. No. 32;
18; Mismatches
AMP (UNDER OF GLUTAMINE)

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  R CONDITIONS OF AF
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L outstation -
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                                                                                                                                                                  the European Bioinformatics Institute. There are no resuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by a
                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=93259940; PubMed=8098326;
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                                                                                                                                                          entities requires a license agreement
                                                                                                                                                                                                                                                                   J. Bacteriol. 175:2961-2969(1993).
-!- CATALYTIC ACTIVITY: ATP + L-gl
                                                                                                                                                                                                                                                                                                                                                                                                                                Glutamine
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                Pfam; PF03951; gln-synt_N; 1.
ProDom; PF001057; Gln synt_C; 1.
TIGRFAMS; TIGR00653; GlnA; 1.
PROSITE; PS00180; GLNA_1; 1.
                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                            Pyrococcus woesei
                                                 InterPro; IPRO04809; GlnA.
InterPro; IPRO01637; GlnA adenyltn.
Pfam; PF00120; gln-synt; I.
Pfam; PF03951; gln-synt_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                Archaea; Euryarchaeota;
                                                                                           interPro;
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                                                                                                                                                                                                                                                                                                                                   Tiboni O.,
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                                                                                                                                                                                                                                                         L-glutamine
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and sequencing of the gene encoding glutamine synthetase I archaeum Pyrococcus woesei: anomalous phylogenies inferred lysis of archaeal and bacterial glutamine synthetase I
          PS00180;
PS00181;
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(Rel. 29, Last sequence update)
(Rel. 37, Last annotation updat
rnthetase I (EC 6.3.1.2) (Glutam
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          GLNA_1; 1.
GLNA_ATP; 1.
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N REF. 1).
IPPDTE (IN REF. 1).
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01-OCT-1993 (Rel. 27, 01-OCT-1993 (Rel. 27, 101-OCT-1993 (Rel. 27, 101-OCT-1993 (Rel. 41, 101-OCT-1994 (Rel. 41, 101-OCT))
                                                                                                                                                                                                                                                                                                                                                                                                                                                            participation in cell cycle regulation in late G1-phase control by E2F-1, pRb, p107 and Sp-1."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.-i- FUNCTION: Component of the inner kinetochore plate. normal kinetochore assembly.
                                                                                                                                   EMBL; M95724; AAA51974.1; -. EMBL; AF151723; AAF73191.1; PIR; A42681; A42681.
                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
Chromosomal protein;
                GO; GO:0005699; C:kinetochore; TAS.
GO; GO:0003677; F:DNA binding activity; TAS
InterPro; IPR007113; Cupin_sup.
                                                                                          MIM; 117141; -.
                                                                                                                Genew; HGNC:1854; CENPC1.
                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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SEQUENCE OF 1-21 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saitoh H., Tomkiel J., Cooke Rothfield N.F., Earnshaw W.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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kinetochore plate.";
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Nuclear protein; DNA-binding;
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Last annotation update)
(CENP-C) (Centromere autoantigen
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SEQUENCE FROM N.A.

MEDLINE=99120557; PubMed=9923682;

MEDLINE=99120557; PubMed=9923682;

Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Land R.A., Ling L.-S.L., Moir D.T., King B.L., Carmel G., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel B.M., Juiang D.M., Juiang D.M., Juiang D.M., Juiang D.M., Juiang D.M., Juiang D.M., Mills S.D., Jiang Q., Taylor D.E., Tummino P.M., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Tummino P.M., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Tummino P.M., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Tummino P.M., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Tummino P.M., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Tummino P.M., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Tummino P.M., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Tummino P.M., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Tummino P.M., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Tummino P.M., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Tummino P.M., Mills S.D., Jiang Q., Taylor D.E., Tummino P.M., Mills S.D., Jiang Q., Taylor D.E., Tummino P.M., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D., Mills S.D.,
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                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                              "Genomic sequence comparison of two unrelated isolates gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                         EMBL; AE001472; AAD05948.1; PIR; E71940; E71940.
                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                          FUNCTION: One of the essential components for the initiation of protein synthesis. Protects formylmethionyl-tRNA from spontaneous hydrolysis and promotes its binding to the 30s ribosomal subunite. Also involved in the hydrolysis of GTP during the formation of the 70s ribosomal complex (By similarity). SUBCELLULAR ICCATTON: CYtoplasmic.
SUBCELLULAR ICCATTON: CYtoplasmic.
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MF_00100;
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943 AA;
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(Rel. 39, Last sequence update)
(Rel. 42, Last annotation updat
initiation factor IF-2.
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8; Mismatches
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NP_BIND 503
NP_BIND 557
DOMAIN 321
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                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the EMropean Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-series.
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=92315338; PubMed=1617731;
Galinski M.R., Medina C.C., Ingravallo P.,
"A reticulocyte-binding protein complex of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGREAMS; TIGRO0487; IF-2; 1.
TIGREAMS; TIGRO0231; small_GTP;
PROSITE; PS01176; IF2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU_D2; 2.
Pfam; PF04760; IF2_N; 1.
ProDom; PD186100; IF2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000795; EF GTPbind. InterPro; IPR004161; EFTU D2. INTERPRO; IPR00178; IF2. INTERPRO; IPR006847; IF2.N. INTERPRO; IPR005225; Small GTP. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DEFM. DE
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    -!- SUBCELLULAR LOCATION: Membrane-bound (Probable).

                                                                                                                                                                                                                                                                                                                                                                                                                  merozoites.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=31273;
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                                                                                                                                                                                                                                                                                                                                                 1 69:1213-1226(1992).
FUNCTION: INVOLVED IN RETICULOCYTE ADHESION.
HUMAN RETICULOCYTE CELLS.
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                                                                                           M88098; AAA29744.1; -.
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                                                                                                                                      an email to license@isb-sib.ch).
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(Rel. 25, Last sequence update)
(Rel. 34, Last annotation update)
binding protein 2 (Fragment).
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28.7%;
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GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

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20; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haemosporida; Plasmodium
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                                                                                                                                                            noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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Best Local Similarity

10.3%; 143741

Score Pred.

82; No.

DB 1; 1e+02;

Length 1251;

Query Match

Malaria; NON_TER NON_TER SEQUENCE

1251 1251

ĀΑ;

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Receptor; Membrane.

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RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
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RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lucy J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
"Sequence and analysis of chromosome 1 of the plant Arabidopsis
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EMBL; U66343;
                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content
                                                                                                                                                                                                           Nature 408:816-820(2000).

-I- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).

-I- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nelson D.E., Glaunsinger B., Bohnert H.J.,
"Abundant accumulation of the calcium-binding molecular chaperone calreticulin in specific floral tissues of Arabidopsis thaliana.", plant Physiol. 114:29-37(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Calreticulin 1 precursor.

CRT1 OR AT1656340 OR F13N6.20 OR F14G9.5.

Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid.

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid.

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid.

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid.
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                                      or send an email to license@isb-sib.ch).
                                                                                   modified
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28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97303616; PubMed=9159940;
                                                          European Bioinformatics Institute. The by non-profit institutions as longified and this statement is not removed. ities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARATH
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PROSITE; PS00803;
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InterPro; IPR000886; ER target.
Pfam; PF00262; calreticulin; 1.
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PIR; C96605; C96605.
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2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate
6: sp_mammal:*
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

16	15	14	13	12	11	10	9	8	7	ტ	ű	4	ω	N	_	Result No.	
108	108	108.5	108.5	109	109	110	110.5	111.5	112.5	112.5	118	795	796	799	799	Score	
13.5	13.5	13.6	13.6	13.6	13.6	13.8	13.8	14.0	14.1	14.1	14.8	99.5	99.6	100.0	100.0	Query	df
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## ALIGNMENTS

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PF00082; S; PR00723 AMS; TIGRO	Pfam; PP02225; PA; I.	IPR000209;	IPR006192;	08.064;		-i- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY AN AMIDE BOND (BY SIMILARITY).	mmun. 69:1593-1598(2001).	"Use of a whole Genome Approach to identify vaccine molecules Affording Protection against Streptococcus pneumoniae Infection.";	S., Johnson S., Koenig S.;	e A., Brewah Y.A., Walsh W., Barren P., Lathigra R., F	C.A., Masure H.R., Tuomanen E.,	Wizemann T.M., Heinrichs J.H., Adamou J.E., Erwin A.L., Kunsch C.,	MEDLINE=21116976: PubMed=11179332:	SEQUENCE FROM N.A.		NCBI_TaxID=1313;	Streptococcus.	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;	Streptococcus pneumoniae.	•	ease (Fragment).	(TrEMBLrel. 23, Last annotation	(TrEMBLrel. 17,	O1-JUN-2001 (TrEMBLrel. 17, Created)	CYAHT'S PRELIMINARY; PRI; ZIIY AA.	ц	

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01-OCT-2001
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MEDIINE-21357209; PubMed-11463916;

Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Umayam L.A., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angiutoli S., Dickinson T., Hickey I Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;

"Complete genome sequence of a virulent isolate of Streptococcus
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             TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
PROSITE; PS50847; GRAM POS_ANCHORING;
PROSITE; PS50840; PA; 1.
PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00138; SUBTILASE_SER; 1.
PROSITE; PS00138; SUBTILASE_SER; 1.
PROSITE; PS00678; WD REPEATS_1; 1.
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InterPro; IPR006192; LPXTG.
InterPro; IPR00137; PA.
InterPro; IPR000209; Peptidase_S8.
InterPro; IPR001680; WD40.
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EMBL; AE007373; AAK74791.1;
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Q8DQP7;
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Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett Hoskins J., Alborn W.E. Jr., Arnold J., Fuller W., Gering DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Gering Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E., LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P., McAhren S.M., McHenney M., McLeaster K., Muly C.W., Nicas T.I. Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P., Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G., Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatruć
                                                                                                                                                                                                                                                                                                                                   "Genome of the bacterium Streptococcus J. Bacteriol. 183:5709-5717(2001).
EMBL; AE008434; AAK99365.1; -.
Hydrolase; Complete proteome.
SEQUENCE 2144 AA; 240436 MW; 8C1B4B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                          Glass
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                                                                                                                                                                                                                                                                                Conservative
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llarity 100.0%;
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proteinase PrtA (EC 3
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Pred. No. 2.1e-51;
; Mismatches 0;
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(EC 3.4.21.-).
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Q9S4M8; Q9S4M8; 01-MAY-2000 01-MAY-2000

(TrEMBLrel.

Created)
Last sequence update)

PRELIMINARY;

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Best Local S
Matches 152
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Pfam; PP00746; Gram pos anchor; 1.
Pfam; PP002225; PA; 1.
Pfam; PP00082; Peptidase_S8; 2.
PFINTS; PR00723; SUBTILISIN.
TIGRFAMS; TIGR01167; LPXTG anchor; 1.
PROSITE; PS50847; GRAM POS ANCHORING; 1.
PROSITE; PS50840; PA; 1.
PROSITE; PS00137; SUBTILASE_HIS; 1.
PROSITE; PS00137; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE_SER; 1.
PROSITE; PS00678; WD REPEATS_1; 1.
Cell wall; Peptidoglycan-anchor; Signal.
SIGNAL 1 19
                                                                                                                                                                                                                                                                         Q8CPK8;
                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
SEQUENCE FROM N.A. STRAIN=ATCC 12228; Zhang Y., Ren S.,
                                                                                                               Staphylococcus epidermidis
Bacteria; Firmicutes; Baci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning and sequencing o
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                                                                                                                                                                                Penicillin-binding
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InterPro; IPR001680; WD40.
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InterPro; IPR006192; LPXTG.
InterPro; IPR003137; PA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1957
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                                                                                      _TaxID=1282;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    EEHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 154
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Pred. No. 4.2e-51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Conservation of structural motifs and antigenic diversity in Plasmodium falciparum merozoite surface protein-3 (MSP-3).", Mol. Biochem. Parasitol. 90:21-31(1997).
EMBL; U08852; AAC47832.1;
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Li X.R., Yu X.B
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Eukaryota; Alveolata;
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"Allelic lineages of the merozoite surface protein Plasmodium reichenowi and Plasmodium falciparum.";
Mol. Biochem. Parasitol. 109:185-188(2000).
EMBL; AJ252286; CAB65754.1; -.
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EMBL; U08851; AAC47831.1; -.
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SIGNAL
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01-NOV-1996 (TrEMBLrel. 01, La
01-OCT-2002 (TrEMBLrel. 22, La
Polymorphic antigen precursor.
Plasmodium falaine.
Plasmodium falciparum Eukaryota; Alveolata; NCBI_TaxID=36329;
                                                                              Hypothetical protein. PFE0325W.
                                                                                                                                                                   Q81436;
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Conservation of structural motifs and antigenic diversity in the Plasmodium falciparum merozoite surface protein-3 (MSP-3)."; mol. Biochem. Parasitol. 90:21-31(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McColl D.J., Silva A., Foley M., Kun J.F., I Thompson J.K., Marshall V.M., Coppel R.L., I "Molecular variation in a novel polymorphic Plasmodium falciparum merozoites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q26019;
01-NOV-1996
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                                                                                                                          01-MAR-2003
                                                                                                                                                                                                               Q81436
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                                                                                                                                              01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95198774; PubMed=7891748;
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                                                                                                                          (TrEMBLrel.
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                                                                                                                                                                                                               PRELIMINARY;
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380 F
43290 MW;
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                                (isolate 3D7)
Apicomplexa;
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POLYMORPHIC ANTIGEN.
; 0986CA1393094CA2 CRC64;
                                       Haemosporida;
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Kemp D.J., Anders R.F.;
c antigen associated with
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                                       Plasmodium
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A Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
A Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
A Feltwell T., Gobbe A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
A Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
A Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
A Knights A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,
A Cliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch E.,
A Oliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch E.,
A Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
A Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
A Sulston J.E., Craig A., Newbold C., Barrell B.G;
Network M. Charles C., Pasmodium falciparum chromosomes 1, 3-9 and 13.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ol-OCT-2000 (TERMBLrel. 15, Las 01-OCT-2002 (TERMBLrel. 22, Las Hypothetical 71.7 kDa protein. PFC0465C, MAL3P4.20. Plasmodium falcinghir
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SEQUENCE FROM ... Baker S., De
Devlin K., Baker S., Ch
Hall N., Bowman S., Ch
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077355;
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Chillingworth T., Christ
                                                                                                                                                                                                      Bowman S., Lawson D., Basham D., Brown D., Chillingworth T., Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T., Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Ho Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule Mungalk K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A Rutter S., Skelton J., Squares R., Squares S., Sulston J.E., Whitehead S., Woodward J.R., Newbold C., Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum (isolate 3D7)
Eukaryota; Alveolata; Apicomplexa;
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                      Pfam; PF01480; PWI; 1.
SMART; SM00311; PWI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99376085;
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                                                                       EMBL; AL008970; CAA15610.2;
InterPro; IPR002483; PWI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=36329;
                                                                                                                                 Nature 400:532-538(1999).
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Baker S., Churcher C
Bowman S., Churcher C
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3008 AA;
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                                                                                                                                                                                nucleotide sequence of chromosome
                                                                                                                                                                                                                                                                                                                                                                                               PubMed=10448855;
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Cherevach I., Chillingworth C.,
Cherevach I., Clark R., Corton C.,
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annotation updat
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J. Neurobiol. 25:1-22(1994).
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01-MAR-2003
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Eukaryota; /
                                                                                                                                                                                                              Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W. Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., Jame Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A. Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S. McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; H
NCBI_TaxID=36329;
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EMBL; L28825; AAC09377.1; -.
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Thompson J.K., Marshall V.M., Coppel R.L., K
"Molecular variation in a novel polymorphic
Plasmodium falciparum merozoites.";
Mol. Biochem. Parasitol. 68:53-67(1994).
                                                                                  EMBL; AE014834; AAN35542.:
SEQUENCE 354 AA; 40119
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                                                                                                                                                                 "Genome sequence of falciparum.";
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Q815F3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9FJK9
Q9FJK9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core everosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                  Hypothetical protein. PFL1275C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence features of the regions of 1,01. physically assigned P1 and TAC clones."; DNA Res. 5:297-308(1998).
EMBL; AB015468; BAB10694.1; -.
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01-MAR-2001 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
Gb|AAF20218.1.
                                                                                                                                                                                                                               01-MAR-2003
                                                                                                                                                                                                                                                      01-MAR-2003
  STRAIN=3D7;
                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99087489; PubMed=9872454;
Nakamura Y., Sato S., Asamizu E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nakamura Y., Sato S.,
                                                                                                                        Plasmodium falciparum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 KPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFE------GKK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RENRVTDTVQNNSNGESK------YVQDLARRIRYDE-EATGSQSAQRIDHPNQK 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLOREEHSOKSDSTKDVTATVLDKNNISSKSTTNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGF--EGKKDAG-----YVINLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PQVNHSQLNE----SHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NVGITEKAFENSPIEETSHRVDDNKRINNQKNFTAAKSSENAVSRVSFGADHKRAEVMGK 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KDTFIKPVFKKIEEKKEE-----ENKPTFDVSKKKDNPQVNHSQLNESHRKE
                                                                                                                                                                                                                                                                                                                                                                                                                                 PMENRDQVRQTESAEKSHRKENVTKSEKPRDQEGVKKTEAKDKDRNKEKKEEKTESINK
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                                                                                                   Alveolata;
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(TrEMBLrel.
(TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             470 AA;
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                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53758 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.5%; Score 107.5;
20.1%; Pred. No. 2.5;
                                                                                                 (isolate 3D7).
Apicomplexa; F
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22,
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Last sequence update)
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                                                                                                   Haemosporida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         470
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edons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                        B
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                                                                                                 Plasmodium.
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Best Local S
Matches 36
                                             MEDLINE=22255705; PubMed=12368864;
Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.
Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
Fraser C.M., Barrell B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22255705; PubMed=12368864;
Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.
Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
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"Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99021743; PubMed=9804551;
Gardner M.J., Tettelin H., Carucci D.J., Cummings L.M., Aravind |
Gardner M.J., Tettelin H., Carucci D.J., Fujii C., Pederson J.,
Koonin E.V., Shallom S., Mason T., Yu K., Fujii C., Pertea M.,
Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Pertea M.,
Salzberg S., Zhou L., Sutton G.G., Clayron R., White O., Smith H
Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.;
Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.;
"Chromosome 2 sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1999 (TrEMBLrel. 10,
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE014848; AAN36341.1; -- Hypothetical protein. SEQUENCE 829 AA; 98816 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium:
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical PFB0680W.
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Nature 419:498-511(2002)
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 282:1126-1132(1998).
talciparum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        falciparum.";
                             "Genome sequence of the human malaria parasite Plasmodium
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                                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EEENKPT-----FDVSKKKDN-PQVNHSQLNESH-RKEDLQREEHSQKSDS
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Hypothetical
SEQUENCE 95
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Kiyosawa H., Hughes J.E., Welker D.L.;
"Dictyostelium discoideum nuclear plasmid
the Ddpl and Ddp2 plasmid families.";
Genetics 148:1117-1125(1998).
EMBL; U00796; AAC18634.1; -
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Best Local S
Matches 43
                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Berkeley;
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NCBI_TaxID=7227;
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TAC and E
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Kaneko T., Kato T.,
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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EMBL; AP002057; BAB03174.1;
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A Manartides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
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A Barndon R.C., Bobayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
A Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
A Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
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Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Fleischmann W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9V7J0 PRELIMINARY; rn.; Q9V7J0, Q9GQ81; Q9V7J0, Q9GQ81; Created) 01-MAY-2000 (TrEMBLrel. 13, Created) 01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CG8421 protein (Aspartyl beta-hydroxylase variant ASPH OR CG8421 OR CG18658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neoptera; Endopterygota; Diptera; Brachycera;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDINEINNGKEDSVKDNVTEIQGNDNSLTNSTSSEPN
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to the EMBL/GenBank/DDBJ databases.
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Pred. No. 30;
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RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Ra Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Ra Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Ra Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Ra Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Ra Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Ra Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Andrew G., Milshina N.V., Mobarry C., Morris J., Meshon D.L., Ra McLeon D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Ra Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Ra Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Ra Reinert K., Remington K., Saunders R.D. C., Scheeler F., Shen H., Ship B.C., Siden-Kiamos I., Simpson M., Strong R., Sun E., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Spier E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X., Ra Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Ra Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Theng Y.H., Zhong W., Zhonu X., Zhu S., Zhu X., Smith H.O., Ra Zience 287:2185-2195(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

SEQUENCE FROM N.A., Matthews B.B., Bayraktaroglu L., Campbell K.

Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.

Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,

Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,

Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,

Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,

Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,

Ashburner M.J., Smith E., Shu S., Smutniak F., Whitfield E.,

Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;

"Annotation of Drosophila melanogaster genome.";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003808; AAF58063.2; --
EMBL; AF289494; AAG40807.1; --
FlyBase; F8gn0034075; Asph.
SEQUENCE 382 AA; 43287 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Adams M.D., Celniker
                                                                                                                                                                                                                                                                                                                                                                              Dinchuk J.E., Henderson N.L., Burn T.C., Huber R., Ho S.P., Link J., O'Neil K.T., Focht R.J., Scully M.S., Hollis J.M., Hollis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20564328; PubMed=10956665;
                                                                                                                                                                                                                                                                                                   'Aspartyl beta -Hydroxylase
                                                                                                                                                                                                                                                        soform of Asph Missing
                                                                                                                                                                         Biol.
                                                                                                                                                                     Chem. 275:39543-39554 (2000)
                                                                                                                                                                                                                                                                                                                                           P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MAR-2000)
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                                                                                                                                                                                                                                                        Catalytic
                                                                                                                                                                                                                                                                                                   (Asph)
        60E5C03AEBFC6E8B CRC64;
                                                                                                                                                                                                                                                                                                   and
                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                   an
                                                                                                                                                                                                                                                            Evolutionarily Conserved
ain Share Exons with
                                                                                                                                                                                                                                                        Exons
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, Busam D.A.,
Dietz S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Campbell K.
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RESULT 23
Q9V7I9
RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addams M.D., Celniker S.E., Holt R.A., Shburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Holt R.A., Shburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Bardon R.C., Rogers Y.-H.C., Blazed R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.-H.C., Blazed R.G., Champe M., Pfeiffer B.D.,
RA Baril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Baril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bolthakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bolthakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bolthakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Boukov B.C., Dunn P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Boukov B.C., Dunn P.,
RA Admis M., Caller A., Domes M., Dugan-Rocha S., Dukov B.C., Dunn P.,
RA Admis M., Salush R., Karpen G.M., Geraz C., Ferriera S., Fleischmann W.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Houck J.,
RA Kinmel B.E., Kodira C.D., Kratt C., Kravitz S., Kulp D., Lai Z.,
RA Kinmel B.E., Kodira C.D., Kratt C., Kravitz S., Kulp D., Lai Z.,
RA Kinmel B.E., Kodira C.D., Kratt C., Kravitz S., Kulp D., Lia X.,
RA Hostin D.M., Nelson K.A., Nixon K., Nusskern D.R., Woshrefi A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Haston D.R., Nelson K.A., Nixon K., Nusskern D.R., Smith T.,
RA Reinert K., Resse M.G.,
RA
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CG8421 protein.
ASPH OR CG8421 OR CG18658
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01-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGTVEATVEATTEATTEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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Pred. No. 5.5;
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                                                     H.O.,
                                                                                                                                                                                                                                                                                                                                                    K.A.,
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Science

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RESULT
Q9GQ82
ID Q9G
AC Q9G
DT 01
DT 01
DT 01
DT 02
COC DC CC
COC CC
RN (1)
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Best Local S
Matches 34
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                                                                             Q9GQ82;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last seque)
01-MAR-2003 (TrEMBLrel. 23, Last annot Asparryl beta-hydroxylase variant 1 (C ASPH OR CG8421 OR CG18658.
Drosophila melanogaster (Fruit fly).
          Eukaryota; Metazoa; Arthropoda; Insueoptera; Endopteryota; Diptera; Brachycera; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AE003808; AAF58064.2; -. FlyBase; FBgn0034075; Asph. SEQUENCE 556 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman G., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith B., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Adams M.D., Celniker
Submitted (MAR-2000)
                                                                                                                                                                                                    Q9GQ82
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SEQUENCE FROM N.A.
Crosby M.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                          TKDVTATVLDKNNISSKST
                                                                                                                                                                                                                                                                                                                                                           PLTEELEEELEEEEPTEEDEPAADEEYEEDEDEENNA--GENITAEDAEEEEEEEDNDD
                                                                                                                                                                                                                                                                                                                                                                                           PVFKKIEEKKEEENKPT-----FDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDS
                                                                                                            (TremBirel. 16, Created)
(TremBirel. 16, Last sequence update)
(TremBirel. 23, Last annotation update)
                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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e EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 101.5;
Pred. No. 8.3;
                                                                                                                                                                                                                                                                                          212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B420980CBD6C357A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                        785
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                                                                  Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   databases
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                                                                Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                556;
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Rogers Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              -NLSKOTFIK
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.
RA Burdon R.C., Rogers Y.-H.C., Blazef R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Horkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerbios B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Gebablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Gebablos B., Delcher A., Donge S., Mays A.D., Dew I., Dietz S.M.,
RA Harris N.I., Harvey D., Helman T.J., Gelbart W.M., Glasser K.,
RA Harris N.I., Harvey D., Helman T.J., Gu Z., Guan P., Harris M.,
RA Harris N.I., Harvey D., Helman T.J., Wei M.-H., Tleeyam C.,
RA Harris N.I., Molira C.D., Kraft C., Kranicz J.R., Houck J.,
RA Harris N.I., Molira C.D., Kraft C., Kranicz J.R., Mcheson D.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kranicz S., Kulp D. Lai Z.,
Liang Y., Lai Z., Liang Y., Lin X.,
RA Merkulbv G., Milshina N.V., Mobarry C., Morris J., Moshreti A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Bealeb J.M.,
RA Melson D.R., Nelson K.A., Stapleton M., Strong R., Sin E.,
RA Shue B.C., Siden-Klamos I., Singson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Klamos I., Singson M., Strong R., Sin E.,
RA Sheng X.H., Zhong F.N., Zhang W., Zhang G., Zhao Q., Zheng L.,
Ra Sheng X.H., Zhong F.N., Zhang W., Zhang S., Yao Q.A.,
Ra Harris N.E., Ra Shen H.N., Smith H.O.,
Ra Sheng X.H., Shan H., Sh
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Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Balzon J., An H., Baldwin D., Banzon J. Besson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
A. Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
C. Hoskins R.A., Hostin B., Moshrefi A.,
C. McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
C. McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
C. McIntosh T.C., Moy M., Murphy B., Patel S., Pfeifer B.,
C. McIntosh T.C., Moy M., Murphy B., Patel S., Pictor C., Tyler D.,
C. M. McIntosh T.C., Moy Park S., Patel S., Pictor C., Tyler D.,
C. M. Milliams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
C. Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
C. Milliams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
C. Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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"Aspartyl beta -Hydroxylase
Isoform of Asph Missing the
Junctin.";
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Dinchuk J.E., Henderson N.L., Burn T.C., Huber R.,
O'Neil K.T., Focht R.J., Scully M.S., Hollis J.M.,
                     Hradecky P.,
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01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2002 (TrEMBLrel. 22,
Merozoite surface protein 3
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                           MEDLINE=20416497; PubMed=10960178;
Okenu D.M.N., Thomas A.W., Conway D.J.;
"Allelic lineages of the merozoite surface protein
Plasmodium reichenowi and Plasmodium falciparum.";
Mol. Biochem. Parasitol. 109:185-188(2000)..
EMBL; AJ252287; CAB85901.1; -.
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InterPro; IPR001440; TPR.
InterPro; IPR00525; Zn MTDeptdse.
PROSITE; PS00142; ZINC_PROTEASE; 1
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01-JAN-1998
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SEQUENCE
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Tyers M., I
"Human CPR
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                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
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      Edwards M.C., Liegeois
Tvers M., Elledge S.J
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MEDLINE=98043401; PubMed=9383053;
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i; Hominidae;
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                   R.A.,
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Genetics 147:1063-1076(1997).
EMBL; AF011794; AAB69314.1; -.
InterPro; IPR004238; LEA.
Pfam; PF02987; LEA; 1.
                                                                                                                                                                                                                                                                                                       Hypothetical protein. SEQUENCE 1130 AA;
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                                                                                                                                                                                                                                                                                                                                                                               Nature 419:498-511(2002).
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Last annotation updat
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6; Mismatches
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Pred. No. 23;
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                      Quail M., Barrell B.;
Submitted (SEP-2002) to the E
EMBL; AL844506; CAD50814.1; -
Hypothetical protein.
SEQUENCE 1859 **
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Best Local Similarity
Matches 30; Conserv
Query Match
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Q8IC27;
01-MAR-2003
01-MAR-2003
01-MAR-2003
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01-MAY-1997
01-MAY-1997
01-MAR-2003
                                                                                                                                                                                       Plasmodium falciparum
Eukaryota; Alveolata;
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                          Hypothetical protein. PF07_0016.
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Hypothetical protein.
SEQUENCE 211 AA; 23955
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"The sequence of C. (
Submitted (FEB-1997)
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Rhabditidae; Peloderinae;
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Submitted (SEP-2001) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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STRAIN-Bristol N2;
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Science 282:2012-2018(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HRKEDLOREEHSOKSDSTKDVTATVLDKNNISSKSTTNNPNK 154
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7 (TrEMBLrel. 03, Las
3 (TrEMBLrel. 23, Las
11 24.0 kDa protein.
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    12
                                      218376 MW;
                                                                                                                                                                                                             Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                      Harris
                                                                                                                                                                                                                                 (isolate 3D7)
                                                                                                                                                                                                                                                                                            23,
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EMBL/GenBank/DDBJ databases.
                                                                                               EMBL/GenBank/DDBJ
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Last
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Pred. No.
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                                      2266544164BD360C CRC64;
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RESULT
Q812Z6
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RA Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
RA Cronin A., Bowles R., Davis P., Dear P., Dearden F., Doggett J.,
RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
RA Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA Cliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch B.,
RA Cliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch B.,
Ra Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
Reguer K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
RA Raylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
Sulston J.E., Craig A., Newbold C., Barrell B.G;
"Sequence of plasmodium falciparum chromosomes 1, 3-9 and 13.";
RMLL, ALS29355; CAD51734.1; -.
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Best Local Similarity
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Q8I3A0;
01-MAR-2003
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01-MAR-2003
                                                                               Q8I2Z6;
01-MAR-2003
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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RESULT 33
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A Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
A Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
A Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
A Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
A Humphray S., Monfortov B., Kyes S., Larke N., Lawson D., Lenmard N.,
A Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lenmard N.,
A Line A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,
Oliver K., Ormond D., Price C., Quall M.A., Rabbinowitsch B.,
Oliver K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
A Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
A Sulston J.E., Craig A., Newbold C., Barrell B.G,
Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
Newbold C., Barrell B.G,
Neurola C., Chang R., Canalla C., Barrell B.G,
Neurola C., Chang R., Canalla C., Barrell B.G,
Neurola C., Chang R., Canalla C., Barrell B.G,
Neurola C., Chang R., Canalla C., Barrell B.G,
Neurola C., Chang R., Canalla C., Barrell B.G,
Neurola C., Chang R., Canalla C., Barrell B.G,
Neurola C., Chang R., Canalla C., Barrell B.G,
Neurola C., Chang R., Canalla C., Barrell B.G,
Neurola C., Chang R., Canalla C., Barrell B.G,
Neurola C., Chang R., Canalla C., Barrell B.G,
Neurola C., Chang R., Canalla C., Barrell B.G,
Neurola C., Chang R., Canalla C., Barrell B.G,
Neurola C., Chang R., Canalla C., Barrell B.G,
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Best Local S
Matches 48
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Q9VQV0;
01-MAY-2000
01-OCT-2002
            MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Everis S.E., Richards S., Ashburner M., Henderson S.N.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B., Bayraktaroglu D., Bolshakov S.,
Berten M. B., Bayran M. B., Bayraktaroglu D., Bolshakov S.,
Berten M. B., Bayran M. B., Bayraktaroglu B., Bolshakov S.,
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NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hraapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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CG31958 OR CG10022.
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                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7227;
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Botchan M.R.,
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22,
23,
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Bouck J.,
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Pred. No. 5.5;
25; Mismatches
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  Brokstein
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RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.
RA Mount S.M., Woy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Syler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
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RA Zheng K.H., Zhong F.N., Zhong W., Zhong G., Zhao Q., Zheng L.,
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RA Zheng K.H., Zhong W., Rubin G.M., Venter J.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                    Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Seatrle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome.",
              InterPro; IPR002048; EF-hand.
Pfam; PF00036; eFhand; 3.
ProDom; PD000012; EF-hand; 1.
SMART; SM00054; EFh; 3.
PROSITE; PS00018; EF HAND; 1.
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Evans C.A., Gocayne J.D.,
Banzon J., An H., Baldwin
Carlson J.W., Center A., C
                                                                                                                                                                     Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases EMBL, AE003578; AAF51062.2; -.
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                                                                                                                               FlyBase; FBgn0051958;
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DelCher A., Deng Z., Mays A.D., Dew I., Dietz
Dup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.
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Dietz S.M.,
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A Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
A Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
A Cronin A., Davise R., Davis P., Dear P., Dearden F., Doggett J.,
A Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
A Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
A Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
A Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
A Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
A Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
A Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
A Cliver K., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,
A Oliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch E.,
A Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
A Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Stevens K.,
A Rajandream M.A., Rutter S., Smith R., Squares S., Stevens K.,
A Rajandream M.A., Rutter S., Smith R., Squares S., Stevens K.,
A Taylor K., Tharp S., Smith R., Squares R., Squares S., Stevens K.,
A Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
A Sulston J.S., Craig A., Newbold C., Barrell B.G;

Network M. C., School C., Barrell B.G;

Network M. C., School C., Barrell B.G.,

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EMBL; AL929354; CAD51629.1;
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24.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Davies P., Mungal K., Benchurcher C., Quail M., Banchot to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                           525287 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Atkin R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23,
                                                                                                                                                                                                                                                                                                      26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .'
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                     Score 98; I
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Churcher C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3D7.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          543F0480E11D9EC1 CRC64;
                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                           542206173C29567A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baker S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4524
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                                                                                                                                                                                                                                                                                                                                                                DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .8
                                                                                                                                                                                                                                                                                                                                     .5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barron A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Berriman M.,
Barrell B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harris B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53;
                                                                                                                                                                                                                                                                                                      75;
                                                                                                                                                                                                                                                                                                                                                                Length 4524;
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                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brooks K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harris D.,
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                                                                                                                                                                                                                                                                                                   Gaps
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Best Local
                                                                                                                    Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Archropoda; Hexapoda; Insecta;

Neoptera; Endopterygota; Diptera; Brachycera; Musco
Ephydroidea; Drosophilidae; Drosophila.

NCBI TaxID=7227;
                                                                                                                                                                                                              GM05229p.

ASPH OR CG8421 OR CG18658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 419:498-511(2002).
EMBL; AE014842; AAN35996.1; -.
Hypothetical protein.
SEQUENCE 449 AA; 52812 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-22255705; PubMed=12368864;
Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K. Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S., Perten M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Frasser C.M., Barrell B.,
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum
Eukaryota; Alveolata;
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                        01-DEC-2001
01-OCT-2002
                                                                                                                                                                                                                                                                                                                 Q95S93;
01-DEC-2001
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01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8IHW3
                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome sequence of the human malaria parasite Plasmodium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKKKRKIIESEEETNINSDDEEEEEEYQRKKQKKQKNSNVSTLSLLEKKKKKKRDSESSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IKPVFKKIE-----EKKEEE------NKPTFDV-----SKKKDNPQVN
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MKNIIQKET-EKKQDTVKEV--
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                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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25.1%; Pred. No. 13;
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Apicomplexa; Haemosporida; Plasmodium.
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19,
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Last
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85B62272D6257C68 CRC64;
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                                                                                                                                                                                                                                                                        sequence update) annotation updat
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                                                                                                                                                                   Muscomorpha;
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                                                                                                                                                                                       Pterygota;
    S., Wan K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49;
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    RESULT 38
Q93424
ID Q9342
AC Q9342
DT 01-JP
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Q9K5S1
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  Q93424; P90801;
01-JAN-1999 (TrEMBLrel. 09,
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yu C., Lewis S.E., Rubin G.M., Submitted (CCT-2001) to the EME EMBL; AY060905; ABJAL28453.1; -. FlyBase; FBGD0034075; Asjh. SEQUENCE 556 AA; 63089 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2003 (TrEMBLrel. 23,
Hypothetical protein BH4017,
Q93424
                                                                                                                                                                                                                                                                                                              Hypothetical SEQUENCE 6
                                                                                                                                                                                                                                                                                                                                                                                       halodurans and genomic sequence comparison Nucleic Acids Res. 28:4317-4331(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus halodurans.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical BH4017.
                                                                                                                                                                                                                                                                                                             Pfam; PF04740; Transposase 30; Hypothetical protein; Complete SEQUENCE 614 AA; 70704 MW;
                                                                                                                                                                                                                                                                                                                                                                         EMBL; AP001520; BAB07736.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Takami H., Nakasone K., Takaki Y., Maeno G
Fuji F., Hirama C., Nakamura Y., Ogasawara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                   dorikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                    'Complete genome sequence of the alkaliphilic bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                      nterPro; IPR006829; Transposase_30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                             386
                                                                                                     110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34;
                                                                                                                                                                                                                        თ
                                                                                                                                                                                                                                                      41;
                                                                                                                                                                                                                                                                     Similarity
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                                                                      GKVIGIVDLGRKYHKGKEDLERRLSKSQIE
                                                                                                   NESHRKEDLQREEHSQKSDSTKDVTATVLD 139
                                                                                                                                  FAGRNIASQL-
                                                                                                                                                              FEGKKDAGYVINLSKDTFIKPVFKKIEEKK--BEENKPTFDVSKKK----DNPQVNHSQL
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                                                                                                                                                                                                                                                      Conservative
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                      26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 97.5;
Pred. No. 17
                                                                                                                                                                                                                                                                  Score 97.5;
Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148
                                                                                                                                                                                                                                                                                                           proteome.
2E3FD6EC74E0294C CRC64;
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                                                                                                                                                                                                                                                       Mismatches
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annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus
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                                                                                                                                                                                                                                                                                    614;
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RESULT
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Best Local S
Matches 42
MEDLINE=22255705; PubMed=12368864;
MEDLINE=2255705; PubMed=12368864;
Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.
Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Eisen J.A., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Valdya A.B.,
Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
DOMAIN
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01-MAR-2003
                                                                                                                                                                                                                    Q8I5T1;
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditidae; Peloderinae; Caer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        precursor.
                                                                                                                                                                Plasmodium
                                                                                                                                                                            PFL0600W.
                                                                                                                                                                                                01-MAR-2003
                                                                                                                                                                                                            01-MAR-2003
                                                                                                                                                                                                                                             Q815T1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z81053; CAB02877.1; -
HSSP; P10968; 2CWG.
WormPep; E02A10.2; CE09116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=6239;
                                                                                                          STRAIN=3D7
                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                      Eukaryota;
                                                                                                                                                                                     Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BRISTOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nterPro;
                                                                                                                                                                                                                                                                 39
                                                                                                                                         ryota; Alveolata;
_TaxID=36329;
                                                                                                                                                                                                                                                                                                                         119
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PR01228; EGGSHELL.
                                                                                                                                                                                                                                                                                                                       QREEHSQKSDSTKDVTATVLDK 140
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23
385
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(TrEMBLrel. 23
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                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                     protein.
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190
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                                                                                                                                                    Apicomplexa;
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23, Last annotation update)
ch 37.0 kDa protein E02A10.2
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                                                                                                                                                                                                                                                                                                                                               EP--KKEEEKKEEEQKE--EVEKKEE----EEKKDEEPKKEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oda; Chromadorea;
Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                     24;
                                                                                                                                                                                                                     Created)
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Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 97;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ
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HYPOTHETICAL
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                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                3D7)
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                                                                                                                                                                                                                                                                                                  371
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                                                                                                                                                                                               sequence update) annotation updat
                                                                                                                                                   Haemosporida;
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                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                                                                                                                                                                                                     48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRC64;
                                                                                                                                                      Plasmodium
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RESULT
Q9STN4
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Best Local S
Matches 35
Query Match
Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical 109.0 kDa protein.
T28D5.30 OR AT4G08340.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosida eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE014846; AAN36209.1;
Hypothetical protein.
SEQUENCE 558 AA; 66487 M
                                                                            EMBL; AL109819; CAB52556.1; -.
EMBL; AL161511; CAB77959.1; -.
InterPro; IPR001760; Opsin.
InterPro; IPR003653; SUMO protease.
Pfam; PF02902; Peptidase C48; 1.
PROSITE; PS00238; OPSIN; 1.
                                                                                                                                                                                                        SEQUENCE FROM N.A.
Lennard N., Quail M.,
Mewes H.W., Lemcke K.,
                                                                                                                                                                                                                                                                                                                     Bevan M., Lenn
Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9STN4;
01-MAY-2000
                                                               PROSITE; PS50600; ULP_PROTEASE;
                                                                                                                                                EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Bevan M., Lennard N.,
                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9STN4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature
                                            Hypothetical protein SEQUENCE 988 AA;
                                                                                                                                                                                             Submitted
                                                                                                                                                                                                                                                                                               Submitted
                                                                                                                                                                                                                                                                                                            Schueller
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                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97
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                                                                                                                                                                                                                                                    idopsis sequencing project;
ad (AUG-1999) to the EMBL/GenBank/DDBJ
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 31;
 Score 97; DB Pred. No. 34; 31; Mismatches
                                                                                                                                                                                            s B., Rajandream M
r K.F.X.;
EMBL/GenBank/DDBJ
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Pred. No. 18;
31; Mismatches
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Mayer K.F.X., I
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19

NGKEMSSTIVSEEDFILPVYKGELEKGY----

-QFDGWEISGFEGKKDAGYVINLSKDTF

Db 502 HVLGAKDVTDVSDPTDKVGVNDVTDASDPTE 532	Qy 123 HSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 154	Db 442 VEPVGDDVRSSGDMSPNPSAANNVREGPATFDIMESEDNPGRDNVAPMEDHIRSEVQLSP 501	EI	::: :     ::  :     ::    :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  ::::	
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Title:
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Maximum Match 100%
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Gapop 10.0 ,
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98	76	4.10	ωĸ	, ,	Result
107.5	119	615	848	848	Score
12.7	14.0	72.5	100.0	100.0	% Query Match
665	778	117	2140	773	% Query Match Length DB
21	23	23	24	22	BB
AAG47777 AAB18278	ABP39023	AAW55096 ABP54590	ABU01020	AAB48343	SUMMARIES
Arabidopsis thalia Plasmodium falcipa	Staphylococcus epi	Streptococcus pneu S. pneumoniae SP04	streptococcus pneu	S. pneumoniae Sp13	Description

			£			
. Human secreted pro	ABB12281	22	2515	10.4	88	45
Human protein SEQ	AAM79319	22	817	10.4	88	44
Human protein SEQ	AAM79318	22	817	10.4	88	43
Human protein sequ	AAB94584	22	258	10.4	88	2
Candida albicans e	ABP73992	23	225	10.4	88	41
Shrimp white spot	AAG85008	22	1141	10.4	88.5	40
Drosophila melanoc	ABB64828	22	281	10.4	88.5	9
Herbicidally activ	ABB93341	23	296	10.5	89	8
Drosophila melanoc	ABB58704	22	1408	0	89.5	37
S. aureus trigger	AAY03189	20	525		89.5	36
	ABP73570	23	516	•	89.5	S
Chlamydia pneumoni	AAY35091	20	511	0	89.5	ω 4
S. aureus trigger	AAY03190	20	402		89.5	ü
Drosophila melanog	ABB58769	22	1183	0	90	ω 2
Shrimp white spot	AAG85023	22	922	0	90.5	3
Human polypeptide	ABP68963	23	801	0	90.5	30
Human colon cances	AAB53319	21	758	0	90.5	29
Human cell cycle :	AAY44364	21	757		90.5	28
Candida albicans e	ABP73209	23	635	0	90.5	27
Human ORFX ORF2661	AAB42897	21	209	0	90.5	26
Staphylococcus epi	ABP40312	23	902	0	91	25
Staphylococcus epi	ABP38188	23	442	0	91	24
Staphylococcus epi	ABP40822	23	309	0	92	23
	AAG82397	22	299	10.8	92	22
Pathogen specific	ABJ18979	24	645	0	92.5	21
Staphylococcus epi	ABP56879	24	654	$\vdash$	93.5	20
Pathogen specific	ABJ19106	24	645	11.0	93.5	19
Plasmodium falcipa	AAB18272	21	2500	ч	96	18
Staphylococcus lug	AAE20967	23	2060	$\mathbf{r}$	96.5	17
Arabidopsis thalia	AAG37132	21	476	1.	96.5	16
Arabidopsis thalia	AAG37133	21	456	۲	96.5	15
Arabidopsis thalia	AAG37134	21	408	•	96.5	14
Novel human diagno	ABG16636	22	2519	11.5	97.5	13
Human MDDT-2 prote	ABP55393	24	0	•	99.5	12
	ABP55413	24		11.7	99.5	11
Drosophila melanog	ABB61977	22	564	12.0	101.5	10

## ALIGNMENTS

RESULT 1 AAB48343 ID AAB4

AAB48343 standard; Protein;

773 AA

AAB48343;

20-APR-2001

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Immunogenic; Sp128; Sp130; pneumococcal; otitis media; nasopharyngeal;
bronchial; lung; blood; infection; immune response; immunotherapy;
antibacterial; auditory; vaccine.
New vaccines comprising Sp128 or Sp130 polypeptides, for treating and
                              WPI; 2001-112197/12.
N-PSDB; AAC84742.
                                                                                                                                                                                                                                                   Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                          S. pneumoniae
                                                                          Adamou JE,
                                                                                                                                    10-JUN-1999;
                                                                                                                                                               09-JUN-2000; 2000WO-US15925
                                                                                                                                                                                                                      WO200076540-A2.
                                                                                                                                                                                            21-DEC-2000.
                                                                                                       (MEDI-) MED IMMUNE INC
                                                                            Choi GH;
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Best Local S
Matches 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to novel immunogenic polypeptides, Sp128 and Sp130 from S. pneumoniae. Vaccines comprising the polypeptides are useful for the treatment and prevention of pneumococcal infections, particularly infections caused by Streptococcus, such as otitis media, nasopharyngeal, bronchial, lung or blood infections. The antigens are used as immunogenic agents to stimulate an immune response. The antisera and antibodies may also be used in diagnosing and treating pneumococcal infections. Recombinant polypeptides serve as a mechanism for tsimulating production of antibodies for use in passive immunotherapy, diagnostic reagents, and as reagents in other processes such as affinity chromatography. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preventing pneumococcal infections, particularly infections caused by Streptococcus, e.g. otitis media, nasopharyngeal, bronchial, lung or blood infections -
                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae infection; immunogen; antigen; diagnosia; ADIS; bacterial pneumonia; asplenia; heart disease; lung disease; alcoholism; kidney disease; diabetes; immunosuppressive disorder; otitis media; pneumococcal septicaemia; sinusitis; meningitis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                          WPI; 2000-195301/17.
N-PSDB; AAZ91806.
                                                                                                                                                              27-JUL-1998;
19-MAR-1999;
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                treatment
                            Streptococcal
                                                                                                     Le Page
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                                                                                                                                  (MICR-) MICROBIAL TECHNICS LTD
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               and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              (first
                proteins and polynucleotides useful prophylaxis of bacterial infections
               prophylaxis
                                                                                                                                                                                                                                                                                                                                                                                                 pneumoniae protein sequence
                                                                                                     Wells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,
                                                                                                                                                              98GB-0016336.
99US-0125329.
                                                                                                                                                                                                         99WO-GB02452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                     JM,
                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54pp; English.
                                                                                                     Hanniffy SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 848; DB 22;
Pred. No. 1.1e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                      Hansbro PM;
                                                                                                                                                                                                                                                                                                                                                                                                   ID3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                              for diagnosis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  773;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 iragments) are useful as immunogens or antigens. Immunogenic or antigenic compositions comprising the proteins are useful as vaccines and also in diagnostic assays. The sequences are useful for the detection or also in diagnostic assays. The sequences are useful for the detection or diagnostic of S. pneumoniae infection, by contacting a sample to be tested with them. Agents capable of antagonising, inhibiting or interfering with the function or expression of the protein or polypeptide are useful in medical compositions in the treatment or prophylaxis of S. pneumoniae infection. As the sequences can be used to treat S. pneumoniae infection, they can be used to treat bacterial pneumonia, which has high rates in young children, the elderly, and in patients with predisposing conditions such as asplenia, heart, lung and kidney disease, diabetes, alcoholism, or with immunosuppressive disorders, especially AIDS. They can also be or with immunosuppressive disorders, especially AIDS. They can also be
                                                                                                                                                                                                                                                                                                                                                                Bacterial meningitis; pneumonia; sepsis; otitis ear infection; antiinflammatory; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                              S. pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                            N-PSDB;
                                                                                                         Masignani V,
                                                                                                                                                                                      27-MAR-2001; 2001GB-0007658
                                                                                                                                                                                                                       27-MAR-2002; 2002WO-IB02163
                                                                                                                                                                                                                                                                                   WO200277021-A2
                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae type 4 strain
                                                                                                                                                                                                                                                                                                                                                auditory;
                                                                                                                                                                                                                                                                                                                                                                                                                                              11-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU01020 standard; Protein; 2140 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 41-42; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABU01020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          used to treat pneumococcal septicaemia,
                                                                                                                                         (GENO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1923
                                                           2003-040579/03
DB; ABX06302.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence represents a Streptococcus pneumoniae protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                щ
                                                                                                                                        CHIRON SPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTVKEFILNKDTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDG
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                                                                                                                                                                                                                                                                                                                                                  respiratory; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2120 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                         GENOMIC RES
                                                                                                                                                                                                                                                                                                                                                                                                              type 4 strain protein from
                                                                                                         Tettelin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 848; DB 21;
Pred. No. 4.3e-74;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            otitis media, sinusitis, and
                                                                                                                                                                                                                                                                                                                                                                                                              coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    derivatives
                                                                                                                                                                                                                                                                                                                                                                    immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                region
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New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media

Claim 1; SEQ ID No 1180; 56pp; English.

fragment,

or ear infection

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteins, treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the nucleic acid cited above or fragments between nucleotides 8-100 of a sequence not defined in the specification, for amplifying a target sequence contained within a Streptococcus nucleic acid sequence, where the first primer is substantially complementary to the target sequence and the second primer is substantially complementary to the complement of the target sequence, and where the parts of the primers having substantial complementarity define the termini of the target sequence to be amplified, assay comprising contacting a test compound with the protein, and determining whether the test compound binds to the protein and a correction and accomposition between the test compound with the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein and a Streptococcus pneumoniae bacterium, where one or more genes encoding the proteins has been rendered inactive. The proteins, nucleic acid molecules, antibody and compositions are useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, particularly S. pneumoniae, such as pneumonia, sepsis, otitis media or ear infection. They are also useful in developing vaccines, diagnostics and antibiotics. The methods are useful for identifying immunodominant proteins. The present sequence is one of the 2469 proteins expressed by the identified coding regions from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragmexpressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS56454. Also included are an antibody which binds one of the
07-MAY-1998
                                                                                 Streptococcus
                                                                                                                         detection; pneumonia; otitis
                                                                                                                                                Streptococcus pneumoniae; antigen; vaccine; infection; diagnosis;
                                                                                                                                                                                           Streptococcus
                                                                                                                                                                                                                                      02-OCT-1998
                                                                                                                                                                                                                                                                                 AAW55096;
                                                                                                                                                                                                                                                                                                                            AAW55096 standard; Protein; 117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTVKEFILNKDTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDG
                                                                                                                                                                                                                                                                                                                                                                                                                                      ESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTVKEFILNKDTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2140 AA;
                                                                                                                                                                                                                                      (first entry)
                                                                                 pneumoniae
                                                                                                                                                                                         pneumoniae SP0043 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                            media; meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 848; DB 24;
Pred. No. 4.4e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 24;
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23-MAY-2002 US2002061545-A1

22-JAN-2001; 2001US-0765272.

97US-0961083

(CHOI/) CHOI G

Streptococcus pneumoniae

X H

04-SEP-2002

(first entry)

Streptococcus pneumoniae; epitope; vaccine; antigenic protein; antibacterial; Streptococcal infection; detection.

S. pneumoniae SP043 protein sequence SEQ ID NO:68

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                                                        ABP54590
                                                                        RESULT 5
                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                     are used to detect Streptococcus infection (by usual hybridisation or amplification methods), also for isolating Streptococcus genes or their allelic variants. The protein can be used similarly to detect specific antibodies in standard immunoassays, especially for diagnosing or monitoring infections. Antibodies which bind the protein are used to detect corresponding antigens, to purify the protein and for passive immunisation (optionally coupled to a toxin). Vaccines are administered, e.g. by injection, orally or through the skin, typically at 0.01-1000 (especially 10-300) mu g/ml per dose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a protein from Streptococcus pneumoniae. The nucleic acid sequence encoding the Streptococcus pneumoniae protein can be useful in vaccines for inducing protective antibodies against Streptococcus pneumoniae, for treatment or prevention of infection e.g. pneumonia, otitis media or meningitis. Probes based on the nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 62; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-272224/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Choi GH,
ABP54590;
                                  ABP54590 standard; Protein; 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protective or therapeutic vaccines,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                          117;
                                                                                                                                                                         108
                                                                                                                                     13
                                                                                                                                                                                                                                        48 YKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSK 107
                                                                                                                                                                                                              1 YKGELEKGYOFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSK 60
                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                         KKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 164
                                                                                                                                   KKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hromockyj A,
                                                                                                                                                                                                                                                                                                                                                                         117 AA;
                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                               72.5%; Score 615; DB 19; 100.0%; Pred. No. 7.3e-53;
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                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kunsch CA;
                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                 Length 117;
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RESULT 6
AAG81779
ID AAG8
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Best Local S
Matches 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABQ84792 to ABQ84904 represents nucleic acids which encode the Streptococcus pneumoniae antigens given in ABP54557 to ABP54669. The S. pneumoniae antigens have antibacterial activity and can be used in vaccines. The S. pneumoniae antigens can also be used to prevent or attenuate a Streptococcal infection in an animal. The polynucleotides encoding the S. pneumoniae antigens can be used to detect Streptococcus nucleic acids. ABQ84905 to ABQ85130 represent primers used in the cloning of S. pneumoniae ORFs (open reading frames) which are used in an example from the present invention.
                     N-PSDB; AAH52629
                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis.

 S. epidermidis

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                                                                                                                                                                                                                                                    09-NOV-2000; 2000WO-US30782
                                                                                                                                                                                                                                                                                                                                                         WO200134809-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-SEP-2001
                                                                                               Kimmerly WJ;
                                                                                                                                                                                                  09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG81779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG81779 standard; Protein; 746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 29; 70pp; English.
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                                                                                                                                                  (GLAX ) GLAXO
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(DILL/)
(DOUG/)
(FANN/)
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                                             2001-316495/33.
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DILLON P J.
DOUGHERTY B.
FANNON M R.
ROSEN C A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      frame protein sequence SEQ ID NO:652.
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Pred. No. 7.3e-53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 117;
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local (
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                            Doucette-Stamm
                                                                                                                                                                  14-AUG-1997;
08-NOV-1997;
                                                                                                                                                                                                                                                                                                                                       30-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP39023;
                                                                                                                                                                                                                                                                                                                                                                                                          US6380370-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP39023 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           no sequences are present for SEQ ID NO:4455 to 4464.
                                                                                               (GENO-) GENOME THERAPEUTICS
                                                                                                                                                                                                                                                                    L3-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -EISGFE-----GKKDAGYVIN--LSKDTFIKPVFKKIEEKKEEENKPTFDVS----K 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDSVNAQSLKP----ITIGNGKQIKQQSVKSGTKVLPHSKVMLMTDGELTMP-DMTGWTK 639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            746 AA;
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97US-064964P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         epidermidis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                epidermidis ORF amino acid sequence SEQ ID NO:3868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          epidermidis.
                            Bush D;
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             reading frame; ORF; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22
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RESULT 8
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Best Local Similarity
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25-FEB-1999

05-MAR-1999

09-MAR-1999

23-MAR-1999

25-MAR-1999

01-APR-1999

06-APR-1999

06-APR-1999

19-APR-1999

19-APR-1999

21-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                     25-FEB-2000;
                                                                                                                                                                                                                                                                       06-SEP-2000
                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                             Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 60255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG47777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG47777 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID 3868; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
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DB; ABN91568.
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                  99US-0123180.
99US-0125588.
99US-0126264.
99US-0126788.
99US-0126795.
99US-0127462.
99US-0128234.
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99US-0128715.
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99US-0130891.
99US-0131449.
99US-0132048.
99US-0132407.
99US-0132484.
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RESULT 9
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Best Local S
Matches 36
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                                                                                                                              (HOFF/) HOFFMAN S.
(CARU/) CARUCCI D.
(GARD/) GARDNER M.
(VENT/) VENTER J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide.
Proteins encoded by chromosome 2 of the human malarial parasite,
                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-NOV-2000
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                                             WPI; 2000-365347/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum chromosome 2 related protein
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                                                                                     Carucci
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99US-0161405.
99US-0161359.
99US-0161359.
99US-0161361.
99US-0161361.
99US-0161992.
99US-0161992.
99US-0161993.
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99US-0159638

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                                                                                     Gardner M,
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Pred. No. 0.06;
32; Mismatches
                                                                                        Venter JC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Also described are: (1) nucleotide sequences (1) vaccines against P. falciparum infection comprising (I) or (II).

(I) and (II) are useful for the development of vaccines against P. falciparum infection. (I) and polyclonal antisera or a monoclonal P. falciparum infection. (I) and polyclonal antisera or of (I), are antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, useful in the detection of infection with P. falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in P. falciparum. Sequencing of the Plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito
Venter JC,
                                                                 23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                   23-MAR-2001; 2001WO-US09231.
                                                                                                                                                       27-SEP-2001
                                                                                                                                                                                       WO200171042-A2
                                                                                                                                                                                                                       Drosophila melanogaster
                                                                                                                                                                                                                                                         pharmaceutical.
                                                                                                                                                                                                                                                                         Drosophila; developmental biology; cell signalling;
                                                                                                                                                                                                                                                                                                         Drosophila melanogaster polypeptide SEQ ID NO 12723
                                                                                                                                                                                                                                                                                                                                             26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                               ABB61977;
                                                                                                                                                                                                                                                                                                                                                                                                               ABB61977 standard; Protein; 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             specifically mentioned within the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70287 and AAB18114 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P. falciparum infection -
                                 (PEKE )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218
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                                 PΕ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KVEENKKSDDHKIEEVKKVEEHEEDEEE--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KDTGEVSELKPHRVT-VTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEI--SGF
                                 CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              665 AA;
Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 321-322; 577pp; English
                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the human malarial parasite,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.5%; Score 106; DB 24.3%; Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              describes proteins and
Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -VKEGVKELEEKKKEEKISDDHKVEENKKSDDHKVEENKKSDDH
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Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 665;
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                                                                                                                                                                                                                                                                           insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (I); and (2)
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ID ABPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiallergic; antiinflammatory; antianaemic; antiparkinsonian; nootropic; anticonvulsant; antiinfertility; antiarteriosclerotic; antiasthmatic; immunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological; antidiabetic; nephrotropic; antigout; thyromimetic; neuroprotective; osteopathic; antiarthritic; antiparasitic; antihelminthic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL11840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                     uropathic; ophthalmological; antirheumatic; haemostatic; antibacterial; virucide; protozoacide; fungicide; gene therapy; cell proliferative; cancer; developmental disorder; neurological disorder; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of the development of th
05-APR-2001;
13-APR-2001;
                                                     30-MAR-2001;
                                                                                                                29-MAR-2002; 2002WO-US09809.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; MDDT; n
antiallergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human MDDT-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence data for this patent did not form specification, but was obtained in electronic at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 12723; 21pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                             WO200278420-A2
                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                          reproductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP55413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP55413 standard; protein; 1384
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                                                                                                                                                                        10-OCT-2002
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2001US-280387P.
2001US-282335P.
2001US-283663P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               molecules for disease detection and treatment; anti-HIV;
                                                                                                                                                                                                                                                                                                                                                disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein SEQ
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Pred. No. 0.29;
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                                                                                                                                                                                                                                                                                                                                                disorder; inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25;
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RESULT 12
ABP55393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes 23 human molecules for disease detection CC and treatment (MDDT-1 to 23) (see ABP55392 to ABP55414). The human CC MDDT-1 to 23 proteins (I) are encoded by the sequences given in ABQ83859 to ABQ83881. (I) can have various activities depending on the cells and Ctissues in which they are expressed. These activities include: anti-HIV; CC antiallergic; antiinfertility; antianaemic; antiparkinsonian; nootropic; anticonvulsant; antiinfertility; antiarteriosclerotic; antiparksthmatic; CC immunosuppressive; antityproid; cytostatic; hepatotropic; dermatological; antidiabetic; nephrotropic; antiagrassitic; antiparkinic; antiparatic; costeopathic; antiarthricii; antiparasitic; neuroprotective; costeopathic; antiarthricii; antiparasitic; neuroprotective; costeopathic; ophthalmological; antitheumatic; haemostatic; antiparatic; curopathic; ophthalmological; antitheumatic; haemostatic; antibacterial; curopathic; ophthalmological; antitheumatic; haemostatic; antibacterial; curopathic; ophthalmological; antitheumatic; haemostatic; antibacterial; curopathic; ophthalmological; antitheumatic; haemostatic; antibacterial; curopathic; ophthalmological; antiparasitic, prolymuclectides conductive used for diagnosing, curopathic; ophthalmological; antiparative (e.g. cancer), developmental curopathic; particularly cell proliferative (e.g. cancer), developmental curopathic; particularly cell proliferative; e.g. cancer), developmental curoparatic, protozoal or helminthic infections. They are also useful in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of proteins associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ramkumar J, Swarren BA, Nguyen DB, Warren BA, Nguyen DB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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18-JAN-2002; 2002US-350702P
25-JAN-2002; 2002US-351749P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human molecules for disease detection and treatment, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (INCY-) INCYTE GENOMICS INC.
                                                                                          1190
                                                                                                                                                                                  1132
                                                                                                                                                                                                                                                                                                                                                         1013 KEFIMLQNEQEISQLK-KEIERTQQRMKEMESVMKEQEQYIATQYKEAIDLGQELRLTRE 1071
                                                                                                                                                                                                                                                                   1072 QVQNSHTELAEARHQQVQAQREIERLSSELEDMKQLSKEKDAHGNHLAEELGASKVREAH 1131
                                                                                                                                      127
                                                                                                                                                                                                                            81
                                                                                                                                                                                                                                                                                                                                                                                                                                                   45;
                                                                                                                                                                                                                                                                                                                                                                                                       4 KEFILNKDIGEVSELKPHRVIVTIONGKEMSSTIVSEEDFILPVYKGELEKGYQF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 207-211; 238pp; English
                                                                                                                                 DLOREEHSOKSDSTKDVTATVLDKNNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arvizu CS,
                                                                                                                                                                                LEARMQAEIKKLSAEVESLKEAYHMEMISHQENHAKWKIS--ADSQKSSVQQLNEQLEKA
                                                                                                                                                                                                                         ----DTFIKPVFKKIEEKKE-----EENKPTFDVSKKKDNPQVNHSQLNESHRKE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1384 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       izu CS, Gandhi AR, Hafal
Swarnakar A, Tang YT, Y
Nguyen DB, Thangavelu K,
Lal PG, Gietzen KJ, Be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.7%;
                                                                                                                                                                                                                                                                                                                 -----GYVINLSK----
                                                                                                                                                                                                                                                                                                                                                                                                                                              32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 99.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hafalia AJA, Ding L, Lu Y;
YT, Yue H, Tran B, Lee SY;
lu K, Yao MG, Elliott VS, Baughn MR;
J, Becha SD, Marquis JP, Kable AB;
                                                                                                                                    153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 63; Gaps
                                                                                                                                                                                                                                                                                                                 80
                                                                                                                                                                                                                                                                                                                                                                                                       58
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XXX

ABP55393

ABP55393 standard;

protein; 1404 AA

Query Match

11.7%;

Score 99.5;

BB 24;

Length 1404;

Sequence

1404

A

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The present invention describes 23 human molecules for disease detection CC and treatment (MDDT-1 to 23) (see ABB55392 to ABB55414). The human CC MDDT-1 to 23 proteins (I) are encoded by the sequences given in ABQ83859 CC ABQ83881 (I) can have various activities depending on the cells and CC tissues in which they are expressed. These activities include: anti-HIV; CC antiallergic; antiinflammatory; antiarteriosclerotic; antiasthmatic; cc antidabetic; aphrotropic; antigout; thyromimetic; antiasthmatic; cc antidabetic; aphrotropic; antigout; thyromimetic; neuroprotective; cc osteopathic; antiarthritic; antiparasitic; hepatotropic; antipactail; cc virucide; protozoacide; and fungicide. (I) and the polynucleotides concoding them can be used in gene therapy. (I) polynucleotides, agonists ce and antagonists from the present invention can be used for diagnosing, treating or preventing disorders associated with aberrant expression of CC MDDT, particularly cell proliferative (e.g. cancer), developmental CC disorders, neurological disorders, or viral, bacterial, fungal, confined and amino acid segments of noticing ansociated with expression of the assessment of the effects of exogenous compounds on the expression of confined and amino acid segments of noticing ansociated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAR-2001; 2001US-280387P.
05-APR-2001; 2001US-28335P.
13-APR-2001; 2001US-28363P.
19-APR-2001; 2001US-285484P.
18-JAN-2002; 2002US-350702P.
25-JAN-2002; 2002US-351749P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; MDDT; molecules for disease detection and treatment; anti-HIV; antiallergic; antiinflammatory; antianaemic; antiparkinsonian; nootropic; anticonvulsant; antiinfertility; antiarteriosclerotic; antiasthmatic; immunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological; antidiabetic; nephrotropic; antigout; thyromimetic; neuroprotective; osteopathic; antiarthritic; antiparasitic; antihelminthic; antipsoriatic; uropathic; ophthalmological; antiparasitic; haemostatic; antibacterial; virucide; protozoacide; fungicide; gene therapy; cell proliferative; cancer; developmental disorder; neurological disorder; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 172-175; 238pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ABQ83860.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human molecules for disease detection and treatment, useful for diagnosing, treating or preventing autoimmune or inflammatory disordies. ALDS, allergy or anemia), multiple sclerosis, osteoarthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-058385/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lu DAM, Arvizu CS, Gandhi AR, Hafalia AJA, Ramthumar J, Swarnakar A, Tang YT, Yue H, Ramthumar J, Swarnakar A, Tang YE, Yao MG, Warren BA, Nguyen DB, Thangavelu K, Yao MG, Emerling BM, Lal PG, Gietzen KJ, Becha SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INCY-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAR-2002; 2002WO-US09809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200278420-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human MDDT-2 protein SEQ ID NO:2.
                                                               of nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reproductive disorder; autoimmune disorder; inflammatory disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INCYTE GENOMICS INC
                                                               acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                               and amino
                                                               acid
                                                               sequences of proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hafalia AJA, Ding L, Lu Y;
YT, Yue H, Tran B, Lee SY;
ilu K, Yao MG, Elliott VS, Baughn
kJ. Becha SD, Marquis JP, Kable AE
                                                               associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders
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printed from WIPO

Gaps

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ABG16636
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               The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical insging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in medical giannestics, forensics, gene mapping, identification of mutations
                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID No 46995; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, us diagnostics, forensics, gene mapping, identification of responsible for genetic disorders or other traits and to be a second to the contract.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAS80823.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human diagnostic protein #16627.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG16636 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLELEE---AQDTVSNLHQQVQDRNEV 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLQREEHSQKSDSTKDVTATVLDKNNI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEARMOAEIKKLSAEVESLKEAYHMEMISHQENHAKWKIS--ADSQKSSVQQLNEQLEKA 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QVQNSHTELAEARHQQVQAQREIERLSSELEDMKQLSKEKDAHGNHLAEELGASKVREAH 1151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
for genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.7%; Pred. No. 1.6; tive 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang
disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ΥŢ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----GYVINLSK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67;
                                                                                                                                                                                                                                                                                                                                                                                                             and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                 mutations
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Best Local S
Matches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid sequences, ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly
                                                                                                                                                       04-MAY-1999
                                                                                                                                                                                                                                                                                                                                                 08-APR-1999
                                                                                                                                                                                                                                                                                                                                                                   06-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1999
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09-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      termination sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana protein fragment SEQ ID NO: 45610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG37134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG37134 standard; Protein; 408 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human
                                                                                                                                                                                                                                       23-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                             29-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hybridisation assay; genetic mapping; gene expression control;
                                                                                                                                                                                                                                                                                                       19-APR-1999
                                                                                                                                                                                                                                                                                                                           L6-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RKEDLQRE----EHSQKSDSTKDV 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKVMVKKDKPVKTETKPSVTEKEVPSKEEPS-----
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29; Mismatches
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pathway;
promoter;

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 25-FEB-1999
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                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                           Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana protein fragment SEQ ID NO: 45609.
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99US-0162142.
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RESULT 16
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Best Local Similarity 25.0%;
Matches 40; Conservative 2:
                  25-FEB-1999

05-MAR 1999

09-MAR 1999

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25-MAR 1999

26-MAR 1999

01-APR-1999

01-APR-1999

16-APR-1999

11-APR-1999

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netic mapping; gene expression control; promoter;
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9; Mismatches
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Matches 40
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The present invention relates to von Willebrand factor binding protein polypeptide (vWb) from Staphylococci. The vWb and immunogens of vwb are useful in vaccines to combat infections caused by Staphylococci. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-OCT-1999
26-OCT-1999
                                                          New von Willebrand factor binding protein from Staphylococci, for determining and treating staphylococcal infection -
                                                                                                                                                                                    06-APR-2001; 2001WO-SE00766
                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                         Staphylococcus lugdunensis
                                                                                                                                                                                                                                                                                                                                                         Staphylococcus lugdunensis von Willebrand factor binding protein.
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                                         Claim
                                                                                                                                             (BIOS-)
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                                                                                                                                                                                                                            WO200228892-A1
                                                                                                                                                                                                                                                                           Peptide
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                                                                                                                                                                                                                                                                                                                             infection.
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                                                                                                                        Frykberg L,
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                                                                                                                                                                                                                                               note= "Mature von Willebrand factor binding protein'
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                                        53pp; English.
                                                                                                                         Jacobsson
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29; Mismatches
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   RESULT 18
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          The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (1) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II). (I) and (II) are useful for the development of vaccines against P. falciparum infection. (I) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in
                                                                                                                                                                                                                                                                                                                                      (HOFF/) HOFFMAN S.
(CARU/) CARUCCI D.
(GARD/) GARDNER M.
(VENT/) VENTER J C.
                                                                                                                                                                                                                    Proteins encoded by chromosome 2 of the human plasmodium falciparum, useful as antimalarial diagnosis of P.falciparum infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium falciparum; antimalaria; malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention is also useful for detection of staphylococcal infection and purifying von Willebrand factor from a complex solution. The present sequence is Staphylococcus lugdunensis vWbl protein.
                                                                                                                                                                                         Disclosure; Page 302-309; 577pp; English
                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                          Hoffman S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-MAY-2000.
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                                                                                                                                                                                                                                      malarial vaccines
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                                                                                                                                                                                                                                      parasite,
and in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NO:129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many
producing hyperimmune allergen, a tissue or are used in a vaccine,
                                                                         Example 7; Page 220; 252pp;
                                                                                                       providing antibody preparation
                                                                                                                  Identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, for preparing vaccine or medicament for treating or preventing e.g. staphylococcal infections, comprises
                                                                                                                                                                                 WPI; 2003-075410/07.
                                                                                                                                                                                                               Tempelmaier B;
                                                                                                                                                                                                                                     Meinke A,
                                                                                                                                                                                                                                                                                                       26-JAN-2001; 2001AT-0000130
                                                                                                                                                                                                                                                                                                                                   21-JAN-2002; 2002WO-EP00546
                                                                                                                                                                                                                                                                                                                                                                   01-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                 WO200259148-A2
                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune disease; HIV; hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hyperimmune; serum-reactive; antigen; partine auto-immunity; vaccine; staphylococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibacterial; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pathogen specific antigen related staphylococcal protein SEQ ID No 414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABJ19106 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the specification.
                                                                                                                                                                                                                                                                         (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                             invention relates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEEEE---KSDDKRD-----DKKNDNTREKNNLDNK 2308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOREEHSOKSDSTKDVTATVLDKNNISSKSTTNNPNK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEKNNLDNKKSFPSNIKVKLEEEEKSDDKRD---DKKNDNTREKNNLDNKKSFPSNIKVK 2280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----SKDTFIKPVFKKIEEKKEEENKPTFDVSKKKUNPQVNHSQLNE----SHRKED:127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KPYKIT---ENNKK-----NEGNEILKKYSIENEEKNNYDKEQNENCILDKDTQCNVNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINL
                                                                                                                                                                                                                             Vytvytska 0,
                                                                                                                                                                                                                                           Nagy E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2500 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                                                                                                                                                          Von
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.3%;
               serum-reactive antigens from a pathogen, host prone to auto-immunity, where the au
                                            to a novel method
                                                                                                                                                                                                                             Ahsen U, Klade C,
Etz H, Dryla A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fungicide; protozoacide; cytostatic; anti-HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30;
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Pred. No. 8.1;
30; Mismatches
                                                                         English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pathogen; tumour; all
l infection; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.1;
                                             for identifying,
                                                                                                                                                                                                                             , Henics T,
Weichhart T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21;
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Hafner M;
                                             isolating and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32;
                 antigens
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comprises providing antibody preparation

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RESULT 20
ABP56879
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus; Staphylococcus epidermidis; MSCRAMM; antibody; microbial surface component recognising adhesive matrix molecule; surface protein; infection; antibacterial; antiinflammatory; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-APR-2003
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                            Patel P,
                                                      Foster TJ,
                                                                                                                                                                                                                                             15-JUN-2001; 2001US-298098P
                                                                                                                                                                                                                                                                                                       17-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2002102829-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     septic arthritis; biomaterial related infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP56879 standard; Protein; 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lmmunosuppressive;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           382 MVMETTNDDYWKDFMVEGQRVRTISKDAKNNTRTIIFPYVEGKTLYDAIVKVHVKTIDYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TTVKEFILNKDTGE-VSELKPHRVTV--TIQNGKEMSSTIVSEEDFILPVYKGELE-KGY 56
                                                                                                                   QUEEN ELIZABETH COLLEGE UNIV PAVIA.
                                                                                                                                                                             INHIBITEX INC
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                         , Roche F,
Syribeys P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       645 AA;
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21.9%;
                         Patti JM,
Speziale
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Pred. No. 2.2;
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                                                                                                                                                       DUBLIN.
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                                                         Hutchins
                                                             'n
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                                                             Hall
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                                                             P
                                                             Domanski P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            endocarditis;
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2003-167481/16

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RESULT 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC The present invention describes an isolated antibody (I) that binds to a CC staphylococcal surface protein selected from any of the 12 sequences of CC 354-2283 amino acids given in ABP56885 to ABP56886. Also described: CC (1) an isolated antisera (II) comprising (I); (2) a diagnostic kit (III) CC comprising (I) and means for detecting binding by (I); (3) diagnosing CC (M1) an infection of Staphylococcus aureus by adding (I) to a sample CC (M1) an infection of Staphylococcus aureus by adding (I) to a sample CC (IV) for treating or preventing an infection of S. aureus comprising (I) and a vehicle, carrier or excipient; (5) treating (M2) or preventing an infection of S. aureus comprising (I), CC and a vehicle, carrier or excipient; (5) treating (M2) or preventing an infection of S. aureus by administering (I) to a human or animal patient; (C (6) producing (M3) an immunological response by administering to a human CC (8) a vaccine (VI) for treating or preventing an infection of S. aureus comprising the surface protein in an amount of the DsqA protein; (7) and C (8) a vaccine (VI) for treating or preventing an infection of S. aureus comprising the surface protein in an amount effective to elicit an immune CC engines, and a vehicle, carrier or excipient. (I) has antinflammatory, antibacterial, immunosuppressive and antiarthritic activities, and can be used in gene therapy. The antibody, composition and vaccine are useful for treating or preventing Staphylococcus architis or biomaterial crelated infections. The present sequence represents Staphylococcus CC epidermidis KrAN protein, which is used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated antibody that binds to a staphylococcal surface protei useful for treating or preventing Staphylococcus aureus infections, such as pneumonia, septic arthritis, endocarditis or biomaterial related infections
                  auto-immunity; vaccine; staphylococcal infection; antibody; cancer; autoimmune disease; HIV; hepatitis.
                                                                                                                                                                           06-MAR-2003
                                                                                                                                                                                                                                                                 ABJ18979 standard; Protein; 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                               hyperimmune; serum-reactive; antigen;
                                                                                  Antibacterial; virucide;
                                                                                                                             Pathogen specific antigen related staphylococcal protein SEQ ID No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 29-30; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention.
                                                                                                                                                                                                                                                                                                                                                                          511 DNKOLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT--PTK 552
                                                                                                                                                                                                                                                                                                                                                                                                                      126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   391 MVMETTNDDYWKDFMVEGQRVRTISKDAKNNTRTIIFPYVEGKTLYDAIVKVHVKTIDYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                             451 GQYHVRIVDKEAFTKANTDKSNKKEQQDNSAKKEATPATPSKPTPSPVEKESQKQDSQKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        336 SAITEFONVOPTNEKMTDLODTKYVVYESVENNESMMDTFVKH-----PIKTGMLNGKKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TTVKEFILNKDTGE-VSELKPHRVTV--TIQNGKEMSSTIVSEEDFILPVYKGELE-KGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABZ22903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    EDLQ----REEHSQKSDSTKDVT-ATVLDKNNISSKSTTNNPNK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGYVINL-SKOTFIKPVFKKIEEKKEEENKPTFDV----SKKKONPQVNHSQLNESHRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QF----DGWEISGFEGKK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     654 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.0%; Score 93.5;
21.9%; Pred. No. 2
                                                                                  fungicide; protozoacide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                             pathogen; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 654;
                                                                                    cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                               allergen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein,
                                                                                    anti-HIV;
                                                                                                                               142.
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RESULT 22 AAG82397

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AAG82397 standard;

Protein; 299

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel method for identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, tumour, allergen, a tissue or host prone to auto-immunity, where the antigens are used in a vaccine, comprises providing antibody preparation from a gainst the specific pathogen, tumour, allergen, tissue or host prone to against the specific pathogen, tumour, allergen, tissue or host prone to cauto-immunity. The hyperimmune serum-reactive antigens comprising any of the 62 sequences of 53-2261 amino acids fully defined in the CC manufacture of a pharmaceutical preparation, particularly a vaccine against staphylococcal infections or colonisation against S. aureus or S. epidermidis. The preparation of antibodies is useful for the manufacture cof a medicament for treating or preventing staphylococcal infections or colonisation against S. aureus or S. epidermidis. The antibody conditations may also be used for diagnostic and imaging purposes. Other conditions that can be treated for diagnostic and imaging purposes. Other infections or aurent for treating or preventing staphylococcal infections or conditions that can be treated for diagnostic and imaging purposes.
                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                      infections caused by viral (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This sequence represents a staphylococcal protein relating to the method for identifying and producing pathogen specific antigens of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, for preparing vaccine or medicament for treating or preventing e.g. staphylococcal infections, comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 21; Page 168; 252pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-075410/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Meinke A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 providing antibody preparation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harinh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JAN-2002; 2002WO-EP00546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tempelmaier
                                                                                                                                                                                                                                                                                                                               Local
                                         126 EDLQ----REEHSQKSDSTKDVT-ATVLDKNNISSKSTTNNPNK 164
                                                                                                                                                            382 MVMETTNDDYWKDFMVEGQRVRTISKDAKNNTRTIIFPYVEGKTLYDAIVKVHVKTIDYD
                                                                              442 GOYHVRIVDKEAFTKANTDKSNKKEQQDNSAKKEATPATPSKPTPSPVEKESQKQDSQKD
                                                                                                                                                                                                                                        327 SAITEFONVOPTNEKMTDLQDTKYVVYESVENNESMMDTFVKH-----PIKTGMLNGKKY 381
                                                                                                                                                                                                 57
                                                                                                                                                                                                                                                                              1 TTVKEFILNKDTGE-VSELKPHRVTV--TIQNGKEMSSTIVSEEDFILPVYKGELE-KGY
                                                                                                                                                                                                                                                                                                                       49;
                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CISTEM BIOTECHNOLOGIES
DNKQLPSVEKENDASSESGKGVTLATKPTKGEVESSTT--PTK
                                                                                                                                                                                                 QF----DGWEISGFEGKK-----
                                                                                                                       AGYVINL-SKDTFIKPVFKKIEEKKEEENKPTFDV----SKKKDNPQVNHSQLNESHRK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vytvytska
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nagy E,
                                                                                                                                                                                                                                                                                                                                                                                                   645 AA;
                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Von Ahsen U,
O, Etz H, I
                                                                                                                                                                                                                                                                                                                                         10.9%; Score 92.5;
21.9%; Pred. No. 2
                                                                                                                                                                                                                                                                                                                       34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J, Klade C,
Dryla A, W
                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                            DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Weichhart
                                                                                                                                                                                                                                                                                                                       74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Henics T,
sichhart T,
                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                     Indels
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Hafner M;
                                                                                                                                                                                                                                                                                                                       67;
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501

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RESULT 23
ABP40822
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AA681454 to AA683120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the sepidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55091 to
                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                       N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4455 to 4464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 18; Page 516; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-316495/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kimmerly WJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus epidermidis SR1 strain; infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG82397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH55098 represent oligonucleotide sequences and primers which in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           epidermidis
                                                                 152
                                                                                                                                                                     64
                                                                                                                                                                                                     \mathfrak{S}
                                                                                                 96
                                                                                                                                 92
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                                                                                                                                                                       SGFE---
                                                                 DREKQAKELVDETKHNVEKIINSVPKHHKKQEVFMEVSSK 191
                                                                                                 EEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQ 135
                                                                                                                                 NKEELIKAKPDLILAHESQKNSAGKVLKSLKDKGVKVVYVKDAQSIDETYDTFKSIGQLT 151
                                                                                                                                                                                                     NKDT-EKSDKKYHRIISLIPSNTEILYRLGIGEDIVGVSTVDDYPKDVKKGKKQFDAMNL
                                                                                                                                                                                                                                   NKDTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFI----LPVYKGELEKG-YQFDGWEI
                                                                                                                                                                                                                                                                                                                                            299
                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000WO-US30782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         endocarditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GROUP LTD
                                                                                                                                                                                                                                                                                                                                          A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0164258
                                                                                                                                                                                                                                                                                       10.8%; Score 92;
24.4%; Pred. No.
                                                                                                                                                                                                                                                                         27;
                                                                                                                                                                   -GKKDAGYVINLSKDTFIKPV------FKKIEEKK 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         frame protein sequence SEQ ID NO:1888
                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                         DВ
                                                                                                                                                                                                                                                                                                         22;
                                                                                                                                                                                                                                                                         60;
                                                                                                                                                                                                                                                                                                         Length 299;
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                         34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              are used
                                                                                                                                                                                                                                                                       Gaps
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RESULT 24
ABP38188
ID ABP38

ABP38188 standard;

Protein; 442

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ABP38188; 24-JUL-2002

(first entry)

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                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                 antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infectior particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequence given in ABP35124 to ABP37960. The S. epidermidis sequences have
                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                SPTO web site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus epidermidis ORF amino acid sequence SEQ.ID NO:5667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-381255/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENO-) GENOME THERAPEUTICS
                                                                                                                                                                                                                                       Local
 162
                                                                        102
                                  96
                                                                                                                                              43
                                                                                                          64 SGFE----
                                                                                                                                                                                                                    39;
                                                                                                                                                                                9 NKDTGEVSBLKPHRVTVTIQNGKEMSSTIVSEEDFI----LPVYKGELEKG-YQFDGWEI 63
                                                                                                                                                                                                                                       Similarity
                                                                        NKEELIKAKPDLILAHESQKNSÄGKVLKSLKDKGVKVVYVKDAQSIDETYDTFKSIGQLT 161
DREKOAKELVDETKHNVEKIINSVPKHHKKQEVFMEVSSK 201
                                EEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQ 135
                                                                                                                                              NKDT-EKSDKKYHRIISLIPSNTEILYRLGIGEDIVGVSTVDDYPKDVKKGKKQFDAMNL
                                                                                                                                                                                                                                                                                   309 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID 5667; 267pp; English.
                                                                                                                                                                                                                    Conservative
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97US-064964P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0134001.
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                                                                                                                                                                                                                                     10.8%;
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                                                                                                          --GKKDAGYVINLSKDTFIKPV-----
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                                                                                                                                                                                                                                   Score 92; DB 23;
Pred. No. 1.1;
                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                    60;
                                                                                                                                                                                                                                                      Length 309;
                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        can be used to
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                                                                                                            FKKIEEKK 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequences
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Staphylococcus

epidermidis ORF amino acid sequence SEQ

ID NO:3033

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RESULT
ABP4031
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Matches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.
          Staphylococcus epidermidis
                                   24-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
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08-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             specification,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          œ
                                                                                                                                                                                                                                                                                                                                                                                                                                          e or inhibit S. epidermidis infection.
The sequence data for this patent did
ification, but was obtained in electro
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                                                                                   standard;
                                                                                                                                                  DSDAENVDEYKENLRKRLSEQKATEAENT-
                                                                                                                                                                                                   GFEEQIEGMKTGDEKDVVVTFPEEYHAEELAGKEATFKTKVNEIKFKDVPELNDEIANEL
                                                                                                                                                                                                                            PVFKKIEEKKEEENK---
                                                                                                                                                                                                                                                  ESIDHSLSHLAEMVVKEDGAVENGDTVNIDFSG-SVDGEEFDGGQAEGYDLEIGSGSFIP
                                                                                                                                                                                                                                                                                                    EDT-EINPVAQPEVNVTQIEKGKDFIFEATVTVEPEVKLGDYKGLEIEKQETDLSDEELQ
                                                                                                                                                                                                                                                                                                                                                                                                      442 AA;
                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID 3033;
                                  ·(first entry)
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gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-055779P
97US-064964P
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                                                                                                                                                                          -SHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTN 160
                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bush
                                                                                                                                                                                                                                                                                                                                                                10.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267pp; English.
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                                                                                     902
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Pred. No. 2.2;
30; Mismatches
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          amino
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in electronic format
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          acid
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          sequence
                                                                                                                                                                                                                           -PTFDVS----KKKONPQVNHSQLNE-
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                                                                                                                                                                                                                                                                                                                                                                            Length 442;
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          SEQ
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          IJ
          NO:5157
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RESULT 26
AAB42897
ID AAB42
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Best Local S
Matches 43
vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidabetic; hypotensive; dermatological; immunosuppressive; antiinflammacory; antiviral; antibacterial; antifungal: antirhammaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus antibacterial;
                                                                                                             Human
                                                                                                                                                                                                     AAB42897 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specification, USPTO web site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-AUG-1997;
08-NOV-1997;
                                                                                                                                           08-FEB-2001
                                                                                                                                                                         AAB42897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                            789 VHDISQ-NGRAAQGVRLMKLGDGQFVSTVAKVNEEDDNEENADEAQQSTTTETADVEEVV
                                                                                                           ORFX ORF2661
                                                                                                                                                                                                                                                                                                                                                                        60 GWEISGFEGKKDAGY-VINLSKDTFIKPVFKKIEEKKEEEN-----KPTFDVSKKK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                               43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        TPVSEYRLSNRGGKGIK----TATITERNGNIVCITTVTGEEDLMVVTNAGVI---IRLD
                                                                                                                                                                                                                                                                                 D----DQTPGNAIHTEGDAEMESVESPENDDRIDIRQDFMDRVNEDIESASDN
                                                                                                                                                                                                                                                                                                              DNPQVNHSQLNESHRKEDLQREE-HSQKSDSTKDVTATVLDKNNISSKSTTNN
                                                                                                                                                                                                                                                                                                                                                                                                                                   TTVKEFILNKDTGEVSELKPHRVTVTIQNGKEMS-STIVSEEDFILPVYKGELEKGYQFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             902 AA;
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                                                                                                                                         (first entry)
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97US-064964P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                epidermidis.
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                                                                                                         polypeptide sequence SEQ ID NO:5322.
                                                                                                                                                                                                     Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 91; DB
Pred. No. 6.1;
31; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
                                                  cardiant;
                                                                                                                                                                                                                                                                                   968
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Matches
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02-APR-1999;
05-APR-1999;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antiheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shimkets RA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coagulation; to inhibit thrombosis; and
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)B; AAC77106.
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                                                                                                                                                                                                                                                                                                                                                                   47;
NPQVNH-----SQLNESHRKEDLQREEHSQKSD--STKDVTATVLDK 150
                                                                                                                                                                                                                                                                                                  GEVSELKPHRVTVTIQNGKEMSSTIVSE--EDFILPVYKGELEKGYQF-----DGWE---
                                                                                                                                                                                                                                     GELQQLSGSQL-----HGKSDSPNVYTEKKEIAILRERLTELERKLTFEQQRSDLWERLY
                                                                                                      VEAKDQNGKQGTDGKKKGGRGSHRAKNKSKETFLGSV-----
                                                                                                                                                                       ----ISGFEGKKDAG----YVINLSKDTFIKFVFKKIEEKKEEENKPTFDVSKKKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 4497-4498; 5507pp; English.
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99US-0127636.
99US-0127728.
2000US-0540763.
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                                                                                                                                                                                                                                                                                                                                                                                                  10.7%; Score 90.5; DB 28.1%; Pred. No. 0.89;
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                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                   56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    209;
                                                                                                                                                                                                                                                                                                                                                                       47;
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8 8 8 8

S

Query Match Best Local Similarity

10.7%;

Score Pred.

90.5; No. 4.

В

23;

Length

635

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                                                               compound catabolism, bis useful for identifying a gene that compound cativity. The method is useful for compound fungal compound cativity. The method is useful for identifying a gene that compound cativity. The method is useful for identifying a gene that contributes to the virulence and/or pathogenicity of a diploid fungal contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent that inhibits the growth of a fungus, a gene contributes to the resistance of a diploid fungus to an antifungal agent that inhibits the growth of a diploid fungus agene contributes to the resistance of a diploid fungus to an antifungal agent that inhibits the growth of a diploid fungus agene contribute of a diploid fungus to an antifungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of a mammalian conspound which modulates the compound catabolism, biosynthetic, transporter, transcriptional, conspound catabolism, biosynthetic, transporter, transcriptional, constituty. The method is useful for identifying a compound having the activity. The method is useful for identifying a compound having the cativity to inhibit growth or proliferation of C. albicans cells and for constitutial Candida ablicans protein used in the method of the invention.

Constitution by C. albicans. The present sequence is that of an activity of a bilicans cells and for the specification but is based on sequence information supplied to Derwent by the C. albication by C. albication and cell in the printed specification by C. albication and cell in the printed specification by C. albication and cell in the printed specification by C. albication and cell in the printed specification by C. albication and cell in the printed specification by C. albication and cell in the printed specification by C. albication and cell in the printed specification by C. albication and cell in the printed specification by C. albication and cel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to constructing (M1) a strain of diploid cells in which both alleles of a gene are modified, comprising one allele by insertion or replacement by a cassette having an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       one allele by insertion or replacement by a cassette having expressible selectable marker and modifying other allele by
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22-AUG-2001;
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    #XFFX#X222222222
                                       The present sequence is cell cycle regulation protein-5 (CECRP-5) analytical method was used to identify this protein CECRPs are activators of cell proliferation or inhibitors of cellular process modulate proliferation. They are used to treat or prevent cell proliferative diseases like cancers, atherosclerosis, cirrhosis,
               hepatitis, psoriasis, deficiency syndrome
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              can be used in gene therapy. The colon cancer antigen polynucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polynucleotides may be used in diagnostics and research, such as for
                                                                          neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities, and
                                                                                                        AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular;
                                                                                                                                                                   Claim 11; Page 1408-1411; 2104pp; English.
                                                                                                                                                                                                             Colon cancer associated gene sequences, referred to antigens, useful for the treatment, prevention, and
                                                                                                                                                                                                                                                                                                                                                                                                  08-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI
                                                                                                                                                                                                                                                                                                                                                                     12-MAR-1999;
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tides may be used in diagnostics and research, such as for identification, and as hybridisation probes. The proteins
                                                                                                                                                                                                                                                                                                           Ruben SM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer; colon cancer antigen;
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Pred. No. 5.3;
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diagnosis of co
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                                                                       New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or
                                                                                                                                                                                                                                                                                                                                                                                 arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                        Parkinson's disease; Alzheimer's disease; autoimmune disease; multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; genome mapping; gene therapy; food supplement; virus; fungucell-proliferative disorder; neurodegenerative disease; bacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human
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                                                                                                                                                                                                                                          05-MAR-2001; 2001US-0799451
                                                                                                                                                                                                                                                                   05-MAR-2002; 2002WO-US05095
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Yang Y,
T, Wang J
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                                                              or coagulation
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                                                                                                                                                                Ma Y, Y
J, Wang
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                                                                                                                                                                                         Goodrich RW,
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                                                                                                                                                          rich RW, Asundi V,
Yamazaki V, Chen
ng D, Drmanac RT;
                                                              disorders
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Pred. No. 5.
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                                                                                                                                                                                          Zhang
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                                                                                                                                                                             Wang
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                                                                                                                                                                                          J,
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The invention relates to an isolated polynucleotide nucleotide sequence selected from any of. 948 sequenc

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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shrimp white spot Bacilliform virus; WSBV; diagnosis; viral infection; antiviral agent; gene expression; antisense construct; transgenic viral resistant shrimp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                            Primary nucleotide sequence of the shrimp white spot Bacilliform (WSBV), useful for producing viral polypeptides that can be used screen for agents that are useful for treating WSBV infection -
                                                                                                                                                                                                                   Χu X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal, parasitic), arthritis, etc.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Parkinson's or Alzheimer's disease), autoimmune diseases (multiple sclerosis, diabetes, lupus) genetic disorders, myeloid or lymphoid disorders, platelet or coagulation disorders, wound, burns, incision,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ABZ11119-ABZ12066) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynucleotides are useful for identifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABP68902-ABP69849) are useful as molecular
Claim 1; Figure 3;
                                                                                                                                                                                                                                                                                                                                                                                                         08-NOV-2000; 2000WO-US28888.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200138351-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      White spot syndrome virus.
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                                                                                                                                              N-PSDB; AAH62803
                                                                                                                                                                                                                                                                (PENY-) PE CORP NY.
(THIR-) THIRD INST OCEANOGRAPHY STATE OCEANI
(SINO-) SINOGENOMAX CO LTD.
                                                                                                                                                                                                                                                                                                                                                             24-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shrimp white spot Bacilliform virus
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                                                                                                                                                                    2001-355877/37.
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                                                                                                                                                                                                                 Yang F, He J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NESHRKEDLQREEHSQKSDSTKDVTATVLDKNNI 153
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626pp; English
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                                                                                                                                                                                                                   Pham L,
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                                                                                                                                                                                                                      Hем,
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The invention relates

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an isolated nucleic acid detection reagent

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RESULT 32
ABB58769
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Best Local
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                                                    New isolated nucleic a
genes from Drosophila
interactions -
                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster polypeptide SEQ ID NO 3099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             control viral gene expression in infected cells and tissues and to create transgenic viral resistant {\tt shrimp}.
                        Disclosure; SEQ ID NO 3099; 21pp + Sequence Listing; English
                                                                                                                                                                                                            23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                       23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                 27-SEP-2001
                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                   pharmaceutical.
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                                                                                                            N-PSDB; ABL02872.
                                                                                                                          WPI; 2001-656860/75.
                                                                                                                                                      Venter JC,
                                                                                                                                                                                                                                                                                                             WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                Drosophila; developmental biology; cell signalling;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB58769 standard;
                                                                                                                                                                                  (PEKE ) PE
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                                                                                                                                                                                  CORP NY.
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                                                                                                                                                      Adams M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein; 1183 AA
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                                                                   detection reagen
for elucidating
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Pred. No. 7;
                                                                                                                                                      Myers EW;
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                                                                                   reagent
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                                                                   nt for detecting cell signalling
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and c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511); expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins
This sequence is the Staphylococcus aureus trigger factor (tig) polypeptide of the invention. Tig polypeptides and polynucleotides are
                                                                              New Staphylococcus aureus trigger factor (tig) polypeptide and polynucleotide, useful as diagnostic reagents and for prevention treatment of Staphylococci aureus infections
                                                                                                                                                                                         Burnham MKR, Fosberry A,
Lawlor EJ, Rosenberg M,
Warren RL;
                                                                                                                                                                                                                                                       (SMIK )
                                                                                                                                                                                                                                                                                                                    29-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                   21-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           wound infection; impetigo; septic arthritis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trigger factor; tig; diagnosis; immune response; bacterial infection; S. aureus infection; otitis media; toxic shock syndrome; conjunctivitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aureus trigger factor protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY03190 standard; Protein; 402
                                                                                                                                                          WPI; 1999-192663/17
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                                                                                                                                                                                                                                                      SMITHKLINE BEECHAM CORP. SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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97US-0057511.
                                                                                                                                                                                                                                                                                                                                                   98EP-0306697
                                               31pp;
                                                  English
                                                                                                                                                                                                      Hodgson JE, Jaworski DD;
Traini CM, Wang M, Ward J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein by identifying mutations in the tig gene, or determining tig polypeptide or mRNA expression levels due to an infection of an organism with the tig gene. They can diagnose the stage and type of infection. Tig polypeptides are also useful for screening compounds which affect activity of the protein by measuring the binding to tig and observing the stimulation or inhibition of the polypeptide function. These can be used
                                                                                                                                                                                                                                                                                        Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
                                                                                                                                                                                                                                                                                                                                                                                                13-SEP-1999 (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                       04-NOV-1998;
21-NOV-1997;
                                                                                                   20-NOV-1998;
                                                                                                                                                                                      WO9927105-A2
                                                                                                                                                                                                                           Chlamydia pneumoniae
                                                                                                                                                                                                                                                                    vaccine; neutralising
                                                                                                                                                                                                                                                                                                                                                       Chlamydia pneumoniae transmembrane protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY35091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful for diagnosing diseases related to over or underexpression of tig
(GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 DAEANTVDEYKENLRKRLAEOKATDAENV----EKEEAITKATDN 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GFEEQLEGMKVDEEKDVVVTFPEEYHAEELAGKEATFKTKVNEIKFKEVPELTDEIANEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VFK-----KIEEKKE-----EE---NKPTFDVS----KKKDNPQVNHSQLNE- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AIDHSLGHLAEMVVKEDGVVENGDTVNIDFSG-SVDGEEFEGGQAEGYDLEIGSGSFI-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----FEGKKDAGYVINLSKDTFIKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DETDIKPVAQPEVSVTQIEKGKDFIFEATVTVEPEVKLGDYKGLEIEKQETELSDDELQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DTGEVSELKPHRVTVT-IQNGKE--MSSTIVSEEDFILPVYKG-ELEK-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----SHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTN 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 402 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                       98US-0107078.
97FR-0014673.
                                                                                                      98WO-IB01890.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.6%;
22.1%;
                                                                                                                                                                                                                                                                      epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 89.5; D; Pred. No. 2.8; 33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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WPI; 1999-357842/30

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RESULT 35
ABP73570
ID ABP73
CC XXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY3584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          especially where the vocanitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome sequence of Chlamydia pneumoniae
                                                                    Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional expression -
                                                                                                                                                                                                                                                                    29-DEC-2000; 2000US-259128P.
20-FEB-2001; 2001US-0792024.
22-AUG-2001; 2001US-314050P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis; signal transduction; DNA replication; cell division; growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Candida albicans essential protein SEQ ID NO 7407.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae
                             Claim 44; SEQ ID NO 7407; 167pp + Sequence Listing; English.
                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                      26-DEC-2001; 2001WO-US49486
                                                                                                                                                                                                                                                                                                                                                                           11-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                         WO200253728-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                            Candida albicans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP73570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP73570 standard; Protein;
                                                                                                                                                                                                                                      (ELIT-) ELITRA PHARM
                                                                                                                                                                    2002-566694/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         975-976; Disclosure; 1912pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 GDLDRVGHDSNEDSTEDSRS---EGGEPSSKSSS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 EDLOREEHSOKSDSTKDVTATVLDKNNISSKSTT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 IKPVFKKIEEKKEEENKPTFD--------VSKKKDNPQVNHSQLNESHRK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23;
                                                                                                                                                                                                     Ή
                                                                                                                                                    ABZ32120.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    511
                                                                                                                                                                                                   Jiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Candida
                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.6%;
                                                                                                                                                                                                                                      INC.
                                                                                                                                                                                                     Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             albicans;
                                                                                                                                                                                                     'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 89.5;
Pred. No. 3
                                                                                                                                                                                                     Bussey H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
                                                                                                                                                                                                     Ohlsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
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XXX

invention

relates to constructing (M1) a strain of diploid fungal

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RESULT 36
AAY03189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC certs in which poth alleles of a gene are modified, compiled, cone allele by insertion or replacement by a cassette having an CC expressible selectable marker and modifying other allele by recombination, of a promoter replacement fragment with a heterologous CC promoter, so that expression of the second allele is regulated by the CC promoter. (M1) is useful for constructing a strain of diploid fungal CC cells in which both alleles modified are useful for identifying a gene that CC cells in which both alleles modified are useful for identifying a gene that CC contributes to the virulence and/or pathogenicity of a fungus, a gene that CC contributes to the virulence and/or pathogenicity of a fungus, a gene that CC contributes to the resistance of a diploid fungus to an antifungal agent that inhibits the growth of a diploid fungus CC and for identifying a therapeutic agent for treatment of a mammalian CC disease. (M1) is useful for identifying a compound which modulates the CC compound catabolism, biosynthetic, preferably enzymatic activity, carbon CC compound catabolism, biosynthetic, transporter, transcriptional, CC translational, signal transduction, DNA replication and cell division CC ability to inhibit growth or proliferation of C. albicans cells and for treating infection by C. albicans. The present sequence is that of an CC essential Candida albicans protein used in the method of the invention.

CC Specification but is based on sequence information supplied to Derwent by the Control of the firm of the control of the printed specification of the printed of the printed control of the control of the printed to the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of
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Best Local

    aureus trigger factor protein sequence.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cells in which both alleles of a gene are modified, comprising one allele by insertion or replacement by a cassette having an
Burnham
                                                                                                      29-DEC-1997;
04-SEP-1997;
                                                                                                                                                                                                                                                                                                     Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                   Trigger factor; tig; diagnosis; immune response; bacterial infection; S. aureus infection; otitis media; toxic shock syndrome; conjunctivit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY03189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY03189 standard;
                                        (SMIK )
                                                                                                                                                                          21-AUG-1998;
                                                                                                                                                                                                                    31-MAR-1999.
                                                                                                                                                                                                                                                                                                                                                 wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     369 KNKGRISRYLANKCSIASRIDNYSEEPTTAFGE-----ILKKQVEDRLKFYDTGSAPMK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37;
MKR,
                                        SMITHKLINE BEECHAM CORP
SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NSDAIKAALALNGQDLAGAEEQKDVDMV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKKEKKDKKEKKDKK--DKKRKSDDGEETPKKKKKKKSKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----DGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKE----EENKPTF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KDTGEVSELKPHRVTVT--IQNGKEMSSTIVSEEDFILPVYKGELEKGYQF-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          516 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
Fosberry A,
                                                                                                         97US-0999339.
97US-0057511.
                                                                                                                                                                                                                                                                                                         aureus.
                                                                                                                                                                          98EP-0306697.
                                                                                                                                                                                                                                                                                                                                             impetigo; septic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.6%; Score 89.5; 23.3%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27;
Hodgson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                    arthritis;
JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -SDEEQVKKEKKEKKEKKEKKDKKEKKEKK
  Jaworski DD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                        conjunctivitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ঠ
                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 37
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                                                                                                                                                                                                                                                                                                                                                                                               ABB58704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC protein by identifying mutations in the tig gene, or determining tig with the tig gene. They can diagnose the stage and type of infection. Tig colypeptides are also useful for screening compounds which affect colypeptides are also useful for screening compounds which affect continuity of the protein by measuring the binding to tig and observing the stimulation or inhibition of the polypeptide function. These can be used in treatment to inhibit or enhance tig activity, in addition to direct administration of tig polypeptides to treat conditions associated with a clack of tig polypeptide, or direct administration of antisense sequences to prevent expression. Tig polypeptides (administered directly, in a cc vector and as a vaccine) and antibodies induce an immune response to include: bacterial infections, especially Staphylococcus aureus conjunctivitis, wound infection, impetigo and septic arthritis etc. Tig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
WO200171042-A2
                                                  Drosophila melanogaster
                                                                                                          Drosophila, developmental biology; cell signalling; pharmaceutical.
                                                                                                                                                                                         Drosophila melanogaster polypeptide SEQ ID NO 2904
                                                                                                                                                                                                                                                                                                            ABB58704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 14; Page 6; 31pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treatment of Staphylococci aureus infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Staphylococcus aureus trigger factor (tig) polynucleotide, useful as diagnostic reagents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-192663/17.
N-PSDB; AAX28174.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lawlor EJ,
                                                                                                                                                                                                                                                    26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                 ABB58704 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conjunctivitis, wound infection, impetigo and septic arthritis etc. Tig polypeptides, polynucleotides and their (ant)agonists can prevent adhesion of bacteria to matrix proteins, and are useful for use on wound and body implants to prevent bacterial infection.
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Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----GYQFDGWEISG--FEGKKDAGYVINLSKDTFIKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLO1840-ABL16175) and the encoded proteins (ABBC101840-ABL16175) and the encoded proteins
                                                                                                                 Herbicidally active polypeptide SEQ ID NO 2552
                                                                                                                                               31-MAY-2002
                                                                                                                                                                                                         ABB93341 standard; Protein; 296 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic a genes from Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Venter JC,
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11-JUL-2000;
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                                                      Arabidopsis thaliana
                                                                                     Herbicidal; plant; agriculture; herbicide
                                                                                                                                                                             ABB93341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 2904; 21pp + Sequence Listing;
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DB; ABL02807.
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                                                                                                                                                                                                                                                                                                                                                                                                       MESKEYSEPLAVKLGEDVSKSPSNESSDTKISEVKGEE--PKWNGELPKTGEQVKQPEKS
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Matches 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequence from plant with nucleic acid or amino acid sequences from non-plant
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  23-MAR-2000; 2000US-191637P
                             23-MAR-2001; 2001WO-US09231.
                                                                                    WO200171042-A2
                                                                                                                Drosophila melanogaster
                                                                                                                                              pharmaceutical.
                                                                                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                     Drosophila melanogaster polypeptide
                                                                                                                                                                                                                  26-MAR-2002
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                                                                                                                                                                                                                                                                        ABB64828 standard;
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43; Conserv
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(THIR-)
(SINO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                        Shrimp white spot Bacilliform virus; WSBV; diagnosis; viral infection; antiviral agent; gene expression; antisense construct;
                                                                                                                                                                                                                              Shrimp white
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence data for this patent did not form specification, but was obtained in electronic i
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                                                                           08-NOV-2000;
                                                                                                    31-MAY-2001.
                                                                                                                             WO200138351-A2
                                                                                                                                                                            transgenic viral
                                                                                                                                                                                                                                                                                 AAG85008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection
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                                                                                                                                                     spot syndrome
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                                                                                                                                                                                                                              spot Bacilliform virus (WSBV)
                                                                           2000WO-US28888
                                                                                                                                                                                                                                                       (first
                                                   99CN-0124717.
                                                                                                                                                                            gene expression; resistant shrimp.
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Matches 30
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                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Figure 3; 626pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primary nucleotide sequence of the shrimp white spot Bacilliform virus (WSBV), useful for producing viral polypeptides that can be used to screen for agents that are useful for treating WSBV infection -
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N-PSDB; AAH62788.
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108 KKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLD--KNNISSKSTTN---NP 162

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01-NOV-1995
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                        REPEAT
                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                    REPEAT
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                                                                                                                                                                                                     MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIJUE 95104835; PubMed=7806212;
Lien L.L., Feener C., Fischbach N., Kunkel L.M.;
"Cloning of human microtubule-associated protein
identification of a related gene on chromosome 1
                                                                                                                                                                                                                                                            entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995
16-OCT-2001
 REPEAT
                                                                                                           REPEAT
                                                                                                                          CHAIN
                                                                                                                                                  PROSITE;
                                                                                                                                                                                           GO; GO:0005875;
                                                                                                                                                                                                                      Genew;
                                                                                                                                                                                                                                 EMBL; L06237; AAA18904.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Microtubule-associated
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                                                                                                                                                                             InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                    both MAP1
                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN: Has a highly basic region with many copies of the sequence KKEE and KKEZ/V, repeated but not at fixed intervals, which is responsible for the binding of the microtubules of the binding of the microtubules of the binding of the prime ICl is coexpressed with MAPIB. It is a polypeptide generated from MAPIB by proteolytic processing. It is free to associate with both MAPIA and MAPIB. It interacts with the amino-terminal region
                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: TO MAPIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: 3 DIFFERENT LIGHT CHAINS, LC1, WITH MAP1A AND MAP1B PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATED MAPIB MAY PLAY A ROLE IN THE CYTOSKELETAL CHANGES THAT ACCOMPANY NEURITE EXTENSION. PROBLEM MAPIB BINDS TO AT LEAST TWO TUBULIN SUBUNITS IN THE POLYMER, AND THIS BRIDGING OF SUBUNITS MIGHT BE INVOLVED IN NUCLEATING MICROTUBULE POLYMERIZATION AND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mics 22:273-280(1994).
FUNCTION: THE FUNCTION OF BRAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STABILIZING MICROTUBULES.
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PF00414; MAP1B
                                                                                                                                                                                                                   HGNC:6836; MAP1B.
                                                                                                                     )0414; MAFIB NEUKAAAA,
PS00230; MAFIB NEUKAAAA,
PANEAT; Phosphorylation
MAPI LIG
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(Rel. 40, Last annotation update)
associated protein 1B (MAP 1B) [Contains: MAP1 light chain
                                                                                                                                                                                                                                                                                                                                                                                    (By
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                                                                                                                                                                                                                                                                                                                                                                                   similarity).
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Primates;
                                                                                                                                                                             MAP1B_neuraxin.
           MAP1 LIGHT CHAIN LC1.
MAP1B 1.
MAP1B 2.
MAP1B 3.
MAP1B 4.
MAP1B 5.
MAP1B 6.
MAP1B 7.
MAP1B 8.
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-QKSSESRKSDDNKDILTHILDFVQNNFSSEIFMNKLLSP 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sociated protein 1B on chromosome 15.";
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IN THE CYTOSKELETAL CHA
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Q14093;
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                                                                                                                REPEAT
REPEAT
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DOMAIN
                                                                                                                                                                                                                                                                      MIM;
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Cylicin II (Multiple-band polypeptide II).
                                                                                                                                                                                                                                                 GO; GO:0005200; F:structural
                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE-95255491; PubMed-7737358;
Hess H., Heid H., Zimbelmann R., Franke W.W.;
"The protein complexity of the cytoskeleton of bovine and heads: the identification and characterization of cylicin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                         SEQUENCE
                                                                                                                                                          REPEAT
                                                                                                                                                                                                                            Cytoskeleton;
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                                                                                                                                                                                                                                                                                                                                         EMBL; Z46788; CAA86752.1;
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                                                                                                                                                                                                                                                                                             Genew;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: POSSIBLE ARCHITECTURAL ROLE DURING
                                                                                                                                                                                                                                                                                                                    137271;
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                                                                                                                                                                                                                                                                                             HGNC:2583;
                         Similarity
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                                                                                                                                                                                                                          protein;
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                         Score 95;
Pred. No.
                                                                                                                                                                                                     constituent of cytoskeleton; TAS. tein; Repeat; Sperm; Spermatogenesis. 31 X 3 AA REPEATS OF K-K-X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 97.5;
Pred. No. 21;
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LYS-RICH (HIGHLY BASIC, CONKEE AND KKEI/V REPEATS).
KKEE AND KKEI/V REPEATS).
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                                                                                                                                                                                   X APPROXIMATE TANDEM REPEATS
                                                                                            D86766599C1809E7 CRC64;
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                                                DB 1;
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                                              Length 348;
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II.";
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38;

Conservative

20;

Mismatches

39;

Indels

26;

Gaps

7;

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RESULT 4
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P41001;
 Isomerase;
NP BIND
ACT SITE
DOMĀIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium falciparum Eukaryota; Alveolata; NCBI_TaxID=5839;
                                                                  SMART; SM00433; TOP2c;
SMART; SM00434; TOP4c;
                                                                                       ProDom; PD000742; DNA_topoisoIV; 1.
SMART; SM00387; HATPase_c; 1.
                                                                                                            Pfam; PF00204; DNA_gyraseB; 1.
Pfam; PF00521; DNA_topoisoTV; 1.
Pfam; PF02518; HATFase_c; 1.
PRINTS; PR00615; CCAATSUBUNTA.
PRINTS; PR00418; TET2FAMILY.
                                                                                                                                                                                                                 EMBL; X79345; -; NOT_ANNOTATED_CDS. HSSP; P06786; 1BGW.
                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed, entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cheesman S., McAleese S., Goman M., Johnson D., Ridley R.G., Kilbey B.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLAFK
                                                        PROSITE;
                                                                                                                                                                   InterPro; IPR003594; ATPbind ATPase.
InterPro; IPR003957; CBFA_NFTB_topis.
InterPro; IPR001241; DNA_topoisoII.
InterPro; IPR002205; DNA_topoisoIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94316496; PubMed=8041616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                topoisomerase
                                                                                                                                                                                                                                                                                               European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Belongs to the type II topoisomerase family
                                                                                                                                                                                                                                                                                                                                                        RELAX ONLY NEGATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLAFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SK--KKDNPQVNHSQLN-----ESHRKEDLQREEHSQKSDSTKD---VTATVLDKNNI 153
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; Topoisomerase; I
144 149
830 830
271 281
308 316
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(Rel.
(Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11,
31,
31,
                       TOPOISOMERASE II; 1.
omerase; DNA-binding; ATP-binding; Nuclear protein.
149 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -GTEKDSKKGKKDS----KKGKDSAIELQAVKADEKKDEDGKKDANKGDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Last sequence update)
, Last annotation update)
(EC 5.99.1.3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (isolate K1 / Thailand).
Apicomplexa; Haemosporida;
                                                                                                                                                                                                                                                                                                                                                        SUPERCOILS.
            DNA CLEAVAGE (BY SIMILARITY) POLY-ASN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                  There are no restrictions ng as its content is in
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                                                 Query Match
Best Local S
Matches 38
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Matches 36
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DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                             Hofmann C.J.B., Rensing S.A., Haeuber M.M., Mart Couch J., McFadden G.I., Igloi G.L., Maier U.-G.
"The smallest known eukaryotic genomes encode a an understanding of nucleomorph functions.";
Mol. Gen. Genet. 243:600-604 (1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1994 (Rel.
01-OCT-1994 (Rel.
28-FEB-2003 (Rel.
                                                                                               PRINTS; PRO0301; HSATSHOCK70.

ProDom; PD000089; HSp70; 1.

PROSITE; PS00329; HSP70 1; 1.

PROSITE; PS00329; HSP70 2; 1.

PROSITE; PS01036; HSP70 3; 1.

ATP-binding; Heat shock; Nucleomorph.

ATP-binding; Heat shock; Nucleomorph.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PYRSA
HS70_PYRSA
                                                                                                                                                                                                                                                                             entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. U
                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Crypt
NCBI_TaxID=3034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P37899;
01-OCT-1994
                                                                                                                                                                                                                                                   EMBL; X72621; CAA51197.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94268506; PubMed=8208251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pyrenomonas salina.
Nucleomorph.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heat shock 70 kDa
                                                                                                                                                                                                                                                                                                                                                                                   MOl. Gen. Genet. 243:600-604(1994).
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                               Pfam; PF00012; HSP70;
                                                                                                                                                                                                                         HSSP; P08109; 1CKR.
                                                                                                                                                                                                           nterPro; IPR001023; Hsp70.
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491
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                                                  l Similarity
38; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIEKVEEAIEFORNVELSNREESNK--FKVARKO-----GPSSMKKKKKKKKKSSDEESE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGDTSDSSEFLVNTLNIKKNTNKKTTTSSNN 1273
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 ILNVSASDKSTGKSNKITITNDKGRLSKEEIERMVEEAE--
                        ILNKDTGEVSELKPHRVTVTIQNG---KEMSSTIVSEEDFILPVYKGELEKGYQFDGWEI
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1227 12
1398 AA;
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                                                 11.0%;
nilarity 24.5%;
Conservative 2
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41,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161029 MW; BAAD7BEE88FE5BE9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     annotation
                                                   26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence update)
                                                 Score 93.5; DE Pred. No. 9.7; 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 95; DB
Pred. No. 17;
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                                                                             DB
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                                                                                                                                                                                                                                                                                         http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Martin W.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53;
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                                                                                                                                                                                                                                                                                                     Usage
                                                                                                                                                                                                                                                                                                                    its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1398;
                                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                           Length
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  -KYKTEDEK-
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                                                                             649;
                                                                                                                                                                                                                                                                                                                                                                                                                           gene:
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                                                   41;
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                                                   Gaps
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RESULT 6
MAPB MOUSE
ID MAPB MOUSE
AC P14873;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Swiss Webster; TISSUE-Brain; MEDLINE=90094539; PubMed=2480963; Noble M., Lewis S.A., Cowan N.J.; "The microtubule binding domain of microtubule-associated protein MAP1B contains a repeated sequence motif unrelated to that of MAP2
                REPEAT
REPEAT
                                                         REPEAT
REPEAT
                                                                                                                                                              88
                                                                                                                                                                                          MGD;
                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [Contains: MAP1 light cha
MAP1B OR MTAP1B OR MTAP5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Microtubule-associated protein 1B (MAP 1B) (MAP1.2) (MAP1(X))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1990
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990
 REPEAT
                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                             REPEAT
                                                                                                    Microtubules;
                                                                                                                                    Pfam;
                                                                                                                                                                                                                       EMBL; X51396; CAA35761.1;
                                                                                                                                                                                                                                                                  entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d tau.";

Cell. Biol. 109:3367-3376(1989).

Cell. Biol. 109:3367-3376(1989).

FUNCTION: THE FUNCTION OF BRAIN MAPS IS ESSENTIALLY UNKNOWN.

FUNCTION: THE FUNCTION OF BRAIN MAPS IN THE CYTOSKELETAL CHANGES PHOSPHORYLATED MAPIB MAY PLAY A ROLE IN THE CYTOSKELETAL CHANGES

THAT ACCOMPANY NEURITE EXTENSION. POSSIBLY MAPIB BINDS TO AT LEAST TWO TUBULIN SUBUNITS IN THE POLYMER, AND THIS BRIDGING OF SUBUNITS TWO TUBULIN SUBUNITS IN THE POLYMER, AND THIS BRIDGING AND IN
                                                                                                                                                            GO:0016358;
GO:0001578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: 3 DIFFERENT LIGHT CHAINS, LC1, LC2 AND LC3, CAN ASSOCIATE WITH MAPLA AND MAPLE PROTEINS

DOMAIN: Has a highly basic region with many copies of the sequence KKEE and KKEI/V, repeated but not at fixed intervals, which is
                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: TO MAPIA.
                                                                                                                                                                                                                                                                                                                                                                                              responsible for the binding of MAP18 to microtubules.
PTM: LC1 IS COEXCRESSED WITH MAP18. IT IS A POLYPEPTIE GENERATED FROM MAP18 BY PROTEOLYTIC PROCESSING. IT IS FREE TO ASSOCIATE WITH BOTH MAP18 AND MAP18. IT INTERACTS WITH THE AMINO-TERMINAL REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STABILIZING MICROTUBULES.
                                                                                                                                                                                          MGI:1306778; Mtap1b
                                                                                                                                                                                                          S07549; QRMSP1.
                                                                                                                                    PF00414; MAP1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
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                                                                                                                    PS00230; MAPIB NEURAXIN; 7
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                                                                                                                                                01578; P:microtubule bundling;
   IPR000102; MAP1B_neuraxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eutheria;
 1874
1891
1908
1925
1942
1959
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(Rel. 14, Last sequence update)
(Rel. 41, Last annotation updat
                                                                                                     Repeat;
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                                                                                                                                                                              P:dendrite morphogenesis;
   2464
1890
1907
1924
1941
1958
1975
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Rodentia;
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                                                                                                       Phosphorylation
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MAP1B 1.
MAP1B 2.
MAP1B 3.
MAP1B 4.
MAP1B 5.
MAP1B 6.
                                                                                        MAP1
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Sciurognathi; Muridae;
                                                                                      LIGHT
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; Murinae; Mus.
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                                                                                                                                        A Mood V, Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

Collins M., Comnor R., Cronin A., Davis P., Feltwell T., Fraser A.,

Gollins M., Comnor R., Cronin A., Davis P., Feltwell T., Fraser A.,

Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

A Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

James K., Jones M., Leather S., McDonald S., McGen J.,

A Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

AN Mooney P., Moule S., Mangall K., Murphy L., Niblett D., Odell C.,

AN Mooney P., Moule S., Pearson D., Quail M.A., Rabbinowitsch B.,

AN Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch B.,

AN Oliver K., O'Neil S., Pearson D., Segger K., Sharp S.,

Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

AN Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

AN Skelton J., Vanstreels E., Rieger M., Walsh S.V., Wazren T., Whitehead S.,

Wedder C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

AN Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

AN Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

AN Geffeau A., Cadieu B., Dreano S., Gloux S., Leurselle B.,

Galibert F., Aves S., J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

AN Galibart F., Agen S., J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

Daga R.R., Cruzado L., Jimenez J., Sanchez M., Garzon A., Thode G.,

Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

AN Cernitti L., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,

AN Cernitti L., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,

AN Cernitti L., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,
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Best Local S
Matches 49
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15-JUL-1998
28-FEB-2003
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014207;
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REPEAT
REPEAT
                                                                        Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Po
Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe."
Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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SPAC6B12.02C
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                   This SWISS-PROT entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces.
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                                                   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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protein C6B12.02c in chromosome
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MAP1B 8.

MAP1B 9.

MAP1B 10.

LYS-RICH (HIGHLY BASIC, (KKEE AND KKEI/V REPEATS).
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ght. It is produced Bioinformatics and
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 and the
                                                                                                                                    Potashkin J.,
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                   through
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   EMBL outstation
                 a collaboration
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European Bioinformatics Institute.

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                                                                                                                                                                                                                                          extrachromosomal DNA of the ascomycete Ascobolus immersus.";
Mol. Gen. Genet. 218:523-530(1989).
-i- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N d
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Pezizomycetes;
Pezizales; Ascobolaceae; Ascobolus.
NCBI_TaxID=5191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1991 (Rel. 19, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Probable DNA polymerase (EC 2.7.7.7).
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                                                       s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                        oken F., Meinhardt F., Esser K.; organello replication and viral affinity of linear
                                                                                                                                                       (BY SIMILARITY). STRONG, TO DNA POLYMERASE TYPE-B FAMILY. STRONG,
                                                                                                                                                                                                      MISCELLANEOUS: THIS DNA POLYMERASE
                                                                                                                                          DNA POLYMERASE OF OTHER FUNGAL AND PLANTS
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                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE-94205265; PubMed-8154186;

MEDLINE-94205265; PubMed-8154186;

BOU G., Esteban P.F., Baladron V., Gonzalez G.A., Cantalejo J.G.,

Remacha M., Jimenez A., del Rey F., Ballesta J.P.G., Revuelta J.L.

"The complete sequence of a 15,820 bp segment of Saccharomyces

"The complete sequence XI contains the UBI2 and MPL1 genes and thr
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01-JUN-1994 (Rel. 29; Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Myosin-like protein MLP1
MLP1 OR YKR095W OR YKR415.
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PIR; S05362;
                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Electrone
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NCBI_TaxID=4932;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccisaccharomycetales; Saccharomycetaceae; Saccharomyces
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Transferase; DNA-directed DNA polymerase;
DNA-binding; Plasmid; Micochondrion.
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         protein of Staphylococcus aureus and Staphylococcus epidermidis.";
Antimicrob. Agents Chemother, 35:2151-2154 (1991).
-i- FUNCTION: DNA GYRASE NEGATIVELY SUPERCOILS CLOSED CIRCULAR DOUBLE-STRANDED DNA IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES THE INTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED DNA RINGS, INCLUDING CATENANES AND KNOTTED RINGS.
-i- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.
-i- SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS PRESDANCIETED ACTIVITY AND CHAINS. THE A CHAIN IS PRESDANCIETED
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                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=ATCC 12228;
Zhang Y., Ren S., Li
Chen Z., Wen Y.;
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01-OCT-1996
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license@isb-sib.ch).
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MEDLINE=98044033; PubMed=9384377;
Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.
Kunst F., Ogasawara N., Moszer I., Bolotin A., Borchert
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Brochert
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Danie
Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institute.
                                                                                                                                                                                                                                                                       Bacillus subtilis.
Bacteria; Firmicutes;
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HSSP; P09097; 1AB4.
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                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                        subtilis chromosome
                                                                                                                                                                     Ogasawara N., Nakai S., Yoshikawa
"Systematic sequencing of the 180
                                                                                                                                                                                                   MEDLINE=96051385; PubMed=7584024;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l'opoisomerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGRFAMs; TIGR01063; gyrA; 1.
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m; PD000742; DNA_topoisoIV;
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                                                                                                                                         chromosome containing 1:1-14(1994).
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3 (Rel. 41, Last annotation update)
-alanine carboxypeptidase precursor (
(DD-carboxypeptidase) (CPase) (PBP5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   893 AA;
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24.9%; Pred. No.
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S->F: RESISTANT TO CIPROFLOXACIN.
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kilobase region of the
replication origin.";
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(See http://www.isb-sib.ch/announce/
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RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Parro V., Pohl T.M., Portetelle B., Porwollik S., Prescott A.M.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tamconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Voshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
RT Subtilis.",
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT Subtilis.",
EMBL; D26185; BAA0524
EMBL; Z99104; CAB1178
EMBL; M13766; AAA2237
PIR; S66040; S66040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waxman D.J., Strominger J.L.;
"Sequence of active site peptides from the penicillin-sensitive alanine carboxypeptidase of Bacillus subtilis. Mechanism of penicillin action and sequence homology to beta-lactamases.";
J. Biol. Chem. 255:3964-3976(1980).
            SubtiList; BG10074; dacA.
InterPro; IPR001967; Ala/AlaCBptasel.
                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Primary structure of the COOH-terminal membranous segment of penicillin-sensitive enzyme purified from two Bacilli."; J. Biol. Chem. 256:2067-2077(1981).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waxman D.J., Strominger J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=81117303; PubMed=6780559;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 390:249-256(1997).
                                                        MEROPS; S11.001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reduced heat resistance of mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteriol.
                                                                                                                                                                                                                                                                                                                          PATHWAY: Peptidoglycan synthesis; final stages. SUBCELIULAR LOCATION: Membrane-associated. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S11; ALSO D-ALANYL-D-ALANINE CARBOXYPEPTIDASE 1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: REMOVES C-TERMINAL D-ALANYL RESIDUES FROM SUGAR-PEPTIDE CELL WALL PRECURSORS.
                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: D-alanyl-D-alanine + H(2)O
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                                                                                        ; BAA05246.1; -.; CAB11786.1; -.; AAA22375.1; -.
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RESULT 12
SPT7_YEAST
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Best Local
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ACT SITE
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                            Transcriptional activator SPT7. SPT7 OR YBR081C OR YBR0739.
        yeast proteins.";
Nucleic Acids Res. 20:2603-2603(1992).
-!- FUNCTION: TRANSCRIPTIONAL ACTIVATO
                                                                                                                                                                                                   Steensma H.Y.
                                                                                                                                                                                                                                                                         MEDLINE-95229044; PubMed=7713415;
Gansheroff L.J., Dollard C., Tan P., Win
"The Saccharomyces cerevisiae SPT7 gene
important for transcription in vivo.";
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01-FEB-1994 (Rel.
01-OCT-1996 (Rel.
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Hydrolase; Carboxypeptidase; F
                                                 Haynes S.R.,
Dawid I B.;
                                                                       SEQUENCE OF 463-523 FROM N.A. MEDLINE=92285152; PubMed=1350857;
                                                                                                       Submitted
                                                                                                                           Andre B.,
                                                                                                                                    STRAIN=S288c
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                                        "The bromodomain:
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Signal; Complete p
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ACYLATED BY PENICILLIN.
E -> Q (IN REF. 3).
E -> Q (IN REF. 4).
; DA6C5B0307D7C117 CRC64;
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Pred. No. 11;
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           ACTIVATOR
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SWISS-PROT entry

SUBCELLULAR SIMILARITY:

Contains 1 bromodomain.

LOCATION: Nuclear.

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RESULT 13
LIP_STAEP
ID LIP_STAEP
AC Q02510;
DT 01-JUN-1994
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Best Local S
Matches 39
       Zhang Y., Ren
           STRAIN=ATCC 12228;
Zhang Y., Ren S., Li
Chen Z., Wen Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                        Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales; Staphylococcus
                                                                                                                                                                             Lipase precursor GEHC OR SE0281.
                                                                                                                                                                                                 28-FEB-2003
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00633; BROMODOMAIN_1; 1.

PROSITE; PS50014; BROMODOMAIN_2; 1.

Transcription regulation; Nuclear protein; Activator; Bromodomain.

DOMAIN 458 528 BROMODOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00503
SMART; SM00297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGD; S0000285; SPT7.
GO; GO:0000124; C:SAGA complex; I
InterPro; IPR001487; Bromodomain.
Pfam; PF00439; bromodomain; 1.
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PIR; S41552; S41552.
HSSP; Q92831; 1B91.
 Submitted
                                         SEQUENCE
                                                                      epidermidis."
                                                                                "Molecular analysis
                                                                                             Farrell A.M.,
                                                                                                    MEDLINE=93171870; PubMed=8436947;
                                                                                                                            SEQUENCE
                                                                                                                                             NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                             Microbiol.
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                                         FROM N
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(NOV-2002)
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                                                                                                                           N.A.,
                                                                                              Foster
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41, Last annotation update)
(EC 3.1.1.3) (Glycerol ester
                                                             139:267-277 (1993)
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                                                                                             T.J.,
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the
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                                                                                             Holland K.T.;
EMBL/GenBank/DDBJ
                    G.,
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databases
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RESULT 14
TIG_STAAM
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Best Local S
Matches 39
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Q99TI6;
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ACT_SITE
ACT_SITE
CONFLICT
CONFLICT
                                                   SEQUENCE FROM N.A.
STRAIN-Mu50 / ATCC 700699, and N315;
MEDLINE-21311952; PubMed-11418146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no room use by non-profit institute.
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              Kuroda M., Ohta T., Uchiyama I., Baba T.,
Cui L., Oquchi A., Aoki K.-I., Nagai Y.,
                                                                                                                                                                              Staphylococcus aureus Staphylococcus aureus
                                                                                                                                                                                                                       Staphylococcus
                                                                                                                                                                                                                                          Trigger factor (TF).
TIG OR SAV1675 OR SA1499 OR MW1619.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                           Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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Kanamori M.,
                                                                                                                                    NCBI_TaxID=158878,
                                                                                                                                                                                                                                                                                    28-FEB-2003
                                                                                                                                                                                                                                                                                                      28-FEB-2003
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MISCELLANEOUS: THE EXPRESSION OF STAPHYLOCOCCUS LIPASE
NEGATIVELY REGULATED BY BACTERIOPHAGE LYSOGENIZATION (I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A47705; A47705.
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; IPR000734; Lipase.
; IPR000379; Ser_estrs_site.
;04650; YSIRK_sigmal; 1.
; TIGR01168; YSIRK_sigmal; 1.
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(Rel. 41, Last )
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                                                                                                                                         es; Bacillales;
158879, 196620;
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77343 MW;
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Maruyama
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LIPASE.
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CHARGE RELAY SYSTEM (BY
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E -> G (IN REF. 1).
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Pred. No.
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RESULT 15

SKM1_YEAST

ID SKM1_Y:

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Best Local :
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  SKM1 YEAST STANDAI
Q12469; Q06940;
01-NOV-1997 (Rel. 35,
01-NOV-1997 (Rel. 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
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InterPro; IPR001179; FKBP PPIABE.
InterPro; IPR005216; Trig_fac.
Pfam; PF00254; FKBP; 1.
TIGREPAMS; TIGR00115; tig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AP003363; BAB57837.1; -. EMBL; AP003134; BAB42766.1; -. EMBL; AP004827; BAB95484.1; -.
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Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I.,
Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui ]
Yamamoto K., Hiramatsu K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A89951; A89951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Whole genome sequencing of aureus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lancet 359:1819-1827(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome and virulence determinants of high virulence community.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lancet 357:1225-1240(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Involved in protein export. Acts as a chaperone by maintaining the newly synthesized protein in an open conformation
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PS00454; FKBP_PPIASE_2; FALSE_NEG.
PS50059; FKBP_PPIASE_3; 1.
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                                                                                                                                                                                                DAEANTVDEYKENLRKRLAEQKATDAENV----EKEEAITKATDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chaperone; Isomerase; Rotamase; 3 248 PPIASE, FKBP-TYPE.
                                                                          STANDARD;
                                                                                                                                                                                                                                             SHRKEDLOREEHSOKSDSTKDVTATVLDKNNISSKSTTN
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    sequence update)
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
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                                                                          B
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DOMAIN

NP BIND

BINDING

ACT SITE

CONFLICT

CONFLICT
                                                                                                                                                PROSITE; PS50108; CRIB; 1.
PROSITE; PS50003; PH DOMAIN;
PROSITE; PS50011; PROTEIN_KI
                                                                                                                                                                                       ProDom; PD000001; Prot ki
SMART; SM00285; PBD; 1.
SMART; SM00233; PH; 1.
SMART; SM00233; PH; 1.
                                                                                                                                                                                                                                                 Pfam; PF00786; PBD; 1.
Pfam; PF00169; PH; 1.
Pfam; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE
                                                                                                                                                                                                                                                                                                                    InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     suppressor gene for tRNA-
delta element.";
Yeast 11:1069-1075(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                         PIR; S51884; S51884.
SGD; S0005473; SKM1.
GO; GO:0000074; P:regulation
                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X69322; CAA49163.1; -.
EMBL; Z48149; CAA88147.1; -.
EMBL; Z74855; CAA99132.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: MAY BE INVOLVED IN CELLULAR SIGNALLING FUNCTIONS. MAY PLAY A ROLE IN MORPHOGENETIC CONTE-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PRO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Characterization of SKM1, a Saccharomyces novel Ste20/PAK-like protein kinase."; Mol. Microbiol. 23:431-444(1997).
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MEDLINE=97197189; PubMed=9044278;
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Serine/threonine-protein kinase SKM1 (EC 2.7.1.-) (Protein kinase
 CONFLICT
                                                                                              DOMAIN
                                                                                                              DOMAIN
                                                                                                                         Transferase;
                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Contains 1 CRIB domain-
-!- SIMILARITY: Contains 1 PH domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vandenbol M., Durand P., Portetelle D., Hilger F.;
"Sequence analysis of a 44 kb DNA fragment of yeast chromosome including the Tyl-H3 retrotransposon, the sufl(+) frameshift suppressor gene for tRNA-Gly, the yeast transfer RNA-Thr-la and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96076631; PubMed=7502582; Vandenbol M., Durand P., Portetel
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                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000095; PAKbox/Rhobndng.
InterPro; IPR001849; PH.
                                                                                                                                                                                                                                                                                                         nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STE20 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                   IPR000719; Prot_kinase.
IPR002290; Ser_thr_pkin
                                                                                                                                                                                                                                                                                                       IPR001245; Tyr_pkinase.
 123
366
406
507
303
320
                                                                                                                       DO11; PROTEIN KINASE DOM; 1.
D108; PROTEIN KINASE ST; 1.
Serine/threonine-protein ki
 136
639
374
406
507
303
306
320
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                                                                                                                                                                                                                                     kinase;
PROTEIN KINASE.
ATP (BY SIMILAR)
ATP (BY SIMILARITY.
BY SIMILARITY.
S -> A (IN REF.
R -> Y (IN REF.
                                                                                                                                                                                                                                                                                                                     pkinase.
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YTP (BY SIMILARITY):
Y SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain.
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                                                                                                                           kinase;
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REF. 1).
REF. 1).
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MBL outstation -
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RESULT 16
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Best Local
           InterPro; IPR006315; A
InterPro; IPR005546; A
InterPro; IPR000710; I
InterPro; IPR004899; E
Pfam; PF03797; Autotra
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01-NOV-1995
28-FEB-2003
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CONFLICT
                                                                                                                                                                                                                                                                                                                                             Poulsen K., Reinholdt J., Kilian M.;
Poulsen K., Reinholdt J., Kilian M.;
"A comparative genetic study of serologically distinct Haemophil
influenzae type 1 immunoglobulin Al proteases.";
J. Bacteriol. 174:2913-2921(1992).
-i- FUNCTION: VIRULENCE FACTOR; CLEAVES HOST IMMUNOGLOBULIN A
PRODUCING INTACT FC AND FAB FRAGMENTS.
-i- CATALYTIC ACTIVITY: Cleavage of immunoglobulin A molecules
certain Pro-|-Xaa bonds in the hinge region. No small molecules
                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss-Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restrate by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haemophilus influenzae.
Bacteria; Proteobacteria; Gam
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAEIN
                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                              MEROPS; S06.001;
                                                                                                        EMBL; M87489; AAA24966.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92234949; PubMed=1373717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=HK715 / Serotype B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mmunoglobulin
                                                                                                                                                                                                                                                        DOMAIN: THE SIGNAL PEPTIDE GUIDES THE PRECURSOR TO THE PERIPLISPACE, AND THE CARBOXY-TERMINAL HELPER DOMAIN ASSOCIATES WITH OUTER MEMBRANE TO FORM A FORE FOR EXCRETION OF THE PROTEASE DOMAIN. THE HELPER DOMAIN IS THEN RELEASED BY AUTOPROTEOLYSIS SIMILARITY).
                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO PEPTIDASE FAMILY S6.
                                                                                                                                                                                                                                                                                                                          substrates are known.
SUBCELLULAR LOCATION: Secreted.
                                                                                           A41859; A41859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         310 LAPSAPATKNHDSKTKWHKEDLLELKNNDDSNEIIMKMKTVAIDVN 355
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Proteobacteria; Gammaproteobacteria;
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(Rel. 32, Last sequence update)
(Rel. 41, Last annotation updat)
lin Al protease precursor (EC 3.
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            Autotransporter;
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                       Pertactin.
                                       IgA_S6
                                                  Autotransporter.
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Pred. No. 27;
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                                                                                                                                               http://www.isb-sib.ch/announce/
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RESULT 17
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01-NOV-1995
28-FEB-2003
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ACT SITE
DOMAIN
                                                                                                                                         Eki T., Naitou M., Hagiwara H., Abe M., Ozaba M., Sasanuma M., Tsuchiya Y., Shibata T., Ktanabe K., Yamazaki M.-A., Tsashiro H., Hanaoka F., Murakami "Fifteen open reading frames in a 30.8 kb region chromosome VI from Saccharomyces cerevisiae."; Yeast 12:177-190(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase; Serine protease; SIGNAL 1 25 CHAIN 26 1014
                                                                                                                                                                                                                                                                                  Yamazaki M., Tashiro H., Eki T.;
"Analysis of the nucleotide sequence of chromosome Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                          Murakami Y., Naitou M., Hagi
Sasanuma S.-I., Sasanuma M.,
Yamazaki M., Tashiro H., Eki
                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical YFR038W.
                                  or send an email to license@isb-sib.ch).
                                             modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                        STRAIN=S288c / AB972;
MEDLINE=96287654; PubMed=8686381;
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=S288c / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00921; IGASERPTASE.
           EMBL; D50617;
                                                                                the European Bioinformatics Institute.
                                                                                                        This
                                                                                                                                                                                                                                                                                                                                              MEDLINE=95400292; PubMed=7670463;
                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                             -!- SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY.
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4932;
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                                                                                          SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                         Genet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YEAST
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                                                                     non-profit institutions as long
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           BAA09277.1;
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helicase in CDC26-SAP155
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                                                                                                                                                                                                                                                                                                                                  Hagiwara H.,
                                                                                                                                                                                                                                                                                                             Eki T.;
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8
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75;
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a Y., Soeda
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                                                                   There are no rest
                                                                                                                                                                                                   Ozawa M., Sasanuma
tanabe K., Ono A.,
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                                            http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A1 PROTEASE. (POTENTIAL).
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                                                                                                                                                                              of.
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Best Local S
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001761; Q17362;
15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Muscle M-line assembly protein unc-89 (Uncoordinated UNC-89 OR CO9D1.1.
                                                                                                          Waterston
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00271; helicase C; 1.

Pfam; PF00176; SNF2_N; 1.

SMART; SM00487; DEXDC; 1.

SMART; SM00480; HELLCC; 1.

SMART; SM00490; HELLCC; 1.

ATP-binding.

ATP-binding.

ATP-binding.

ATP-BIND 247 254 ATP (POTENTIAL).

SITE 352 355

SEQUENCE 778 AA; 88730 MM; 3E6C0857B5EABD84 CRC6
                                                                                                                                                                  STRAIN-Bristol N2;
Du Z., Le T.T., Wilson R.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
   ++
                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                            MEDLINE-96180278; PubMed-8603916;
Benian G.M., Tinley T.L., Tang X., Borod
"The Caenorhabditis elegans gene unc-89,
assembly, encodes a giant modular protei
                                                                                                                                                                                                                                                                                                                                           STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001410; DEAD.
InterPro; IPR001650; Helicase
InterPro; IPR000330; SNF2_N.
                                                                                                                                          REVISIONS
                                                                                                                                                                                                                                                                transduction domains.
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=6239;
                                                                                                                                                                                                                                    2
these signals, localizes, and then participates in assemiline.

M-line.

TISSUE SPECIFICITY: Localizes to the middle of A-bands.

SIMILARITY: Contains 1 DBL-homology (DH) domain.
                                                           nitted (APR-2002) to the EMBL/GenBank/DDBJ databases. FUNCTION: Structural component of the muscle w-line. Myofilament lattice assembly begins with positional cues laid down in the basement membrane and muscle cell membrane. UNC-89 responds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S0001934; YFR038W. rPro; IPR001410; DE
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                                                                                                                                                                                                                    N.A.
                                                                                                                                                                                                                                                   132:835-848(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                          Nematoda;
                                                                                                                                                                                                                                                                                                                                                             FUNCTION,
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                             SPECIFICITY
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Pfam; PF00041; fn3; 1:
Pfam; PF00047; ig; 47.
Pfam; PF00169; PH; 1:
Pfam; PF05177; RCSD; 5:
Pfam; PF005177; RCSD; 5:
Pfam; PF00010; SH3; 1:
Pfam; PF00010; SH3; 1:
SMART; SM00408; IGC2; 23.
SMART; SM00326; RhOGEF; 1:
SMART; SM00326; SH3; 1:
SMART; SM00326; SH3; 1:
PROSITE; PS50010; DH 2; 1:
PROSITE; PS50010; DH 2; 1:
PROSITE; PS50031; PH DOMAIN
PROSITE; PS50002; SH3; 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WormPep; C09D1.1; CE30426.
InterPro; IPR003961; FN III.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR007598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003049; PH.
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-!- SIMILARITY: Contains 49 immunoglobulin-like C2-type domains.
-!- SIMILARITY: Contains 1 PH domain.
-!- SIMILARITY: Contains 5 RCSD domains.
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EMBL; AF003131; AAB54132.2;
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InterPro; IPR007850;
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; IG_LIKE; 49
; PH_DOMAIN;
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Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
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15-SEP-2003 (Rel. 42, Last annotation update)
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MEDLINE=2108560; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K.,
Kawai J., Shinagawa A., Shibata K.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                 01-OCT 1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ribonucleic acid trafficking protein 1 (5'-
(EC 3.1.11-) (P116).

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NCBI_TaxID=4932;
                                            Eukaryota; Fungi; Ascomycota; Saccharomycetales; Saccharomycetales;
                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes,
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MGI:1355295; Nsbpl.
GC:0005654; C:nucleoplasm; IDA.
GC:0003682; F:chromatin binding activity; IDA.
GC:0006356; P:regulation of transcription from Pol I prom.
GC:0006356; P:regulation of transcription from Pol I prom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         brain, lung, pancreas and eye.

DEVELOPMENTAL STAGE: Highest levels are found in 7-day-old embryos. Levels in the 7-day-old embryo are 4-fold higher than the adult and almost 10-fold higher than in later embryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a transcriptional activator.
SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: Widely expressed submaxillary gland, thymus, kidney an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE HMG-14/HMG-17 PROTEIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M00527; HMG17; 1.
PS00355; HMG14_17; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     requires a license agreement (S
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                             GOPEEDGKEDLHEEVGKEDLHEEDGKEGOPEEDGKEI 274
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406 AA;
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M -> V (IN REF. 1).
N -> H (IN REF. 2).
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Best Local
             Query Match
                                                                                                               Nuclear
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Landt O.,
Submitted
                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by small fine in the requires a license arrows.
                                                                                                                                                                                                                                        EMBL; S61567; AAB26818.1; -.
EMBL; M95626; AAA33960.1; -.
EMBL; L106011; AAA16950.1; -.
EMBL; Z11746; -, NOT ANNOTATED CDS.
EMBL; Z74956; CAA99240.1; -.
PIR; S20126; S20126.
                                       SEQUENCE
                                                                                                                                                                             GO; GO:0005634; C:nucleus; IDA.
GO; GO:000634; F:5'-3' exoribonuclease a
GO; GO:0006365; P:335 primary transcript
GO; GO:0006396; P:RNA processing; IMP.
                                                                                                                                                                                                                             SGD;
                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUL-1996) to the -!- FUNCTION: May function i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kenna M., Stevens A., McCammon M., Douglas M.G.;
"An essential yeast gene with homology to the exonuclease-
XRN1/KEM1 gene also encodes a protein with exoribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae required for the trafficking of mRNA.";
                                                                            MUTAGEN
                                                                                                                                                     Pfam; PF03159;
                                                                                                                                                                                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                                                                           -!- COFACTOR: Requires magnesium.
-!- SUMCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: Belongs to the 5'-3' exonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bohn C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hall B.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93268292; PubMe Aldrich T.L., di Segni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kenna M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93109318;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amberg D.C., Goldstein A.L., Cole "Isolation and characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92331925; PubMed=1628825; Amberg D.C., Goldstein A.L., Cole C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Valens M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structure
                                                                                                                                                                  nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: May function in the processing and/or trafficking of nuclear mRNA. May be involved in general transcription as well. Possesses 5'->3' exoribonuclease activity degrading poly(A) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                            mainly 5'-AMP.
COFACTOR: Requires magnesium.
                                                                                                                                                                                                                               S0005574; RAT1.
                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
                                                                                                  r protein; Hydrolase; 1
525 528
793 797
955 999
 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FROM N.A.
Hiesel R.,
I (JUL-1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM
                                                                                                                                                             IPR004859; Put_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the yeast TAP1 protein: depend on the DNA context of the target Biol, 13:3434-3444(1993).
                                       1006
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                                       A,
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Segni G., McConaughy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=8417335;
                                                                            683
                                                                                                                                                                                                                                                                                                                                           license agreement (See http://www.isb-sib.ch/announce,
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10.2%;
19.0%;
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to the
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EMBL/GenBank/DDBJ databases.
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                                                                                                                                         Nuclease;
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 Score
Pred.
                                                   YEAST
                                                             TRANSCRIPTION OF THE PROMOTER-DEFECTIVE
                                                                            Y->H: IN ALLELE TAP1-1; ACTIVATES
                                                                                       CONTAINS 2 X
YSGN REPEATS.
                                                                                                                           POLY-GLU
                                      T SUP4 TRNA(TYR)
  No. 50;
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target gene
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              Length 1006
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Adul Rahman R.N.Z., Jongsareejit B., Fujiwara S., Imanaka Tedul Rahman R.N.Z., Jongsareejit B., Fujiwara S., Imanaka Tedul Rahman R.N.Z., Jongsareejit B., Fujiwara S., Imanaka Tedul Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rahman Rah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D86222; BAA20530.1; -. HSSP; P06201; 1LGR. InterPro; IPR001691; GLN_synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics and the EMBL outsi
the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                   TIGRFAMs;
                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IFR004809; GlnA.
InterPro; IPR001637; GlnA adenyltn.
Transon oln-synt; I.
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10; PF00120; gln-synt; 1.
20; PD001057; Gln synt_C; 1.
20; PD001057; GlnA; 1.
21TE; PS00180; GLNA_1; 1.
21TE; PS00180; GLNA_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: ATP + L-glutamate +
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YEEAVEDGVSFDGSSIPGFEGIEDSDLIFKADPSTYAEIPWEGIGRVYGYIYKGDEPYQA
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(Rel. 37, Last sequence update)
(Rel. 37, Last snnotation update)
(Rel. 37, Last annotation update)
ynthetase (EC 6.3.1.2) (Glutamate--ammonia ligase)
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                                                                                                               10.1%;
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O THE GLUTAMINE SYNTHETASE FAMILY.
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                                                                                                                  Pred.
                                                                                                                  Score 86;
Pred. No.
                                                                                                                                                                                        AMP (UNDER CONDITIONS OF ABUNDANT GLUTAMINE) (BY SIMILARITY).
; 9426DCCFEEF18168 CRC64;
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                                                                                                                       22;
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                                                                              RA KUMSET, POGRAGMATA N., MOSZEY I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borrilst S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
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RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
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RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizmo M., Moesti D., Nakai S., Noback M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
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RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sekiguchi J., Sendaie Y., Sadaie Y.,
RA Sekiguchi J., Sendaie H., Kapoport G., Shin B.S., Soldo B.,
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RA Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Vasamortti A.,
Natari A., Wati A., Wedler E., Wedler H., Weitzenegger T.,
Vata K., Vasumoto K., Vasumoto K., Vata K.,
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P39793;
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01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Penicillin-binding protein 1A/1B (PBP1) [Includes: Penicillin-
insensitive transglycosylase (EC 2.4.2.-) (Peptidoglycan TGase);
Penicillin-sensitive transpeptidase (EC 3.4.-.-) (DD-transpeptidase)].
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    Bacteriol.

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des for penicillin-binding protein
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                                       Yamane K., Yasu
in E., Yoshikawa
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                                                                                                                                                                                                                                                  В.
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SubtiList; BG10954; ponA.
InterPro; IPR003661; PN III.
InterPro; IPR001264; Glyco trans 51.
InterPro; IPR001460; Transpeptdse.
Pfam; PF00912; Transglycosyl; 1.
Pfam; PF00905; Transpeptidase; 1.
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EMBL; L47838; AAB3845;
EMBL; Z99115; CAB14148
PIR; I40529; I40529.
                                                                                                                              Peptidoglycan synthesis; Cell wall; Transferase; Hydrolase; Multifunctional enzyme; Transmembrane;
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SMART; SM00060; FN3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
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increased levels of divalent cations for growth.";
J. Bacteriol. 180:4555-4563(1998).
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             TRANSMEM
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                                                                                               Antibiotic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISCELLANEOUS: CELLS LACKING THE PROTEIN REQUIRE INCREASED LEVELS OF MG(2+) OR CA(2+) FOR GROWTH AND GERMINATION. APPROXIMATELY 50% OF CELLS WITHOUT THE PROTEIN CONTAIN ABNORMAL FTSZ RINGS, SUGGESTING IT IS INVOLVED IN SEPTUM SYNTHESIS; INCREASED LEVELS OF MG(2+) OR CA(2+) ONLY PARTIALLY ELIMINATE THE SEPTATION DEFECTS. SIMILARITY: Contains 1 fibronectin type III domain.

SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATHWAY: Peptidoglycan synthesis; final stages. SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN, OVER THE WHOLE CELL AT LOW CONCENTRATIONS. ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: CELL WALL FORMATION. SYNTHESIS OF CROSS-LINKED PEPTIDOGLYCAN FROM THE LIPID INTERMEDIATES. THE ENZYME HAS PENICILLIN-INSENSITIVE TRANSGLYCOSYLASE N-TERMINAL DOMAIN (FORMATION OF LINEAR GLYCAN STRANDS) AND A PENICILLIN-SENSITRANSPEPTIDASE C-TERMINAL DOMAIN (CROSS-LINKING OF THE PEPT SUBUNITS) (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DIVISION SITE IN VEGETATIVE CELLS.
DEVELOPMENTAL STAGE: EXPRESSION IS
DECREASES DURING SPORULATION AND I
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resistance; Completé proteome.

1 37 CYTOPLASMIC (POTENTIAL).
38 58 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
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AAB38459.1; -.
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Best Local (
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ACT SITE
SEQUENCE
                                                                                                            Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human of the complete sequences of 100 new cDNA clones from brain who code for large proteins in vitro "
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DOMAIN
                                                              DNA Res. 4:141-150(1997).
-i- FUNCTION: May function as a nuclear chaperone and the assembly/disassembly of macromolecular complex
                                                                                                                                                                                                                                                                                               Garbarino J.E., Gibbons I.R.;
"Expression and genomic analysis
conserved ADA protein distantly r
BMC Genomics 3:18-18(2002).
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This SWISS-PROT entry is copyright. It is produced through a copyright. It is produced through a copyright.
                                                                                                                                                                                                                                Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                            TISSUE=Brain,
                                                                                                                                                                                                                                                         TISSUE=Testis;
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                                                                                                                                                                                                        SEQUENCE OF 3550-5596 FROM N.A.
                                                                                                                                                                                                                                            Tracey A.;
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                                    SUBCELLULAR LOCATION: Nuclear SIMILARITY: Contains 1 VWFA do
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01-OCT-1993 (Rel. 27, Cr
01-OCT-1996 (Rel. 34, La
15-SEP-2003 (Rel. 42, La
Probable ATP-dependent R
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Ripmaster T.L., Vaughn G.P., Woolford J.L.
"A putative ATP-dependent RNA helicase invocerevisiae ribosome assembly.";
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                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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SMART; SM00327; VWA; 1.
                                                         SEQUENCE FROM N.A.
MEDLINE=93087480; PubMed=1454790;
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InterPro; IPR003593; AAA ATPASE
InterPro; IPR002035; WF_A.
Pfam; PF00004; AAA; 1
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GO:0003754; F:chaperone act
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2-dependent RNA helicase DR
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Pred. No.
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RA Benes V., Brueckner M., Pelius L., Albermann K., Andre B., Ansorge W., Ra Benes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A., Ra Entian K.-D., Floeth M., Goffeeu A., Hebling U., Heumann K., Ra Entian K.-D., Floeth M., Goffeeu A., Hebling U., Heumann K., Ra Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D., Ra Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M., Ra Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M., Ra Portetelle D., Purnelle B., Scholler P., Schwager C., Schwarz S., Ra Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P., Ra Vidermedeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E., Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.; RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII."; RL Laure 387:87-90(1997).
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Best Local S
Matches 38
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NP BIND
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Pfam;
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EMBL; X91488; CAA62783.1;
EMBL; Z73113; CAA97452.1;
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"Sequence analysis of the CEN12 region of Saccharomyces cerevisiae
a 43.7 kb fragment of chromosome XII including an open reading fran
homologous to the human cystic fibrosis transmembrane conductance
regulator protein CFTR.";
reast 12:693-708(1996).
                                                                                                                                                          SEQUENCE
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SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY.
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S0003931; DRS1.
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PF00271; helicase C; 1.
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----GWEI--SGFEGKKDAGYVINLSKDTFIKPVFKK--
                                          ILDSSDDEKVEAKK---TTKKRKGKN-NKKKVSEGDNLDEDVHEDLDAGFKFDLDADDTT
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Pred. No. 43;
29; Mismatches
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KKRKGKNNKKKVSEGDNLDEDVHEDLD -> MTKKSRLRRL
RRSGRVRITRKRLVRGITSMRMFMRTWT (IN REF. 1).
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                                                                                                                                            RGA1 YEAST STANDARD; PRT; 1007 AA. P39083; P39934; O1-FEB-1995 (Rel. 31, Created) O1-FEB-1995 (Rel. 31, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update)
                                    This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stevenson B.J., Ferguson B., de Virgilio C., Bi E., Pringle J.R., Ammerer G., Sprague G.F. Jr.; "Mutation of RGA1, which encodes a putative GTPase-activating protein for the polarity-establishment protein Cdc42p, activates the pheromone-response pathway in the yeast Saccharomyces cerevisiae."; Genes Dev. 9:2949-2963(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WEDLINE=97344368; PubMed=9200815; Walencia A., Rechmann S., Teodoru Voss H., Benes V., Andrade M.A., Valencia A., Rechmann S., Teodoru Schwager C., Paces V., Sander C., Ansorge W.; "DNA sequencing and analysis of 130 kb from yeast chromosome XV.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-97060020; PubMed-8904341; MEDLINE-97060020; PubMed-8904341; Wiemann S., Rechmann S., Benes V., Voss H., Schwager C., Vicek (Stegemann J., Zimmermann J., Erfle H., Pacces V., Ansorge W.; Stegemann J., Tarlie H., Pacces V., Ansorge W.; "Sequencing and analysis of 51 kb on the right arm of chromosome from Saccharomyces cerevisiae reveals 30 open reading frames."; Yeast 12:281-288(1996).
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"The LIM domain-containing Dbml GTPase-activating protein is required for normal cellular morphogenesis in Saccharomyces cerevisiae.";
Mol. Cell. Biol. 16:1376-1390(1996).
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Stevenson B.J., Ferguson B., de Virgilio
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                                                                                           SIMILARITY: Contains 2 LIM zinc-binding domains. SIMILARITY: Contains 1 Rho-GAP domain.
SWISS-PROT entry is copyright. It is produced through a centre the Swiss Institute of Bioinformatics, and the EMBL
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t 13:655-672(1997).
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                                 collaboration
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RESULT 26

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RGO; GO:0004871; F:signal transducer activity; IPI.

RGO; GO:0004871; F:signal transducer activity; IPI.

RGO; GO:0007015; P:actin filament organization; IMP.

RGO; GO:0007118; P:apical bud growth; IPI.

RR GO; GO:0007125; P:invasive growth; IPI.

RR GO; GO:0007125; P:invasive growth; IPI.

RR GO; GO:0007124; P:sisotropic bud growth; IPI.

RR GO; GO:0007124; P:pseudohyphal growth; IPI.

RR GO; GO:0007124; P:signal transduction during conjugation with...

RR GO; GO:0007264; P:small GTPase mediated signal transduction; IPI

RR GO; GO:0007264; P:small GTPase mediated signal transduction; IPI

RR GO; GO:0007264; P:small GTPase mediated signal transduction; IPI

RR GO; GO:0007264; P:small GTPase mediated signal transduction; IPI

RR GO; GO:0007264; P:RhoGAP.

RR InterPro; IPR000198; RhoGAP.

RR PFADDOM; PF00412; LIM; 1.

RR PFADOM; PF00427; LIM; 2.
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Best Local (
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EMBL; X90518; CAA62108.1; -.
EMBL; X94335; CAA64046.1; -.
EMBL; Z75035; CAA649326.1; -.
EMBL; X90950; CAA62445.1; -.
EMBL; L02617; AAA35153.1; -.
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SMART; SM00132; LIM; 2.
SMART; SM00324; RhoGAP; 1.
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SGD; S0005653;
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DOMAIN 13
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LIM 2.
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Pred. No. 59;
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STANDARD; P Q9ER21; Q9QW92;

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Littauer U.Z., Prior P., Gundelfinger E.D., Sch
"Neuraxin, a novel putative structural protein
nervous system that is immunologically related
associated protein 5.";
EMBO J. 8:2879-2888(1989).
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MAP1B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Isolation and sequencing of the 5' associated protein (MAPIB)-encoding Gene 172:307-308(1996).
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STRAIN-Sprague-Dawley; TISSUE-Testis;
MEDLINE-96257242; PubMed-8666295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003
Microtubule
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                                                                                                                                                                                             DEVELOPMENTAL STAGE: In cerebral cortex, spinal cord and sciatic nerve levels are high early in development but decrease during postnatal development and are low in adults. In dorsal root ganglia levels remain high throughout development. INDUCTION: By nerve growth factor. INDUCTION: By nerve growth factor. OOMAIN: Has a highly basic region with many copies of the sequence KKEE and KKEI/V, repeated but not at fixed intervals, which is responsible for the binding of MAPIB to microtubules. FTM: IC1 is coexpressed with MAPIB. It is a polypeptide generated for the sequence of the sequence of the sequence of the sequence responsible for the binding of MAPIB to microtubules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    with MARIA and MAPIB proteins.
with MARIA and MAPIB proteins.
TISSUE SPECIFICITY: Nervous system (spinal cord, brain stem,
TISSUE, and arabrum). Not expressed in liver, spleen, kidney,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stabilizing microtubules.
SUBUNIT: 3 different light chains, LC1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphory ated MAPIB may play a role in the cyroskeletal changes that accompany neurite extension. Possibly MAPIB Binds to at least two tubulin subunits in the polymer, and this bridging of subunits might be involved in nucleating microtubule polymerization and in
CAUTION: A C-terminal fragment of this protein (residues 1597 2459) was originally described as neuraxin in Ref.3.
                                                                SIMILARITY: TO MAPIA
                                                                                                                                         PTM: LC1 is coexpressed with MAP1B. It is a polypeptide generated from MAP1B by proteolytic processing. It is free to associate with both MAP1A and MAP1B. It interacts with the amino-terminal region
                                                                                                              of MAP1B (By similarity).
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d protein 1B (MAP 1B) (Neuraxin)
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and Glial tumor;
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ated to microtubule-
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Best Local S
Matches 40
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MEDLINE=21848401; PubMed=11859360; Wood V., Gwilliam R., Rajandream M.A., Lyne Sgouros J., Peat N., Hayles J., Baker S., Ba Brooks K., Brown D., Brown S., Chillingworth Collins M., Connor R., Cronin A., Davis P., Gentles S., Goble A., Hamlin N., Harris D.,
                                                                                                                                                             16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein C106.14c in chromosome I
                                                                                                                                                                                               Q10342; Q9UI
01-OCT-1996
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EMBL; X60370; CAC16162.1; -.
EMBL; X16623; CAA34620.1; AL
PIR; A56577; A56577.
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                                                                                                           Schizosaccharomycetales; Schizosaccharomyces.
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Pfam; PF00414; MAP1B neuraxin; 10.
PROSITE; PS00230; MAP1B NEURAXIN; 8.
Microtubules; Repeat; Phosphorylation.
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                                                                   STRAIN=972;
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                                                                            SEQUENCE FROM N.A.
                                                                                               NCBI_TaxID=4896;
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naromycetales; Schizosaccharomycetaceae;
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GLU-RICH.

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Pred. No. 1
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          , Baker S., Basham D., Bowma
Chillingworth T., Churcher
A., Davis P., Feltwell T., E
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(See http://www.isb-sib.ch/announce/
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RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Oliver K., O'Neil S., Pearson D., Ouail M.A., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Kelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whithead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
"The genome sequence of Schizosaccharomyces pombe.";
Nature 415:871-880(2002).
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Tames K., Jones L., Moule S.,
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Q8CST4;
15-SEP-2003
15-SEP-2003
15-SEP-2003
SEQUENCE FROM N.A. STRAIN=ATCC 12228; Zhang Y., Ren S.,
                                                                 NCBI_TaxID=1282;
                                                                                    Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales;
                                                                                                                                        Translation initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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 Ren S., Li
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559
719 AA;
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(Rel. 42, Last sequence update)
(Rel. 42, Last annotation update)
initiation factor IF-2.
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HAMAP; MF 00100; -; 1.
Pfam; PP00009; GTP EFTU; 1.
Pfam; PP03144; GTP EFTU D2; 1.
Pfam; PP04760; IF2_N; 2.
ProDom; PD186100; IF2; 1.
                                                                                                                                                                                                                                                                                                                                                                             P75062;
01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
16-OCT-2001 (Rel. 4
                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; PubMed=9948633;
MEDLINE=97105885; PubMed=9948633;
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                                                                                                                                                                                                                                                                                            Mycoplasma pneumoniae. Bacteria, Firmicutes;
                                                                                pneumoniae.";
Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                        Hypothetical lipoprotein MPN052 OR MP102.
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TIGREAMS; TIGRO0231; small_GTP; 1.
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                       <del>-</del>
                                                                                                                           "Complete sequence
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                       SIMILARITY:
                                                                 SUBCELLULAR
                                           Potential).
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                       SOME,
                                                                 LOCATION:
                                                                                                                                                                                                                                                                                                                                        35, Created;
35, Last sequence update;
40, Last annotation update;
protein MG040 homolog precur
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238 G
281 G
334 . G
79343 MW;
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                                                                                  24:4420-4449(1996)
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                       J
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                       T. PALLIDIUM
                                                                 Attached
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GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

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M; 07FB5A6A59CF970C CRC
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                       TMPC.
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                                                                 the
                                                                                                                                                                                                                                                                                                                                                         precursor
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                                                                 membrane
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                                                                                                                           the
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                                                                                                                           bacterium Mycoplasma
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=Rd / KW20 / ATCC 51907;
STRAIN=Rd / KW20 / ATCC 51907;
STRAIN=Rd / KW20 / ATCC 51907;
STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=99350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Fleischmann R.D., Adams M.D., Tomb J.-F., Dougherry B.A., Merrick J.M.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherry B.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherry B.A., Kirkness E.F.,
Kerlavage A.R., Liu L.-I., Glodek A., Kelley J.M.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Scott J.M., Spriggs T., Hedblom E., Cotton M.D.,
Scott J.D., Shirley R., Liu L.-I., Saudek D.M., Brandon R.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Immunoglobulin A1 protease precursor (
IGA OR IGA1 OR H10990.
Haemophilus influenzae.
Bacteria; Proteobacteria; Gammaproteob
                                                                                                                                                                                                                                       STRAIN=Serotype D;
Wright A., Fishman Y.,
Submitted (MAY-1991) t
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                                                                                                                                                                                                                                                                                                                                   Pasteurellaceae; Haemophilus.
NCBI_TaxID=727;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GAO_HAEIN
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657 H
27 N
71671 MW;
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                                                                                                                                                                                                                                         Tai F., Plaut A.G.;
o the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                              Gammaproteobacteria; Pasteurellales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36;
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; 6147B1A5673606A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 84.5;
Pred. No. 44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      update) (IGA1 protease).
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RESULT 31
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CONFLICT
                                                                                                                                                                                                                                                                                                              Pfam; PF03797; Autotransporter; Pfam; PF02395; IGA1; 1. Pfam; PF03212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                     InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                     PIR; H6
MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X59800; -; NOT ANNOTATED CDS EMBL; U32779; AAC22651.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter J.C.;
"Whole-genome random sequencing and
Rd.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fine L.D., Fritchman J.L., Gnehm C.L., McDonald L.A.,
                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                 Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 269:496-512(1995)
                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                       PRINTS; PR00921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION:
                                                                                                                                                                                                                                                                        Complete
                                                                                                                                                                                                                                                                                            rigrfams; Tigr01414; autotrans_barl; 1.
                                                                                                                                                                                                                                                                                                                                                                                           TIGR; HI0990; -
                                                                                                                                                                                                                                                                                                                                                  [nterPro;
                                                                                                                                                                                                                                                                                                                                                           [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Secreted.

SUBCELLULAR LOCATION: Secreted.

DOMAIN: THE SIGNAL PEPTIDE GUIDES THE PRECURSOR TO THE PERIPLA SPACE, AND THE CARBOXY-TERMINAL HELPER DOMAIN ASSOCIATES WITH OUTER MEMBRANE TO FORM A PORE FOR EXCRETION OF THE PROTEASE DOMAIN. THE HELPER DOMAIN IS THEN RELEASED BY AUTOPROTEOLYSIS SIMILARITY).

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: VIRULENCE FACTOR; CLEAVES HOST IMMUNC PRODUCING INTEGET FC AND FAB FRAGMENTS.
CATALYTIC ACTIVITY: Cleavage of immunoglobulin certain Pro-|-xaa bonds in the hinge region. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       substrates are known.
                                                                                                                                                                                                                                                                                                                                                                                                                H64106; H64106.
                                                               76
                                                                                    24;
                                                                                                                                                                                                                                                                                                                                                                                                     ; S06.001; -.
                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             non-profit institutions as long and this statement is not removed
                                                                                                                                                                                                                                                                      proteome
SOPOETSAEETTAASTDETTIADNSKRSKPNR 1379
                    -- QKSDSTKDVTATVLDKNNISSKSTTNNPNK 164
                                          INTGSATAITETAEKSDKPQTETAASTEDASQHKANTVADNSVANNSESSDPKSRRRSI
                                                               INLSKOTFIKPVFKKIEEKKEEENKPTFDVSKKKONPQVNHSQLNESHRKEDLQREEHS-
                                                                                                                                                                                                                                                                                                                                                IPR006315; Autotransport.
IPR005546; Autotransporter.
IPR000710; IgA_S6.
IPR004899; Pertactin.
                                                                                                                                                                                                                                                                                 Serine protease;
                                                                                                                                                    1015
288
253
272
464
866
1036
1074
                                                                                     Conservative
                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                      IGASERPTASE.
                                                                                                                                                    1014
1694
288
288
254
272
464
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1036
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Small K.V., Fraser
                                                                                     15;
                                                                                                                                        MW;
                                                                                                                                                                                                                                                                                  Transmembrane;
                                                                                                Pred.
                                                                                                         Score
                                                                                                                                                                                                                            HELPER PEPTIDE PROBABLE.
                                                                                                                                                                                                                                                 IMMUNOGLOBULIN
                                                                                                                                                                                                                                                               POTENTIAL
                                                                                       Mismatches
                                                                                                                                                                        A (IN REF. )
E (IN REF. )
T (IN REF. )
D (IN REF. )
                                                                                                                                C52427013F93178C CRC64;
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                                                                                               84.5;
No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                  (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    There are no
                                                                                                                                           REF.
                                                                                      лВ 1;
1.2e+02;
эв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOST IMMUNOGLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Geoghagen N.S.
aser C.M., Smit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as
                                                                                                                                                                                                                                                                                  Zymogen; Signal;
                                                                                                                                                                                                                                          (POTENTIAL).
                                                                                                                                                                                                                                                    A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          its content
                                                                                                                                                                                                                                                    PROTEASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haemophilus influenzae
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                                                                                                          Length 1694;
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RESULT 32
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Best Local S
Matches 50
                         Q00799;
01-APR-1993
01-APR-1993
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Oocyte;

MEDLINE-9322498; PubMed=8468323;

Fujiwara S., Kawahara H., Makabe K.W.,

"A complementary DNA for an ascidian er

"A complementary DNA for an ascidian er
                                                                               RBP2
Reticulocyte RBP2.
                                                                                           PLAVB
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                            Nuclear protein; Developmental protein.

DOMAIN

98

143

ASP/GLU-RICH (ACIDIC).

DOMAIN

219

228

ASP/GLU-RICH (ACIDIC).

DOMAIN

219

ASP/GLU-RICH (ACIDIC).

NUCLEAR LOCALIZATION S.

DOMAIN

444

451

NUCLEAR LOCALIZATION S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein N1.";
J. Biochem. 113:189-195(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Halocynthia roretzi
Eukaryota; Metazoa;
Stolidobranchia; Pyu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1994
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00515; TPR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D13541; BAA02741.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001440; TPR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way iffied and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CELLS OF METAMORPHOSED JUVENILES.
SIMILARITY: TO XENOPUS LAEVIS HISTONE BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEVELOPMENTAL STAGE: THIS PROTEIN IS DETECTED OF ALL CELLS IN EMBRYOS AND LARVAE BUT IS NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY: EMBRYO AND LARVAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: MAY FUNCTION AS A
                                                                               PLAVB
                                                                                                                                                                                                   393
                                                                                                                                                452
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                                                                                                                                                                                                                            ISGF----EGKKDAGYVINLSKDTFIK--PVFK----KIEEKKEEENKPTFDVSKKKDNP
                                                                                                                                                                                                                                                       KEIISECKEVGELKELIP-----
                                                                                                                                                                                                                                                                                 KEFILN-KDTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWE
                                                                                                                                               DEDNQPAESKENESKKAKQEETEEATNGHSAVKKDT-DVTDKNGTNGHSKT--PKK
                                                                                                                                                                                                   -SPFRQASEGESSSGLGASTSDDKPCSTIPIRKVAPTSVPVAKDSPSDITHLVRRKRPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBRYONIC CELL DIVISIONS.
                                                                                                                                                                                                                                                                                                                                                               219
444
465
510 AA;
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(Rel.
(Rel.
                       (Rel. 25, Created)
(Rel. 25, Last sequence update)
(Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                           Conservative
            binding
                                                                                                                                                                        QVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTINNPNK 164
                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tzi (Sea squirt).
oa; Chordata; Urochordata; Ascidiacea;
Pyuridae; Halocynthia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40,29
                                                                                                                                                                                                                                                                                                                                                                56871 MW;
                                                                                                                                                                                                                                                                                                                      9.98;
           protein
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                           25;
                                                                                                                                                                                                                                                                                                                     Score
Pred.
             N
                                                                                                                                                                                                                                                                                                                                                                           NUCLEAR LOCALIZATION SIGNAL NUCLEAR LOCALIZATION SIGNAL
                                                                                                                                                                                                                                                                                                                                                                D9961E5953E976FF CRC64;
                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOSOME ASSEMBLY FACTOR DURING
                                                                                                                                                                                                                                                                                                                         N 64
                                                                              1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         embryonic nuclear antigen Hgv2 the amphibian histone-binding
                                                                                                                                                                                                                                                       -DINSKI---EDVILA--KKQMQK---LDG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                         36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Satoh N.;
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                                                                                                                                                                                                                                                                                                                                    ۳.
                                                                                                                                                                                                                                                                                                           61;
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                                                                                                                                                                                                                                                                                                           40;
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RESULT 33
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Best Local S
Matches 42
                                                                                                                                                                                                                                                                PEA
FENR_
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NON_TER
SEQUENCE
                                                                                                             PETH.
Pisum sativum (Garden pea).
Pisum sativum (Garden pea).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
Spermatophyta; Magnoliophyta; Papillonoideae; Vicieae; Pisum.
                                                                                                                                                                                  01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ferredoxin--NADP reductase, leaf isozyme, chl.
(EC 118.1.2) (FNR).
                                                           STRAIN=cv. Little
Newman B.J., Gray
                                                                                                                                                                                                                                       P10933;
01-JUL-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no rest
use by non-profit institutions as content
modified and this statement is not removed. Usage by an
entitles requires a license agreement (See http://www.isb-
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
SEQUENCE
                                    reductase
                                                                                     SEQUENCE FROM
                                                                                                           NCBI_TaxID=3888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=31273;
                        Plant Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M88098; AAA29744.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              merozoites."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92315338; PubMed=1617731;
Galinski M.R., Medina C.C., Ingra
"A reticulocyte-binding protein c
                                                "Characterisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium vivax (strain Belem).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Membrane-bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: INVOLVED IN RE HUMAN RETICULOCYTE CELLS
                                                                                                                                                                                                                                                                PEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a en the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69:1213-1226(1992).
                                                                                                                                                                                                                                                                                                                             433
                                                                                                                                                                                                                                                                                                                                                      152
                                                                                                                                                                                                                                                                                                                                                                              373
                                                                                                                                                                                                                                                                                                                                                                                                                                313
                                                                                                                                                                                                                                                                                                                                                                                                       105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 253 REIMNKKDEIKSYLSEIKEYKDKCTTEISNSKRGKDKIEFLEKFKPNEESNSNKVNINEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
OF 270-360 FROM N.A.,
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                                                                                                                                                                                                                                                                                                                                                      SIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEFILNKD--TGEVSELKPH--RVTVTIQNGKEMSSTI-----VSEEDFILPVYKGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor; Membrane
                                                                                                                                                                                                                                                                                                                                                                                                      VSK--KKDNPQV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKGYQFDGWEISGFE-GKKDAGYVINL--SKDTFIKPVFKK----IEEKKEEENKPTFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1251 12
1251 AA;
                        Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                      154
                                                                                                                                                                                                                                                                                                                              435
                                                                                     N.A.
                                                                                                                                                                                                                                                                STANDARD;
                        10:511-520(1988)
                                                of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1251
                                                                        Marvel; TISSUE=Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143741 MW;
                                                full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IN RETICULOCYTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 84; DB
Pred. No. 96;
37; Mismatches
 AND
                                                                                                                                                                                                                                                                                                                                                                                                      NHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLD--KN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54BA51C7404AC572 CRC64;
 MUTAGENESIS
                                                 CDNA
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                                                                                                                                                                                                   chloroplast precursor
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EMBL; L15567; AAB59304.1; -.
PIR; S04030; S04030.
PDB; 1QFZ; 01-SEP-99.
PDB; 1QGQ; 01-SEP-99.
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Nat. Struct. Biol. 6:847-853(1999).
-i- FUNCTION: MAY PLAY A KEY ROLE IN REGULATING THE RELATIVE AMOF CYCLIC AND NON-CYCLIC ELECTRON FLOW TO MEET THE DEMANDS (PLANT FOR ATP AND REDUCING POWER.
-i- CATALYTIC ACTIVITY: Reduced ferredoxin + NADP(+) = oxidized ferredoxin + NADPH.
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MEDLINE=99396739; PubMed=10467097;
Deng Z., Aliverti A., Zanetti G., Arakaki A.K., (
Orellano E.G., Calcaterra N.B., Ceccarelli E.A.,
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MISCELLANGOUS: FUR IS PROBABLY ATTACHED TO THE MEMBRANE BY A SPECIFIC BINDING PROTEIN.
SIMILARITY: WITH OTHER SPECIES FUR.
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SUBCELLULAR LOCAT
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BY SIMILARITY.
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Y->W, F, S.
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Thylakoid; Membrane;
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                                                               related-protein 1.
U2AF1-RS1 OR U2AFBPL
Homo sapiens (Human).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo NCBI_TaxID=9606;

Chordata; Craniata; Vertebrata; Euteleostomi;

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                             Plasmodium falciparum
Eukaryota; Alveolata;
NCBI_TaxID=5837;
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                                                                                                                     Glutamic
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                                                                                                                                                                                                                       GARP_PLAFF
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Pfam; PF00642; zf-CCCH; 2.
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EMBL; U51224;
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Biochem. Biophys. Res. Commun.
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Dejong P.J., Plass C., Chapman V.M
"Absence of imprinting in UZAFBPL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96163878; PubMed=8586425;
Kitagawa K., Wang X., Hatada I., Yamaoka
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GO:0005634; C:nucleus; NAS.
GO:0003723; F:RNA binding a
GO:0003723; R:RNA_rec_mo
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SIMILARITY: Contains 1 RNA recognition motif (
SIMILARITY: Contains 2 C3H1-type zinc fingers.
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Chapman V.M., Hayashizaki
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Yamazaki M., Tashiro H., Yokoyama K., Sor
"Molecular cloning of cDNA encoding a hum
expression is induced by adenovirus type
Agric. Biol. Chem. 54:3163-2170/1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HS9A_HUMAN STANDARD; PRT; 731 AA. P07900; Q9BVQ5; 01-AUG-1988 (Rel. 08, Created) 01-APR-1990 (Rel. 14, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Heat shock protein HSP 90-alpha (HSP 86). HSPCA OR HSPC1 OR HSP90A.
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                                                                                                                                                                                                                                                                                                                                    TISSUE=Peripheral blood lymphocytes; MEDLINE=89386066; PubMed=2780322;
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Mol. Biochem. Parasitol. 31:199-202(1988).
                                                                                                                      SEQUENCE FROM N.A. MEDLINE=91242090;
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44; Conser
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                                                                                                                         PubMed=1368637;
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Pred. No. 54;
33; Mismatches
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15 X 3 AA TANDEM REPEATS OF K-K-X.
9 X APPROXIMATE TANDEM REPEATS.
5 X APPROXIMATE TANDEM REPEATS.
POLY-GLU.
7 X APPROXIMATE TANDEM REPEATS.
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Catarrhini; Hominidae,
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heat-shock protein whose
E1A in HeLa cells.";
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A Strausberg R.D., Collins F.S., Wagner L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Carninci P., Prange C.,

Daratchenko L., Malek J.A., Gunaratne P.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Daratchenko J., Hulyk S.W.,

Villalon D.K., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Morley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Villalon D.K., Morley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Villalon D.K., Morley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Villalon D.K., Morley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Dalkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

M. Generch A., Schein J.E., Jones S.J.M., Marra M.A.,

Generch A., Schein J.E., Jones S.J.M., Marra M.A.,

M. Generch A., Schein J.E., Jones S.J.M., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=89343979; PubMed=2527334; Hickey E., Brandon S.E., Smale G., "Sequence and regulation of a gene heat shock protein."; mol. Cell. Biol. 9:2615-2626(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Placenta;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-311 FROM N.A.
MEDLINE=90076956; PubMed=2591742;
Walter T., Drabent B., Krebs H., Tomalak M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome assignment of related Gene 56:29-40(1987).
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MEDLINE=98324997; PubMed=9660753; Young J.C., Obermann W.M., Hartl F.U.; "Specific binding of tetratricopeptide
                                                                                                                                                                                                                                                                                                                                                                                                   Tanaka M., Tanaka T., Mitsui Y., Yamamoto M., Submitted (SEP-1996) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Generation and initial analysis of more human and mouse cDNA sequences."; proc. Natl. Acad. Sci. U.S.A. 99:16899-16
                                                                                                               threonine
                                                                                                                                                                                         MEDLINE=90008887;
                                                                                                                                                                                                               PHOSPHORYLATION
                                                                                                                                                                                                                                                                                     conserved serines that are
                                                                                                                                                                                                                                                                                                     "Two human 90-kDa heat
                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-20, AND PHOSPHORYLATION MEDLINE=89123325; PubMed=2492519;
                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 538-731 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene 83:105-115(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning and analysis of a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Benecke B.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Placenta;
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                                                                                                                                                                          Lees-Miller S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning and nucleotide
                                                          INTERACTION WITH OM34
                                                                                                                                                                                                                                                  Biol. Chem. 264:2431-2437(1989)
                                                                                                                             e human double-stranded DNA-
90-kDa heat-shock protein,
                                                                                               Chem.
                                                                                                                 residues."
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                                                                                               264:17275-17280(1989)
                                                                                                                                                                          Anderson C.
                                                                                                                                                                                                             BY DS-DNA KINASE.
                                                                                                                                                                                                                                                                                                                            Anderson C
                                                                                                                                                                                         PubMed=2507541;
 tetratricopeptide
                                                                                                                                                                                                                                                                                 shock proteins are are phosphorylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence of the murine hsp84 cDNA and
f related sequences.";
                                                                                                                                 DNA-activated
ein, hsp90 alph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86-kDa heat-shock-protein-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encoding a human 89-kilodalton
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                                                                                                                                   alpha
 repeat
                                                                                                                                   protein kinase phospl
ha at two NH2-termina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    than 15,000 full-length
                                                                                                                                                                                                                                                                                   phosphorylated in vivo at in vitro by casein kinase
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CONFLICT
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TRANSFAC;
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                                                                                                                                                                                                                                          MIM; 140571; -.
GO; GO:0005737; C:cytoplasm;
GO; GO:0003773; F:heat shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X15183; CAA33259.1; -.
EMBL; X07270; CAA30255.1; -.
EMBL; M27024; AAA63194.1; -.
EMBL; M30626; AAA36023.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C-terminal 12-kDa domain of hsp90.";
J. Biol. Chem. 273:18007-18010(1998)
                                                                                                                              SMART; SM00387; HP
PROSITE; PS00298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinf
the European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hydrolysis.";
J. Cell Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "In vivo function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF MEDLINE=99034582; PubMed=9817749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein chaperone by Cell 89:239-250(1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97262065; PubMed=9108479
                                                                                                                                                                                             InterPro; IPR003594; ATPbind ATPase.
InterPro; IPR001404; Hsp90.
Pfam; PF02518. Hamma--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBUNIT: Homodimer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: Molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Crystal structure
                                                                                                                                                                                                                                                                                                                          A32319; HHHU86.
1YER; 22-APR-98.
1YES; 22-APR-98.
1YET; 22-APR-98.
1BYQ; 28-OCT-98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (By similarity)
                                                                                                                                                                           PF02518; HATPase C; 1.
PF00183; HSP90; 1.
                                                                                                                                                                                                                                                                                                                                                                                                       BC000987; AAH00987.1; -. D87666; BAA13430.1; -. D87666; BAA13431.1; -.
                                                                                                                              ; PR00775; HEATSHOCK90
SM00387; HATPase_c; 1
E; PS00298; HSP90; 1.
                                                                                                                                                                                                                                                                                            HGNC:5253; HSPCA.
                                                                  ATP-binding;
0 0 0
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ion of Hsp90 is dependent on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of an Hsp90-geldanamycin complex: targeting
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                                                                                                                  Heat shock; Phosphorylation; 3D-structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interacts with
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n ATP binding and
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L outstation -
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Baster E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Baril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gebion K., Doup L.E., Downes M., Dayan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferrac C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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                                                                                                                                                                                                                                                                                                                       STRAIN=Berkeley;
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                                                                                                                                                                                                                                                                                                                                                                                 Ephydroidea; Drosophilidae; Drosophila.
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(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
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Pred. No. 5
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      K.A.,
                                                                               1 P.,
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RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Lilang Y., Lin X.,
RA Liu X., Mattel B., McIncosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.N., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Rainert K., Remington K., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stepleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Rubin G.M., Janu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RI T'the genome sequence of Drosophila melanogaster.";
Excence 287:2185-2195(2000)
                                                                                                                                                                                                          Best Loo
Matches
                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDINE-2246069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S. Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This
                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgn0033062; CG7843.
Pfam; PF04959; ARS2; 1.
                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE003784; AAM68343.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. U entities requires a license agreement (See httentities requires a license agreement)
                                                                                                                                                                                                                                                                                                                  Hypothetical VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Annotation of the Drosophila melanogaster euchromatic systematic review.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q9V9K7-2; Sequence=VSP_000327;
-!- SIMILARITY: BELONGS TO THE ARS2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lewis S.E.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Short
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
392
                                  119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q9V9K7-1;
                                                                                                                                                                                                          l Similarity
36; Conserv
LKEKYDVEDGLRAE - - QKTEAEKD
                                                                                                                                      KVLDEKPKDPVVYERKAEOMOSVKEVEKTINSPKEEMSEADPVSTORKPVRPVNSDGENW
                                                                                                                                                                       EVSELKP-----HRVTVTIQNGKEMSSTI-----VSEEDFILPVYKGELEKGYQFDGW
                                  LNESHRKEDLOREEHSOKSDSTKD
                                                                     DDDDAENSAPKKELAEDSKDSDSKPEDKQLNKKKTKKRKRNSSDDDSSSSSESSSSSDEEK
                                                                                                    EISGFEGKKDAGYVINLSKDTFIKPVFKKIEE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                      equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
                                                                                                                                                                                                        9.8%;
nilarity 25.0%;
Conservative 2:
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                                                                                                                                                                                                                                                                                                                  protein; 3
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                                                                                                                                                                                                                                                                               107221 MW;
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                                                                                                                                                                                                        Score 83.5; Di
Pred. No. 77;
23; Mismatches
                                                                                                                                                                                                                                                                             Missing (in isoform Short).
/FTId=VSP_000327.
v; OC1AF09E02E8AB0B CRC64;
                                  142
413
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                                                                                                                                                                                                            68;
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                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                            Indels
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RESULT 38

RESULT 38

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A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Rosak S.A., McEwan P.J., McSernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length

RT muman and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

C METHYNONI-ENDAT AND MPNA
                                                                                                           This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are use by non-profit institutions as long as its modified and this statement is not removed. Usage entities requires a license agreement (See http://or send an email to license@isb-sib.ch).
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Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara P.
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi (
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Ninomiya K., Iwayanagi T.,
Ninomiya K., Iwayanagi T.,
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30-MAY-2000 (Rel. 39, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Eukaryotic translation initiation factor 3 su
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MEDLINE=99041954; PubMed=9822659;
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Mammalia; Eutheria;
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AUG-2000) to the EMBL/GenBank/DDBJ
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GK; 075822;
MIM; 603910;
                                                                                                                                 STRAIN=Rd / KW20 / ATCC 51907;

MEDLINE=95350630; PubMede77542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Gocayne J.D. Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M. Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Greber C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.
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DOMAIN
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Bacteria; Proteobacteria; Gam
Pasteurellaceae; Haemophilus.
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01-NOV-1995
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                                                                                                                                                                                                                                                                                                                "A functional tonB gene is required virulence expression by Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003
                                                                                                            Whole-genome
FUNCTION: INTERACTS WITH OUTER MEMBRANE RECEPTOR PROTEINS THAT CARRY OUT HIGH-AFFINITY BINDING AND ENERGY DEPENDENT UPTAKE INTO THE PERIPLASMIC SPACE OF SPECIFIC SUBSTRATES. IT COULD ACT TO TRANSDUCE ENERGY FROM THE CYTOPLASMIC MEMBRANE TO SPECIFIC ENERGY-REQUIRING PROCESSES IN THE OUTER MEMBRANE, RESULTING IN THE RELEASE INTO THE PERIPLASM OF LIGANDS BOUND BY THESE OUTER
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ders J.D., Cope
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E -> G (IN REF. 1).
A -> T (IN REF. 2).
8 83624235424445AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gammaproteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 83; DB
Pred. No. 21;
25; Mismatches
                                                                                                           and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                     L.D.,
                                                                                                                                                                                                                                                                                                                influenzae type b.";
                                                                                                                                                                                                                                                                                                                            for both utilization
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                                                                                                                                                                                                                    Clayton R.A., Kirkness E.F., Dougherty B.A., Merrick J.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pasteurellales;
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                                                                                                                                    M., Brandon R
n N.S.M.,
, Smith H.O.,
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Best Local
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SEQUENCE
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VARIANT
VARIANT
                                                               Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
DOMAIN
                                                 NCBI_TaxID=9606;
                                                                                                                              16-OCT-2001 (Rel. 40, Created)
28-FEB-2003 (Rel. 41, Last seq
15-SEP-2003 (Rel. 42, Last ann
                                                                                                                                                          ADSV HUMAN
Q9Y6Ū3; Q8WU97;
16-OCT-2001 (Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
VARIANT
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Transport; Protein transport; Inner membrane; Periplasmic; Transmembrane; Signal-anchor; Repeat; Virulence; Complete F. DOMAIN

7 CYTOPLASMIC (POTENTIAL).

TRANSMEM 8 27 SIGNAL-ANCHOR (POTENTIAL).

DOMAIN 28 270 PERIPLASMIC (POTENTIAL).

DOMAIN 28 270 PERIPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U04996; AAA60460.1; -.
EMBL; U32771; AAC21917.1; -.
PIR; F64057; F64057.
TIGR; H10251; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con entitles requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
               TISSUE=Skin
                          SEQUENCE FROM N.A.
                                                                                                                   Adseverin
MEDLINE=22388257; PubMed=12477932;
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InterPro; IPR006260; TonB_C.
Pfam; PF03544; TonB; 1.
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                                                                                                                    (Scinderin)
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                                                                                                                                                                                     STANDARD;
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                                                               Chordata;
Primates;
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                                                                                                                              sequence update)
annotation update)
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E -> K (IN STRAIN TN106).
D -> N (IN STRAIN TN106).
MISSING (IN STRAIN TN106).
G -> E (IN STRAIN TN106).
G -> E (IN STRAIN TN106).
K -> Q (IN STRAIN TN106).
E -> X (IN STRAIN TN106).
E -> X (IN STRAIN TN106).
C -> R (IN STRAIN TN106).
C -> R (IN STRAIN TN106).
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Pred.
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GLU/LYS/PRO-RICH
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                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X 2 AA TANDEM REPEATS OF E-P.
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                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                  Length 270,
                                                                                                                                                                                                                                                                                                                                                                                                               CRC64;
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A Isogai T., Ota T., Hayashi K., Sugano S., Takahashi-Fujii A., Hara H.,
XI Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
XI Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
XI Arita M., Nabekura T., Ishii S., Komai F., Hara R., Yamamoto J.,
XI Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
XI WEDO human cDNA sequencing project. ".
XI WEDO human cDNA sequencing project.";
XI Submitted (MAY-2001) to the EMEL/GenBank/DDBJ databases.
XI Submitted (MAY-2001) to the EMEL/GenBank/DDBJ databases.
XI Submitted (MAY-2001) to the EMEL/GenBank/DDBJ databases.
XI Submitted (MAY-201) to the EMEL/GenBank/DDBJ databases.
XI Submitted (MAY-201) to the EMEL/GenBank/DDBJ databases.
XI Submitted (MAY-201) to the EMEL/GenBank/DDBJ databases.
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XI Submitted (MAY-201) to the EMEL/GenBank/DDBJ databases.
XI Submitted (MAY-201) to the EMEL/GenBank/DDBJ databases.
XI Submitted (MAY-201) to
        CONFLICT
                                                                                                                                 Cytoskeleton; F
DOMAIN 364
REPEAT 146
REPEAT 265
REPEAT 265
REPEAT 398
REPEAT 523
REPEAT 626
SITE 112
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Klausmer R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Bichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as more modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                    SMART;
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PRINTS; PR00597; GELSOLIN.
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EMBL; AC005281; AAD15423.1; -.
EMBL; AC0077778; BAB55361.1; -.
HSSP; P02640; 2VIL.
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Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Rutterfield Y.S.N., Krzywinski M.I., Stalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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Isogai T., Ota T., Hayashi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kalicki J., Smith-Craig Submitted (JUL-1998) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001974; Gelsolin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 248-715 FROM N.A.
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SM00262; GEL;
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                                                                                                                                                         g; Repeat; Calcium; Capping protein.
ACTIN-SEVERING (POTENTIAL).
ACTAN - SEVERING (POTENTIAL).
ACTIN - BINDING.
GELSOLIN-LIKE 1.
GELSOLIN-LIKE 2.
GELSOLIN-LIKE 3.
GELSOLIN-LIKE 4.
GELSOLIN-LIKE 5.
GELSOLIN-LIKE 5.
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Query Match Query Match Best Local Similarity 23.1%; Pred. No. 62; Matches 34; Conservative 30; Mismatches 47; Indels 3 22 RVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGK	tch 9.8%; Score 83; DB 1; Length 715; al Similarity 23.1%; Pred. No. 62; 34; Conservative 30; Mismatches 47; Indels 36; Gaps 5 22 RVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYV 75
	96; Gaps

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Minimum Maximum
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Perfect score:
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            PRINTS;
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Nucleic Acids Res. 22:2547-2551(1994).
-!- FINCTION: COMPROL OF TOPOLOGICAL STATES OF DNA BY TRANSIENT
BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPOISOMERASE I.
MAKES DOUBLE-STRAND BREAKS.
-!- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
of double-stranded DNA.
-!- SUBUNIT: Homodimer (By similarity).
                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
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                                    Pfam; PF00204; DNA_gyraseB; 1.
Pfam; PF00521; DNA_topoisoIV; 1.
Pfam; PF02518; HATPase_c; 1.
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InterPro; IPR002205; DNA_topoisoIV.
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PD000742; DNA_topoisoI
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(Rel. 31, Last seq
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                                                                                                                              NOT_ANNOTATED_CDS
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39, Last annotation update)
II (EC 5.99.1.3).
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 _topoisoIV; 1.
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Pred. No. 14;
38; Mismatches
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RESULT 3
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SEQUENCE
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PROSITE;
            the European Bioinformatics Institute. The use by non-profit institutions as not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomycetaceae;
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STRAIN=S288C / AB9
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or send an email to license@isb-sib.ch).
                                                                                                   This
                                                                                                                                                     Science 265:2077-2082(1994)
                                                                                                                                                                                                        Vaudin M.;
                                                                                                                                                                                                                                                                                                                          MEDLINE=94378003; PubMed=8091229;
                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                     -!- SIMILARITY: TO YEAST YFL042C.
                                                                                                                                                                                     "Complete nucleotide sequence
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                                          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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SM00434; TOP4c;
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(Rel. 31, Last sequence update)
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TOPOISOMERASE II; 1.

pomerase; DNA-binding; ATP-binding; Nuclear protein.

149 ATP (POTENTIAL).

830 DNA CLEAVAGE (BY SIMILARITY).

281 POLY-ASN.

316 POLY-ASN.
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              noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                       chromosome
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                                                                                                                                                                                                                                                          Mouser
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Pfam; PF02893; GRAM; 1.
SMART; SM00568; GRAM; 1.
Hypothetical protein; Transmembrane.
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16-OCT-2001
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Lien L.L., Feener C., Fischbach N., Kunkel L.M.;
Lien L.L., Feener C., Fischbach N., Kunkel L.M.;
"Cloning of human microtubule-associated protein 1B and the identification of a related gene on chromosome 15.";
Genomics 22:273-280(1994).
-I- FUNCTION: THE FUNCTION OF BRAIN MAPS IS ESSENTIALLY UNKNOWN.
PHOSPHORYLATED MAP1B MAY PLAY A ROLE IN THE CYTOSKELETAL CHA
THAT ACCOMPANY NEURITE EXTENSION. POSSIBLY MAP1B BINDS TO AT
TWO TUBULIN SUBUNITS IN THE POLYMER, AND THIS BRIDGING OF SU
MIGHT BE INVOLVED IN NUCLEATING MICROTUBULE BOLYMERICANION A
STABILIZING MICROTUBULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                  This
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                                                                                                                                                                                                                                                                                              SUBUNIT: 3 DIFFERENT LIGHT CHAINS, LC1, LC2 AND LC3, CAN ASSOCIATE WITH MAPLA AND MAPLE PROTEINS.

DOMAIN: Has a highly basic region with many copies of the sequence KKEE and KKEI/V, repeated but not at fixed intervals, which is responsible for the binding of MAPLE to microtubules.

PTM: LC1 is coexpressed with MAPLE It is a polypeptide generated from MAPLE by proteolyric processing. It is free to associate with both MAPLA and MAPLE. It interacts with the amino-terminal region
                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr
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                                                                                                                                                                                                                                                 of MAP1B (By similarity). SIMILARITY: TO MAP1A.
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  L06237;
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                                                                      non-profit institutions as long and this statement is not removed requires a license agreement (See
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                                                 email to license@isb-sib.ch).
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P54112;
01-OCT-1996
          Steedharan S., Peterson L.R., Fisher L.M.;

"Ciprofloxacin resistance in coagulase-positive and -negative staphylococci: role of mutations at serine 84 in the DNA gyrase A protein of Staphylococcus aureus and Staphylococcus epidermidis.",

Antimicrob. Agents Chemother. 35:2151-2154(1991).

-i- FUNCTION: DNA GYRASE NEGATIVELY SUPERCOILS CLOSED CIRCULAR DOUBLE-STRANDED DNA IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES THE INTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED DNA RINGS, INCLUDING CATENANES AND KNOTTED RINGS.

-i- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.

-i- SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS RESPONSIBLE FOR DNA
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                                                                                                                                                                         Hess H., Heid H., Zimbelmann R., Franke W.W.;
"The protein complexity of the cytoskeleton of bovine and human synheads: the identification and characterization of cylicin II.";
Exp. Cell Res. 218:174-182(1995).
-!- FUNCTION: POSSIBLE ARCHITECTURAL ROLE DURING SPERMATOGENESIS.
BE INVOLVED IN SPERMATID DIFFERENTIATION.
-!- SUBCELLULAR LOCATION: CALYX; SPERM HEAD CYTOSKELETAL STRUCTURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF03989; DNA GyrasēA Č; 6.
ProDom; PD000742; DNA topoisoIV; 1.
SMART; SM00434; TD04C; 1.
TIGRPAMS; TIGR01063; GyrA; 1.
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EMBL; S72603; AAB20672.1; -.
PIR; A49832; A49832.
HSSP; P09097; 1AB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cylicin II (Multiple-band
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                                                                          This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                rissuE=Testis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
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                          European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                         TISSUE SPECIFICITY: Testis.
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893 AA;
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        EMBL; X15982; CAA34
PIR; S05362; S05362
                                                      use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                  extrachromosomal DNA of the ascomycete Mol. Gen. Genet. 218:523-530(1989).
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=2/I;
                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Pezizomycotina; Pezizomycetes; Pezizales; Ascobolaceae; Ascobolus.
                                                                                                                                                                                                                                                                                                                                                                                         Probable DNA polymerase (EC 2.7.7.7).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                   (BY SIMILARITY)
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                                             email to license@isb-sib.ch).
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(Rel. 37, Last annotation update)
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DNA_pol_B.

InterPro; IPR004868; DNA_pol_B_2.
Pfam; PF03175; DNA_pol_B_2; 1.
SMART; SM00486; POLBC; 1.

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                   PRINTS, PRO0301; HEATSHOCK70.

PRODOM; PD000089; Hsp70; 1.

PROSITE; PS00297; HSP70 2; 1.

PROSITE; PS00329; HSP70 3; 1.

PROSITE; PS01035; HSP70 3; 1.

ATP-binding; Heat shock; Nucleo
                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Transferase; DNA-directed DNA polymerase; DNA replication; DNA-binding; Plasmid; Mitochondrion.

SEQUENCE 1202 AA; 138279 MW; 51D41FCEBDBF2CDE CRC64;
  SEQUENCE
                                                                                                                                                                                      InterPro; IPR001023; Hsp70.
Pfam; PF00012; HSP70; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleomorph.
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                                                                                                                                                                                                                                                                     S42488; S42488.
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  B627B08FF90C9164 CRC64;
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J ADSV HUMAN
AC Q9Y6Ü3; Q8WU97;
AC 16-OCT-2001 (Re-
-FEB-2003 (P
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RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
"Generation and initial analysis of more than 15,000 full-length
"Thuman and mouse cDNA sequences.",
In Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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                   Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Mishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H., Tahase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.; Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.; "NEDO human CDNA sequencing project."; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Ca(2+)-dependent actin filament-severing protein that the organization of the microfilament network undermeath the plasma membrane. In vitro, also has barbed end capping and pullaring activities in the presence of Ca(2+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kalicki J., Smith-Craig
Submitted (JUL-1998) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 248-715 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-527 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adseverin (Scinderin).
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15-SEP-2003 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDK 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILNKDTGEVSELKPHRVTVTIQNG---KEMSSTIVSEEDFILPVYKGELEKGYQFDGWEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ databases
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Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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This

SIMILARITY: BELONGS TO THE VILLIN/GELSOLIN FAMILY. SIMILARITY: Contains 6 gelsolin-like repeats.

SWISS-PROT entry is copyright. It is produced through

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MAPB MOUSE
ID MAPB MOUSE
AC P14873;
DT 01-APR-1990
DT 01-APR-1990
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is incommercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed.
                                                                                                                                                      01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Microtubule-associated protein 1B (MAP 1B) (MAP1.2)
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EMBL; AC005281; AAD15423.1; -.
EMBL; AK027778; BAB55361.1; -.
HSSP; P02640; 2VIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART;
         STRAIN=Swiss Webster; TISSUE=Brain; MEDLINE=90094539; Pubmed=2480963; Noble M. Lewis S.A. Cowan N.J. "The microtubule binding domain of
                                                                                                                                [Contains: MAP1 light cha
MAP1B OR MTAP1B OR MTAP5.
                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytoskeleton;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001974; Gelsolin.
                                                         SEQUENCE FROM N.A.,
                                                                               NCBI_TaxID=10090
                                                                                                Mammalia;
                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                             351 DQSDGFGKVYVTEKVAQIKQIPFDASKLHSSPQMAAQHNMVDDGSGKVEIWRVENN 406
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                                                                                                                                                                                                                                                                                                                                                                           239
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                                                                                                                                                                                                                                                                                                                                                   63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; PR00597; GELSOLIN.
SM00262; GEL; 6.
eleton; Actin-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                           KOIFVWKGKDANPQERKAAMKTAEEFLOOMNYSKNTQIQVLPEGGETPIFKOFFKDWRDK
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                                                                                                                                                                                                                                                                                                                                                                                                 VVKDFARNTTVKEFILNKDTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGEL
                                                                                             Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
715 i
                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                   -IEEKKEEENKPTFDVSKKKDNPQV--NHSQLNESHRKEDLQREEHS
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715
76
                                                                                            Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188
307
451
564
668
119
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80508 MW;
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                                                          AND DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                   10.4%;
        Cowan N.J.;
ing domain of
                                                                                                                                              chain LC1].
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GELSOLIN-LIKE 2.
GELSOLIN-LIKE 4.
GELSOLIN-LIKE 5.
GELSOLIN-LIKE 5.
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Pred.
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POLYPHOSPHOINOSITIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLYPHOSPHOINOSITIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTIN-SEVERING
                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -> H (IN REF. 2).
45FBE42CBCBFDDB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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No.
motif unrelated to that
                                                                                                                                                                                                                    2464 AA.
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16;
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(POTENTIAL).
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                                                                                                                                                         (MAP1 (X))
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 t of MAP2
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RESULT 11
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ID DACA_B
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DACA BACSU STANDARD;
P08750;
01-AUG-1988 (Rel. 08, Created)
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J. Cell Biol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Microtubules;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X51396; CAA35761.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                        NIAMOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000102; MAP1B_neuraxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN: Has a highly basic region with many copies of KKEE and KKEI/V, repeated but not at fixed intervals, responsible for the binding of MAPIB to microrubules PW, LC1 IS COEXPRESSED WITH MAPIB. IT IS A POLYPEPTI FROM MAPIB BY PROTECTIVITIC PROCESSING. IT IS FREE TO FROM MAPIB BY PROTECTIVITIC PROCESSING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell Biol. 109:3367-3376(1989).

FUNCTION: THE FUNCTION OF BARAIN MAPS IS ESSENTIALLY UNKNOWN.

PHOSPHORYLATED MAPIB MAY PLAY A ROLE IN THE CYTOSKELETAL CHANGES

THAT ACCOMPANY NEURITE EXTENSION. POSSIBLY MAPIB BINDS TO AT LEAST

TWO TUBULIN SUBUNITS IN THE POLYMER, AND THIS BRIDGING OF SUBUNITS

MIGHT BE INVOLVED IN NUCLEATING MICROTUBULE POLYMERIZATION AND IN

STABILIZING MICROTUBULES

SUBUNIT: 3 DIFFERENT LIGHT CHAINS, LC1, LC2 AND LC3, CAN ASSOCIATE

SUBUNIT: 3 DIFFERENT LIGHT CHAINS, LC1, LC2 AND LC3, CAN ASSOCIATE

SUBUNIT: 3 DIFFERENT LIGHT CHAINS, LC1, LC2 AND LC3, CAN ASSOCIATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO:0016358; P:dendrite morphogenesis; GO:0001578; P:microtubule bundling; II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: TO MAPIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGI:1306778; Mtap1b.
                                                                                              673
                                                                                                                                                                                                       584
                                                                                                                       133
                                                                                                                                                                           74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00414; MAP1B_neuraxin;
                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                    QATESKP-----KVTKDKVVKKEIKTKLEEKKEE--KPKKEVVKKEDKTPL---KKDEK
                                                                                                                                                                 SGFEGKKDAGYVINLSKDTFIKPVFK-KIEEKKEEENKPTFDVSKKKDNPQVNHSQLNES
                                                                                                                                                                                                                               KEFILNKDTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS00230; MAP1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAPIA AND MAPIB. IT INTERACTS WITH THE
                                                                                              PRKEEVKKEIKKEIKKEERKELKKEVKKETPLKDAKKEVKKEEKKEVKKEEKEPKK
                                                                                                                       HRKEDLQRE----
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1908
1925
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1942
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1993
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                                                                                                                                                                                                                                                                                                             AΑ;
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1907
1924
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1958
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2043
2060
787
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                                                                                                                                                                                                                                                                                                           WW;
                                                                                                                                                                                                                                                                       Score 93;
Pred. No.
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MAP1B 10.
LYS-RICH
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MAP1B 2.
MAP1B 3.
MAP1B 4.
MAP1B 5.
MAP1B 6.
MAP1B 7.
                                                                                                                                                                                                                                                                                                                                                                               MAP1B
MAP1B
MAP1B
MAP1B
MAP1B
MAP1B
                                                                                                                                                                                                                                                                                                                            KKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bundling;
                             PRT;
                                                                                                                       -EHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 174
                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lation
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                                                                                                                                                                                                                                                                                                                             (HIGHLY BASIC,
KKEI/V REPEATS
                                                                                                                                                                                                                                                                       61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           There are no
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                                                                                                                                                                                                                                                                                   Length 2464;
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Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

Kobayashi Y., Koetter P., Koningstein G., Kroch S., Kumano M.,

Kobayashi Y., Koetter P., Koningstein G., Kroch S., Kumano M.,

Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,

Kurita K., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

Kurita K., Lepidus A., Liu H., Masuda S., Mauel C., Medigue C.,

Kurita K., Lepidus A., Liu H., Masuda S., Mauel C., Medigue C.,

Kurita K., Lepidus A., Liu H., Masuda S., Mauel C., Medigue C.,

Kurita K., Lepidus A., Liu H., Masuda S., Mauel C., Medigue C.,

Kurita K., Lepidus A., Liu H., Masuda S., Mauel C., Medigue C.,

Kurita K., Lepidus A., Liu H., Masuda S., Mauel C., Medigue C.,

Kurita K., Lepidus A., Portetelle D., Porwollik S., Park S.H.,

Kurita K., Lepidus A., Portetelle D., Porwollik S., Park S.H.,

Kurita K., Lepidus A., Portetelle D., Porwollik S., Prescott A. M.,

Kurita K., Lepidus A., Portetelle D., Porwollik S., Prescott A.,

Kurita K., Lepidus A., Seror S.J., Serror F., Soffone F.,

Kurita K., Kurita K., Kurita K., Vandaru K., Serror P., Shin B.S., Soldo B.,

Kurita A., Wanbutt R., Wandenbol M., Vannier F., Vassarotti A.,

Vantiers P., Wipat A., Yanamoto H., Yannae K., Yasumoto K., Yata K.,

Kandari K., Lapidus A., Yanamoto H., Yannae K., Yasumoto K., Yata K.,

Kandari K., Lapidus A., Yanamoto H., Yannae K., Yasumoto K., Yata K.,

Kandari K., Lapidus A., Yanamoto H., Yannae K., Yasumoto K., Yata K.,

Kandari K., Lapidus A., Yanamoto H., Yannae K., Yasumoto K., Yata K.,

Kandari K., Kandari K., Yanamoto K., Yasumoto K., Yata K.,

Kandari K., Yanamoto K., Yasumoto K., Yata K.,

Kandari K., Yanamoto H., Yanamoto K., Yasumoto K., Yata K.,
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Viari A., Wambutt R., W
Winters P., Wipat A., Y
Voshikawa F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waxman D.J., Strominger J.L.;
"Sequence of active site peptides from the penicillin-sensitive alanine carboxypeptidase of Bacillus subtilis. Mechanism of penicillin action and sequence homology to beta-lactamases.";
J. Biol. Chem. 255:3964-3976(1980).
                                       Waxman D.J.,
                                                                                                                                                                                                                                  protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=168
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peptidase) (DD-carboxypeptidase) (CI
"Primary
                                                                       MEDLINE=81117303;
                                                                                                                  SEQUENCE OF 414-443
                                                                                                                                                                                                                                                             "Reduced heat resistance of mutagenesis of the Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=80182289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 32-102
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28-FEB-2003 (Rel. 41,
                                                                                                                                                                                              Bacteriol.
                                                                                                                                                                                                                                                                                                                                                                                        J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complete
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tic sequencing of the 180 kilobase region of the
chromosome containing the replication origin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                    Roberts
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                                   Strominger
                                                                                                                                                                                              167:257-264 (1986)
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                                                                       PubMed=6780559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=6768745;
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                                                                                                                                                                                                                                                                                                                                                                                    Johnstone
   COOH-terminal
                                                                                                                                                                                                                                                                 mutant spores
subtilis gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zumstein E., Yoshikawa
ce of the Gram-positive
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                                                                                                                                                                                                                                                                                                                                                                                    Piggot
   membranous
                                                                                                                                                                                                                                                                 encoding
                                                                                                                                                                                                                                                                                                         after cloning
                                                                                                                                                                                                                                                                                                                                                                                P.J.,
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bacterium Ba
segment of
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, Henaut A.,
Tones L.,
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n Bacillus
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RESULT 12
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Poulsen K., Reinholdt J., Kilian M.; "A comparative genetic study of serologically distinct Haemophilus influenzae type 1 immunoglobulin Al proteases.";
                                                                                                                 IGA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D26185; BAA05246.1; -.
EMBL; Z99104; CAB11786.1; -.
EMBL; M13766; AAA22375.1; -.
                                  STRAIN=HK715 / Serotype MEDLINE=92234949; PubMed
                                           STRAIN=HK715
                                                                                                                                      01-NOV-1995
28-FEB-2003
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                                                       SEQUENCE
                                                                                    Pasteurellaceae;
                                                                                            Bacteria;
                                                                                                         Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00725; DADACBPTASE1.
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European Bioinformatics Institute. Th
by non-profit institutions as long
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                                                                                              Proteobacteria;
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E -> Q (IN REF. 4).
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InterPro; IPR005546; Autotransporter.
InterPro; IPR007710; IGA_S6.
InterPro; IPR004899; Pertactin.
Pfam; PF03797; Autotransporter; 1.
Pfam; PF03795; IGAL; 1.
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- FUNCTION: VIRULENCE FACTOR; CLEAVES HOST IMMUNOGLOBULIN A PRODUCING INTACT FC AND FAB FRAGMENTS.

- CATALYTIC ACTIVITY: Cleavage of immunoglobulin A molecules at certain Pro-|-Xaa bonds in the hinge region. No small molecule
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SUBCELLULAR LOCATION: Secreted.
SUBCELLULAR LOCATION: Secreted.
DOMAIN: THE SIGNAL PEPTIDE GUIDES THE PRECURSOR TO THE PERIPLASMIC DOMAIN: THE SIGNAL PEPTIDE GUIDES THE PROCIATES WITH THE SPACE, AND THE CARBOXY-TERMINAL HELPER DOMAIN ASSOCIATES WITH THE SPACE, TO FORM A PORE FOR EXCRETION OF THE PROTESSE DOMAIN. THE HELPER DOMAIN IS THEN RELEASED BY AUTOPROTEOLYSIS (BY SIMILARITY).
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RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones M., Leather S., McDonald S., McLean J.,
RA James K., Jones J., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Qliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Weltjens I., Vonstreels E., Rieger M., Schaefer M., Whitehead S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Reinhardt R., Pohl T.M.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Shpakovski G.V., Usesry D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
RI Nature 415;871-880(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Schizosaccharomycete Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein C6B12.02c SPAC6B12.02C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z98531; CAB11064.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GeneDB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21848401;
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    -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T39009;
                                                                                                      394
                                                 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPombe;
                                                                                                                                                                                                                                        Similarity
                                                 GWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQL
                                                                                                      TSENPFQLNVAANAVSTIPVYRTTKTKMKKNRFKYVEVEKLPDLILESY
                                                                                                                                                        TTVKEFILNKDTGEVSELKPHRVTVTIQNGKEMSSTIVSE-EDFILPVYKGELEKGYQFD
                                                                                                                                                                                                                                                                                                                                                                       755
866
915
977
1033
1336
1645
                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
697 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T39009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPAC6B12.02c;
                                                                                                                                                                                                                                                                                                                     AA;
GKKAPKFLRVFARSSSHIP---KMIRRKROMDSKKYFSFDKESDROVIDOVLS
                                                                                                                                                                                                                                                                                                                                            775
886
935
937
1053
1356
1665
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                                                                                                                                                                                                                                        10.3%;
                                                                                                                                                                                                                                                                                                                     217432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane
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POTENTIAL.
POTENTIAL.
POTENTIAL.
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POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                        Score 92.5;
Pred. No. 4:
                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                 POLY-LEU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                        8AD3BBCE32397C29 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                           49
                                                                                                                                                                                                                                                                 ВB
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                                                                                                                                                                                                                                                                 Length 1888;
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130

NESHRKEDLQREEHSQKSDS-TKDVTATVLDKN-----NISSKSTTNN

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NSB1_MC
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max., Rubin G.M., Hong L.,

A Hopkins R.F., Jordan H., Moore T., Max., Rubin G.M., Hong L.,

A Hopkins R.F., Jordan H., Moore T., Max., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Barownstein M.J., Wacan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Hitting M., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

A Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Haleseley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Balakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

"Generation and initial analysis of more than 15,000 full-length

Thuman and mouse cDNA sequences "Foot Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. Cont. C
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NSB1 MOUSE STANDARD,
Q9JL35; O88832; Q8VC71; Q9CUW1;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-comme binding protein 1 (Nucleosome binding
               Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Pleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Buttnoich S., Hill D., Hofmann M., Hune D.A., Kamiya M., Lee N.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleosome binding pr
45) (GARP45 protein).
NSBP1 OR GARP45.
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                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J; TISSUE=Hippocampus; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 7-195 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Onoda G., Suzuki N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., FUNCTION, SUBC
SPECIFICITY, AND DEVELOPMENTAL STA
MEDLINE=20158948; PubMed=10692437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-45, a novel nucleosomal binding protein with developmentally regulated expression."; siol. Chem. 275:6368-6374(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DWYSGKHELVQQSHSYKKPSDSKSVGGNIFSVNSKKHSVNINAKTAANN 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SEP-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION, SUBCELLULAR VELOPMENTAL STAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ťo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H., Honda T., Sato H., Kuwanc EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
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a tissue-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kuwano
ya M., Lee N.H.,
Mombaerts P.,
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Best Local S
Matches 48
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CONFLICT
SEQUENCE
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GO; GO:0005654; C:nucleoplasm; IDA.
GO; GO:0003682; F:chromatin binding activity;
GO; GO:0006356; P:regulation of transcription
InterPro; IPR000079; HMG 14-17.
Pfam; PF01101; HMG14-17; 1.
SMART; SM00527; HMG17; 1.
PROSITE; PS00355; HMG14-17; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB018374; BAA33783.2; -. EMBL; BC021626; AAH21626.1; -. EMBL; AK013748; BAB28982.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                            Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF213454; AAF30179.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 409:685-690(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Functional annotation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY: Widely expressed with highest levels submaxillary gland, thymus, kidney and liver and lowest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a transcriptional activator. SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     brain, lung, pancreas and eye.

DEVELOPMENTAL STAGE: Highest levels are found in 7-day-old embryos. Levels in the 7-day-old embryos are 4-fold higher the adult and almost 10-fold higher than in later embryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE HMG-14/HMG-17 PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Binds specifically to nuclear core particles and acts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced throw
                                105
 223
                                                                                                                              126 KANIQDVEKDEDGKE---HKDTGE-----EVEDGKIEEEGLNEKPGTAKSED--
                                                                                            54 ILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKD-----TFIKPVFKKIEEK 104
                                                                                                                                                                                              48;
                                                                                                                                                              ۳
                                                                                                                                                                                                             Similarity
DGKCKEEENK---EVGKEGQPEEDGKEDLHEEVGKEDLHEEDGKEGQPEEDGKEI
                                                                                                                                                                                                                                                                          ----KEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREE--HSQKSDSTKDV 153
                                                                -AEVSKDEEEKGDNEKG-----EDGKEEGDEKEEEKDDKEGDTGTEKEVKEQNKEAEED
                                                                                                                                                             KIVVKDFARNTTVKEFILNKDTGEVSELKPHRVTVTIQNGK-----EMSSTIVSEEDF
                                                                                                                                                                                                                                                             406 AA;
                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                74
390
                                                                                                                                                                                                                                                              45344 MW;
                                                                                                                                                                                                             10.3%;
                                                                                                                                                                                              20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       full-length mouse cDNA
                                                                                                                                                                                                             Score 92; DB
Pred. No. 10;
                                                                                                                                                                                                                                                           1 -> V (IN REF. 1).
7 -> H (IN REF. 2).
59A4305613EC9679 CRC64;
                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            It is produced through a collaboration -
                                                                                                                                                                                                                              1;
                                                                                                                                                                                              59;
                                                                                                                                                                                                                                                                                                                                                                                             from
                                                                                                                                                                                                                           Length 406
                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           embryonic
                                                                                                                                                                                                                                                                                                                                                                                             prom.
                                                                                                                                                                                              48;
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                                                                                                                                                                                              Gaps
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RESULT 15
SPT7 YEAST STANDARD; PRT; 1332 AA.

ID SPT7 YEAST STANDARD; PRT; 1332 AA.

AC P35177;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-CT-1996 (Rel. 34, Last annotation update)
DT Transcriptional activator SPT7.

GN SPT7 OR YERO81C OR YER0739.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaee; Saccharomycetes.
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                                                                                Query Match
Best Local S
Matches 50
                                                                                                                                                                                                                                                                                                EMBL; L22537; AAC37424.1; -.
EMBL; X76294; CAA53940.1; -.
EMBL; Z35950; CAA85026.1; -.
EMBL; M87651; AAA35087.1; -.
PIR; S41552; S41552.
HSSP; Q92831; 1B91.
                                                                                                                                       SMART; SM0029'; BNUTU, ... 1.

PROSITE; PS00633; BROMODOWAIN_1; 1.

PROSITE; PS50014; BROMODOWAIN_2; 1.

Transcription regulation; Nuclear protein; Activator;

Transcription regulation; BROMODOWAIN.

458 BROMODOWAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restrate by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The Saccharomyces cerevisiae SPT7 gene encodes a very acidic protein important for transcription in vivo."; Genetics 139:523-536(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae chromosome Yeast 10:959-964(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=S2880;
MEDLINE=95076715; PubMed=7985423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95229044; PubMed=7713415; Gansheroff L.J., Dollard C., Tan P.,
                                                                                                                                    SEQUENCE
                                                                                                                                                                                                    PRINTS; PRO0503; BROMO; SMART; SM00297; BROMO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic Acids Res.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Andre B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=S288c;
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Steensma H.Y.;
                                                                                                                                                                                                                                                                                      TRANSFAC; T04835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yeast proteins.";
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                                                                                                                                                                                                                                 Pfam; PF00439; bromodomain; 1.
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                                                                                                                                                                                                                                             ; S0000285; SPT7.
GO:0000124; C:SAGA complex; I
erPro; IPR001487; Bromodomain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: TRANSCRIPTIONAL
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                                                                                              Similarity
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1332 AA;
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                                                                                                                                     152616 MW;
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InterPro; IPR000734; Lipase.
InterPro; IPR000737; Ser_estrs_site.
Pfam; PF04650; YSIRK signal; 1.
TIGRFAMs; TIGR01168; YSIRK signal; 1.
PROSITE; PS00120; LIPASE SER; 1.
PROSITE; PS00120; LIPASE SER; 1.
Hydrolase; Lipid degradation; Zymogen; Signal
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last amoutation update)
Lipase precursor (EC 3.1.1.3) (Glycerol ester
GEHC OR SE0281.
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Q02510;
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PIR; ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fatty acid anion.
-!- SUBCELLULAR LOCATION: Secreted.
-!- MISCELLANEOUS: THE EXPRESSION OF STAPHYLOCOCCUS LIPASE
-!- MEGATIVELY REGULATED BY BACTERIOPHAGE LYSOGENIZATION (L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (NOV-2002) to -i- CATALYTIC ACTIVITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute.
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DB 1;

Length 688

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RESULT 17
YFK8_YEAST
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Best Local
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                        InterPro; IPRO01410; DEAD.
InterPro; IPRO0150; Helicase C.
InterPro; IPRO0330; SNF2 N.
Pfam; PF00271; helicase C; 1.
Pfam; PF00271; helicase C; 1.
SMART; SM00480; HELICC; 1.
SMART; SM00490; HELICC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995
01-NOV-1995
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murakami Y., Naitou M., Hagiwara H., Sasanuma S.-I., Sasanuma M., Tsuchiya Yamazaki M., Tashiro H., Eki T.; "Analysis of the nucleotide sequence Saccharomyces cerevisiae.";
                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                             MEDLINE=96287654; PubMed=8686381; Eki T., Nairou M., Hagiwara H., Abe M., Ozawa M., Sasanuma M., Tsuchiya Y., Shibata T., Wtanabe K., Yamazaki M.-A., Tashiro H., Hanaoka F., Murakami Y "Fifteen open reading frames in a 30.8 kb region o chromosome VI from Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=S288c / AB972;
MEDLINE=95400292; PubMed=7670463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomyc
Saccharomycetales; Saccharomycetaceae; Sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P43610;
                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical
Hypothetical protein; ATP-binding.
                                                                                                                                                  EMBL; D50617;
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                                                                                                                                                                                                                                                                                                                  Yeast 12:177-190(1996)
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                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Nuclear (Potential).
SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY.
                                                                                                                       $56293; $56293.
$0001934; YFR038W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KQEDSQKENLSKQDTQSSKTTDLL-----RATAQNQSK 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NKENEAFVQNHSEE----KPQQEQVELEKHASENNQTLHSKAAQSNEDVKTKPSQLDNTAA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKKDAGYVINLSKOTFIKPVFKKIE-EKKEEENKPTFDVSKKKDNPQV--NHSQLNESHR 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NKNVNEKSNVN----SITENESLHNETPKNEDWI-----QQQKDSQNDNKSESVVEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NKDTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 41, Last annotation updat
(Rel. 41, Kast annotation CDC26-SAP
                                                                                                                                                  BAA09277.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                AB972;
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               Nuclear
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tsuchiya
T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomycotina; Saccharomycetes; cetaceae; Saccharomyces.
              protein;
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CDC26-SAP155
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/a Y., Soeda
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            DNA-binding;
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               Helicase;
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                                                                                                                                                                                                                                                EMBL outstation
                                                                                                                                                                                                                                               a collaboration -
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RESULT 18
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Best Local S
Matches 44
                                                                                                                                                                                                                                                                                           MEDINE-1311952; PubMed-11418146;

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., S., Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.; Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.; Puruya K., Sayahylococcu
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28-FEB-2003 (Rel.
28-FEB-2003 (Rel.
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SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIG OR SAV1675 OR SA1499 OR MW1619. Staphylococcus aureus (strain Mu50 / Staphylococcus aureus (strain M315), Staphylococcus aureus (strain MW2). Bacteria; Firmicutes; Bacillales; Sta MCBI TaxID=158878, 158879, 196620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIG_STAAM
Q99TI6;
                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                             Baba T., Takeuchi F., Kuroda M., Yuzaw
Nagai Y., Iwama N., Asano K., Naimi T.
Yamamoto K., Hiramatsu K.;
"Genome and virulence determinants of
                                                                                                                                                                                                                                 STRAIN-MW2;
                                                                                                                                                                                                                                                                                      aureus
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=Mu50 / ATCC 700699,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trigger factor (TF).
TIG OR SAV1675 OR SA1499 OR
                                                                                                                                                                                              STRAIN=MW2;
MEDLINE=22040717; PubMed=12044378;
MEDLINE=2-1040717; PubMed=12044378;
                                                                                                                                                  acquired MRSA.";
                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                        ancet
                                                                                 SIMILARITY:
                                                                                                                       cet 359:1819-1827(2002). FUNCTION: Involved in b
                                                                                                           maintaining the newly
                                                                                               (By similarity)
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                                                                                                                                                                                                                                                                        357:1225-1240(2001).
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                                                                                                                                                                                                                                               FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNMSNGVNYREKEVNDLTADISDSDSDLDSEDNKHGKGDNDTAPIWLQDDVHSDEDI----
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352
778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 41, Created)
(Rel. 41, Last sequence up
(Rel. 41, Last annotation
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                                                                                 BELONGS TO THE FKBP-TYPE PPIASE FAMILY. TIG SUBFAMILY.
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355
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                institutions as long
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                                                                                                           protein export.
synthesized pro
                                                                                                                                                                                                                                                                                                                                                                                                                           and N315;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 90; DB
Pred. No. 28;
29; Mismatches
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                                                                                                           protein
                                                                                                                                                               high virulence community.
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There are no restrictions
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Usage
                its content
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an open conforma
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                                                                                                                                                                                                      Oguchi
                                                                                                            conformation
                                          a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42;
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RESULT 19
PIK1 YEAST
ID PYK1
AC P3910
DT 01-FE
DT 01-FE
DT 01-FE
DT 01-FE
DT 01-OC
DE Phosp
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GN PIK1
OS Sacch
OC Eukar
OC Sacch
OC Sacch
OX NGB1
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Best Local S
Matches 50
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PIK1 YEA
P39104;
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01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Phosphatidylinositol 4-kinase PIKI (EC 2.7.1.67)
(PtdIne-4-kinase)
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PROSITE; PS00453; FKBP_PPIASE 1; FALSE_NEG.
PROSITE; PS00454; FKBP_PPIASE 2; FALSE_NEG.
PROSITE; PS50059; FKBP_PPIASE 3; 1.
Cell_division; Chaperone; Isomerase; Rotama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP003134; BAB4
EMBL; AP004827; BAB9
PIR; A89951; A89951.
                                                                                                                                                                       SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=94069320; PubMed=8248783;
Flanagan C.A., Schnieders E.A., E
                                                                                                                                                                                                                                                                                                                 STRAIN=JK9-3D;
MEDLINE=94252322; PubMed=8194527;
Garcia-Bustos J.F., Marini F., St.
"PIK1, an essential phosphatidylii
yeast nucleus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIK1 OR YNL267W OR N0795.

Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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STRAIN=S288c / F
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InterPro; IPR005215; Trig_fac.
                                                                                   Science
                                                                                                         "Phosphatidylinositol 4-kinase: yeast cell viability.";
                                                                                                                                                               Flanagan C.A., Thorner J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4932;
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                                                                                   262:1444-1448(1993)
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; BAB42766.1; -.
; BAB95484.1; -.
     FY1679;
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Pred. No. 16
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                                                                                                                                                                                     Emerick A.W.,
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EMBL; 120220; AAA34873.1; -.
EMBL; X92494; CAA63231.1; -.
EMBL; Z71543; CAA6374.1; -.
PIR; A49335; A49335.
SGD; S0005211; PIK1.
                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Immunoglobulin Al protease precursor (EC 3.1GA OR IGA1 OR HI0990.
Haemophilus influenzae.
                                                                                                                                                                                                                    IGAO HAEIN
P44969;
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                      Bacteria; Proteol Pasteurellaceae;
                                                                                                                                                                                                                                                                      HAEIN
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SMART; SM00146; PI3KC; I.
PROSITE; PS00915; PI3 4 KINASE
PROSITE; PS00916; PI3_4 KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0005634; C:nucleus; IDA:
GO; GO:0016288; P:cytokinesis;
GO; GO:0006892; P:post Goldi tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --
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Yeast 12:505-514(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
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SIMILARITY: BELONGS TO THE P13/P14-KINASES FAMILY.
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CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol = 1-phosphatidyl-1D-myo-inositol 4-phosphate.
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                                                                                                                                                                                                                                                                                                                                                                                                                    122
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PS00916; PI3_4_KINASE_2; 1.
PS50290; PI3_4_KINASE_3; 1.
PS50290; PI3_4_KINASE_3; 1.
PS50290; PI3_4_KINASE_3; 1.
PS50290; PI3_4_KINASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                    PKYLDNSYVHRTYDGKNINR-----
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                      Proteobacteria; Gau
laceae; Haemophilus
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1066 AA;
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                                                                                                                                                                                                                                             STANDARD;
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PI3_PI4_kinase.
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                                                Gammaproteobacteria;
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Pred. No. 43;
                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                       TIGRFAMs; TIGR01414; autotrans_barl; 1.
Hydrolase; Serine protease; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF03797; Autotransporter; 1. Pfam; PF02395; IGA1; 1. Pfam; PF03212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR005315; Autotransport.
InterPro; IPR005546; Autotransporter.
InterPro; IPR000710; IGA S6.
InterPro; IPR004899; PerTactin.
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EMBL; U32779; AAC222631.1; -.
PIR; H64106; H64106.
MEROPS; S06.001; -.
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m Rd.} ";
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Wright A., Fishman Y.,
Submitted (MAY-1991) t
                                                                                                                                                                                                                                                                                                                                                                                    Complete
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CATALYTIC ACTIVITY: Cleavage of immunoglobulin A molecules at certain Pro-|-xaa bonds in the hinge region. No small molecule substrates are known.

SUBCELLULAR LOCATION: Secreted.

SUBCELLULAR LOCATION: Secreted.

SUBCELLULAR LOCATION: THE SIGNAL PEPTIDE GUIDES THE PRECURSOR TO THE PERIPLASMIC SPACE, AND THE CARBOXY TERMINAL HELPER DOMAIN ASSOCIATES WITH THE OUTER MEMBRANE TO FORM A PORE FOR EXCRETION OF THE PROTEASE DOMAIN. THE HELPER DOMAIN IS THEN RELEASED BY AUTOPROTEOLYSIS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO PEPTIDASE FAMILY S6.
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o the EMBL/GenBank/DDBJ databases
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                                                                       EN -> GV (IN REF. 1).
G -> A (IN REF. 1).
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A -> G (IN REF. 1).
Score 89.5;
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                                                                                          Hypothetical | CONFLICT 5: CONFLICT 5: SEQUENCE 85:
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P25588; P25589; P27513; P87003;
01-MAY-1992 (Rel. 22, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Hypothetical 97 9 kDa protein in CHA1-KRR1 intergenic region.
YCL061C OR YCL61CYCL60C.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YEAST
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SGD; S0000566; YCL061C.
GO; GO:0006347; P:chromatin silencing at HML and HGO; GO:0006348; P:chromatin silencing at telomere; GO; GO:000076; P:DNA replication checkpoint; IGI.
                                                                                                                                                                                                                                                                                     EMBL; X59720; CAA42405.1;
EMBL; X53998; -; NOT_ANNO:
PIR; S74279; S74279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 384-596 FROM N.A.
STRAIN=ATCC 28383 / FL100;
MEDLINE=90384830; PubMed=2169608;
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Rasmussen S.W., von Wettstein
Submitted (MAR-1992) to the EN
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
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  l Similarity
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RESULT 22
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  FENR PEA
P10933;
01-JUL-1989
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01-JUL-1989 (Rel. 11, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ferredoxin--NADP reductase, leaf isozyme, chloroplast precursor [Precurs of 1.18.1.2) (FNR).
                                                                                                                                             "A productive NADP+ binding mode of ferredoxin-NADP revealed by protein engineering and crystallographic Nat. Struct. Biol. 6:847-863 (1999).

-I- FUNCTION: MAY PLAY A KEY ROLE IN REGULATING THE OF CYCLIC AND NOW-CYCLIC ELECTRON FLOW TO MEET TO PLANT FOR ATP AND REDUCING POWER.

-I- CATALYTIC ACTIVITY: Reduced ferredoxin + NADP(+) ferredoxin + NADPH.
                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (1.70 ANGSTROMS).
MEDLINE=99396739; PubMed=10467097;
Deng Z., Aliverti A., Zanetti G., Arakaki A.K., Ottado J., Orellano E.G., Calcaterra N.B., Ceccarelli E.A., Carrillo N.,
                                                                                                                                                                                                                                                                                                                    Orellano E.G., Calcaterra N.B., Carrillo N. "Probing the role of the carboxyl-terminal reductase by site-directed mutagenesis and
                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=cv. Little Marvel; TISSUE=Leaf; Newman B.J., Gray J.C.; "Characterisation of a full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pisum sativum (Garden pea)
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                        Karplus P.A.,
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                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 270-360 FROM N.A., AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                        lant
                                                                                                                                                                                                                                                                                                          Biol. Chem. 268:19267-19273(1993).
        COFACTOR: FAD.

COFACTOR: FAD.

PATHMAY: FINAL STEP IN LINEAR PHOTOSYNTHETIC ELECTRON TRANSPORT CHAIN; IT HAS ALSO BEEN IMPLICATED IN CYCLIC ELECTRON FLOW AROUND PHOTOSYSTEM I, ITS ROLE BEING TO RETURN ELECTRONS FROM FERREDOXIN TO THE CYTOCHROME B-F COMPLEX.

SUBUNIT: MOROMER:
SUBCELLULAR IOCATION: CHLOROPLAST; STROMAL SIDE OF THE THYLAKOID MEMBRANE IN THE VICINITY OF THE PHOTOSYSTEM I IN THE NON-STACKED AND FRINCE PORTION OF THE MEMBRANE.

MISCELLANEOUS: FNR IS PROBABLY ATTACHED TO THE MEMBRANE BY A SPECIFIC BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 415
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                                                                                                                                                                                                                                                                                                                                           Carrillo N.,
                                                                                                                                                                                                                ferredoxin-NADP + crystallographic
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                                                                                                                                                                                                                                                                                                                     region of ferredoxin-NADP+ deletion analysis.";
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                                                                                                                                                           NADP(+) =
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EMBL; L15567; AAB59304
EMBL; L15567; AAB59303
EMBL; L15567; AAB59304
PIR; S04030; S04030.
PDB; 1QFZ; O1-SEP-99.
PDB; 1QG0; O1-SEP-99.
PDB; 1QG0; O1-SEP-99.
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s; PR00371; FPNCR.
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IPR001433; Oxred_FAD/NAD(P)
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; AAB59349.1;
; AAB59303.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3D-structure.
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BY SIMILARITY.
NADP (RIBOSE PART) (BY SIMILARITY).
Y->W,F,S.
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                                                                                                                                                                                                                                                       148 IGDFGDSKTVSLCVKRLVYTNDAGEVVKGVCSNFLCDLKPGSEVKITGPVGKEMLMPKDP 207
                                                                                                                                                                                                                                                                                                                           208 NATVIMLGTGTGIAPPRSFLWKMP-FEKHEDYQFNGLAWLFLG------VPTSSSL 256
                                                                                                                                                                                                                                                                                           ----SSTIVSEEDFILPVYKGELEKGYQFDG--WEISGFEGKKDAGYVINLSKDT 92
                                                                                                                                                                                                                       4 VKDFARNTT----VKEFILNKDTGEV-----SELKP-HRVTVTIQNGKEM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Martin H., Mendoza A., Rodriguez-Pachon J.M., Molina M., Nombela C., "Characterization of SKM1, a Saccharomyces cerevisiae gene encoding a novel Ste20/PAK-like protein kinase.";
Mol. Microbiol. 23:431-444(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    delta element.";
Yeast 11:1069-1075(1995).
-!- FUNCTION: MAY BE INVOLVED IN CELLULAR SIGNALLING OR CYTOSKELETAL
FUNCTIONS: MAY PLAY A ROLE IN MORPHOGENETIC CONTROL.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKM1 YEAST STANDARD; PRT; 655 AA.
012469; Q06640;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Serine/threonine-protein kinase SKM1 (EC 2.7.1.-) (Protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vandenbol M., Durand P., Porteteile D., Hilger F.; Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV including the Tyl-H3 retrotransposon, the sufil(*) frameshift suppressor gene for tRNA-Gly, the yeast transfer RNA-Thr-la and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                       51;
                                                                                                                                                   Length 360;
                                                                                                                                                                                                                                                                                                                                                            93 FIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQ 139
                                                                                                                                                                                                                                                                                                                                                                                  54; Indels
                                                                                                                   40194 MW; 7F1CC10DEBBA7B24 CRC64;
                                                                                                                                                       DB 1;
                                                                                                                                                   9.8%; Score 87.5; D
24.6%; Pred. No. 19;
tive 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Contains 1 CRIB domain. SIMILARITY: Contains 1 PH domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-S288C / GRP88;
MEDLINE-97197189; PubMed-9044278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96076631; PubMed=7502582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75490 D).
SKMI OR YOL113W OR HRA655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X69322; CAA49163.1;
                                                                                                                                                                                         Conservative
 319
322
337
339
351
353
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                                                                                                   355 360 AA;
                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                         41;
                                                                                                                                                                                                                                                                                           44
                                                                                                                   SEQUENCE
STRAND
                                                                                                     STRAND
                                 HELIX
                                                                   HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                YEAST
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SHIFFF
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255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      256 TNIEDNKVREEGR-----VHVSKESTADSQTKQLGKKEQKVIQSHLRRHDNNSTFRPHR 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 YIINKRTNSIK----RSVSRTLRKGK-----TDSILPVYQSELKPFPRPSDDDYKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Structure of a Plasmodium falciparum gene that encodes a glutamic acid-rich protein (GARP).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-89040048; PubMed=2903445;
Triglia T., Stahl H.-D., Crewther P.E., Silva A., Anders R.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310 LAPSAPATKWHDSKTKWHKEDLLELKONDDSNEIIMKMKTVAIDVN 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium NCBI_TaxID=5837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 KKDNPQV--NHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKN 161
                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50003; PH_DOMAIN; 1.
PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN KINASE_ST; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 PILNKDTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S -> R (IN REF. 1).
M -> T (IN REF. 1).
A -> V (IN REF. 1).
i lf6CBC85FE10D385 C
                                                                            cycle; IGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 13, Last sequence update)
(Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.8%; Score 87.5; Dilarity 20.5%; Pred. No. 35; Conservative 36; Mismatches
                                                                        GO; GO:0000074; P:regulation of cell
InterPro; IPR000095; PAKbox/Rhobndng.
InterPro; IPR001849; PH.
                                                                                                                           InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR001245; Tyr pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glutamic acid-rich protein precursor.
                                                                                                                                                                                                                                                         ProDom; PD000001; Prot_kinase; 1.
SMART; SM00285; PBD; 1.
SMART; SM00233; PH; 1.
SMART; SM00220; S_TKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1990 (Rel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75331 MW;
                                                                                                                                                                                PEam; PF00786; PBD; 1.
PEam; PF00169; PH; 1.
PEam; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
EMBL; Z74855; CAA99132.1;
PIR; S51884; S51884.
SGD; S000847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                468
655 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
hes 34; Conserv
                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1990
15-JUL-1999
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P13816;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
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Rad50 provides an ATP-dependent control of mrell by unwindin and/or repositioning DNA ends into the mrell active site (By
                                                   similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profilt institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 ILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKK-----EE 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 VPTTSNDNLKNAHNNN--EIS---SSTDPTNIINVNDKDNENSVDKKKDKKEKKHKKDKK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 ENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQ-----KSDSTKDVTATVLDKNN 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 KDFARNTTVKEFILNKD----TGEV---SELKPHRVTVTIQNGKEMSSTIVSEE----DF 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 KCFSNGLLKNQNILNKSFDSITGRLLNETELEKNK-----DDNSKSETLLKEEKDEKDD 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y., Sakai M., Ogura K., Oteuka R., Nakazawa H., Takamya M., Ohfuku Y., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Yoshizawa T., Kudoh Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kikuchi H., "Complete sequence and gene organization of the genome of a hyper-thermophilic archaebacterium, Pyrococcus horikoshii OT3.", DNA Res. 5:55-76(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rad50/mrell complex possesses single-strand endonuclease activity and ATP-dependent double-strand-specific exonuclease activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pyrococcus horikoshii.
Archaea; Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
9.8%; score 0..., ---
Best Local Similarity 24.1%; Pred. No. 37;
Matches 46; Conservative 35; Mismatches 73; Indels 37;
                                                                                                                                                                                                                                                                                                                                                GLUTAMIC ACID-RICH PROTEIN.

15 X 3 AA TANDEM REPEATS OF K-K-X.

9 X APPROXIMATE TANDEM REPEATS.

5 X APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 X APPROXIMATE TANDEM REPEATS. POLY-GLU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2A8F85606496EA9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA double-strand break repair rad50 ATPase.
RAD50 OR PH0929.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        879 AA
     Biochem, Parasitol, 31:199-202(1988).
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                                                                                                                                                                                                                                                                                                       Repeat; Malaria; Antigen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80551 MW;
                                                                                                                                                                                                                                                      EMBL; J03998; AAA29605.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163 ISSK--STTNN 171
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192 LDEEMVSEINN 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    576
605
654
678 AA;
                                                                                                                                                                                                                                                                                  PIR; A54514; A54514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=53953;
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058687;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 KGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQ 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIINE-96180278; PubMed-8603916; Benian G.M., Tinley T.L., Tang X., Borodovsky M.; Renian G.M., Tinley T.L., Tang X., Borodovsky M.; The caenorhabditis elegans gene unc-89, required for muscle M-line assembly, encodes a giant modular protein composed of Ig and signal transduction domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UN89 CAEEL STANDARD; PRT; 6632 AA.
001761; 071362;
15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Muscle M-line assembly protein unc-89 (Unccordinated protein 89).
UNC-89 OR C09D1.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 879;
sumilarity).
-!-SUBUNIT: Forms a complex with mre11 (By similarity).
-!- SUMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 9.8%; Score 87.5; 21.0%; Pred. No. 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 VNHSQLNESHRKEDLQREEHSQK 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        644 KVTSQLNELQRKFDQKKYEEKRE 666
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                                                                                                                                                                                                                                                                                                  EMBL; AP000004; BAA30025.1; -. PIR; C71083; C71083.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 21.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Du Z., Le T.T., Wilson R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
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Length 6632;
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                                                                        Waterston R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
C.:- FUNCTION: Structural component of the muscle M-line. Myofilament assembly begins with postitional cues laid down in the lattice assembly begins with postitional cues laid down in the basement membrane and muscle cell membrane. UNC-89 responds to these signals, localizes, and then participates in assembling an M-line.
C.:- TISSUE SPECIFICITY: Localizes to the middle of A-bands.
C.:- SIMILARITY: Contains 1 BBL-homology (DH) domain.
C.:- SIMILARITY: Contains 49 immunoglobulin-like C2-type domains.
C.:- SIMILARITY: Contains 1 PH domain.
C.:- SIMILARITY: Contains 1 SR3 domains.
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REMBL; AR03131; AAB5413.2; -

REMBL; AR03131; AAB5413.2; -

REMBL; AR03131; AAB5413.2; -

REMBL; AR03131; AAB5413.2; -

REMBL; AR03131; AB5413.2; -

REMBL; AR031.1; CE3040.6

RICEPPO; IPR003161; FM III.

RICEPPO; IPR003169; IQ_MC.

RICEPPO; IPR001849; PH.

RICEPPO; IPR001849; PH.

REMPERO; IPR001849; PH.

REMPERO; IPR001851; RASD.

REMPERO; IPR001852; SH3.

REMPERO; IPR001852; SH3.

REMPERO; IPR00185; RASD.

REMPERO; IPR00185; RASD.

REMPERO; IPR00185; RASD.

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REMRET; SM00325; RAGGE; 1.

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IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 6.

IG-LIKE C2-TYPE 6.

THR-RICH.

RCSD 1.

RCSD 2.

RCSD 2.

RCSD 3.

RCSD 4.

RCSD 4.

RCSD 4.

RCSD 5.

IG-LIKE C2-TYPE 7.

IG-LIKE C2-TYPE 7.

IG-LIKE C2-TYPE 7.

IG-LIKE C2-TYPE 8.

IG-LIKE C2-TYPE 9.

IG-LIKE C2-TYPE 9.

IG-LIKE C2-TYPE 10.
                                                        REVISIONS
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EMBL; L06011; AAA16950.1; -.
EMBL; Z11746; -; NOT ANNOTATED_CDS.
EMBL; Z74956; CAA99240.1; -.
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                                                             EMBL; S61567; AAB26818.1; -. EMBL; M95626; AAA34960.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       merozoites.";
Cell 69:1213-1226(1992).
                                                                                                                         PIR; S20126; S20126
SGD; S0005574; RAT1
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7;
                                       69 DGWE---ISGFEGKKDAGYVINLSKDTFIKPV----FKKIEEKK--EEENKPTFDVSKKK 119
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=92331925; PubMed=1628825;
Amberg D.C., Goldstein A.L., Cole C.N.;
Sicolation and characterization of RAT1: an essential gene of
Saccharomyces cerevisiae required for the efficient nucleocytoplasmic
trafficking of mRNA.";
                        11 TTVKEFILNKOTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDF--ILPVYKGELEKGYQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Valens M.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
-!- FUNCTION: May function in the processing and/or trafficking of
nuclear mixNA. May be involved in general transcription as well.
Possesses 5'->3' exoribonuclease activity degrading poly(A) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND EXORIBONUCLEASE ACTIVITY.
MEDLINE=93109318; PubMed=8417335;
Kenna M., Stevens A., McCammon M., Douglas M.G.;
"An essential yeast gene with homology to the exonuclease-encoding XRNI/KEMI gene also encodes a protein with exoribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transcription
                                                                                                                                          1242 ESVVVEKQDLSSS----EVQKEIAQQVKEASPEATTTITMETSLTSTKTT 1287
                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                            120 DNPOVNHSOLNESHRKEDLOREEHSOKSDSTKDVTATVLDKNNISSKSTT 169
  20;
                                                                                                                                                                                                                                       01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ribonucleic acid trafficking protein 1 (5'-3' exoribonuclease)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aldrich T.L., di Segni G., McConaughy B.L., Keen N.J., Whelen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Bohn C., Bolotin-Fukuhara M., Daignan-Fornier B., Dang D.V.,
  80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M.;
EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structure of the yeast TAP1 protein: dependence of activation on the DNA context of the target gene."; Mol. Cell. Biol. 13:3434-3444(1993).
                                                                                                                                                                                                                 PRT; 1006 AA
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activity.";
Mol. Cell. Biol. 13:341-350(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93268292; PubMed=8497260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mainly 5'-AMP.
COFACTOR: Requires magnesium.
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RAT1 OR HKE1 OR TAP1 OR YOR048C.
  33;
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Submitted (JUL-1996) to the
  Conservative
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  37;
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                                                                                                                                                                                                                  YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : | : : : : : | | : | | : | 461 ANEGNEEAIAKVKQQSDKNNELMKDISKEEIDDAVSKANKTNFNLAEVMKQKIINKKHRL 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 -----KPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQ------LUSSHRK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: INVOLVED IN RETICULOCYTE ADHESION. SPECIFICALLY BINDS TO HUMAN RETICULOCYTE CELLS.
-!- SUBCELLULAR LOCATION: Membrane-bound (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 IQNGKEMSSTIVSEEDFILPVY--KGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YSGN REPEATS.
Y->H: IN ALLELE TAPI-1; ACTIVATES
TRANSCRIPTION OF THE PROMOTER-DEFECTIVE
YEAST SUP4 TRNA (TYR) ALLELE SUP4A53T61.
MW; 5DDD580245F3BI2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONTAINS 2 X SRYD, 2 X NNNY, AND 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDLOREEH-----SQKSDSTKDVTATVLDK-----NNISSKSTT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 1006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
BEDLINE-2315318; PubMed=1617731;
Galinski M.R., Medina C.C., Ingravallo P., Barnwell J.W.;
"A reticulocyte-binding protein complex of Plasmodium vivax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005634; C:nucleus; IDA.
GO; GO:0004534; F:5'-3' exoribonuclease activity; IDA.
GO; GO:0006365; P:35S primary transcript processing; IMP.
GO; GO:0008306; P:RNA processing; IMP.
InterPro; IPRO3159; XRN N: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nuclear protein; Hydrolase; Nuclease; Exonuclease; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-CTT-1996 (Rel. 34, Last annotation update)
Reticulocyte binding protein 2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ź
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 86.5;
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                                                                                                                                                                                                                             ----VSEEDFILPVYKGELEKGYQFDGWEISGFE-GKKDAGYVINL--SKDTFIKPVFKK 100
                                                                                                                                                                                                                                                                                           ----IEEKKEEENKPTFDVSK--KKDNPQV-----NHSQLNESHRKEDLQREEHS 144
                                                                                                                                                                                                                                                                                                                                                      2 IVVKDFARNTTVKEF----ILNKD---TGEVSELKPH--RVTVTIQNGKEMSSTI--- 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                defensive genes.";
Biochim. Biochim. Acta 1477:112-121(2000).
-!- FUNCTION: ACTIVATES A LIPID-BASED SIGNAL TRANSDUCTION PATHWAY IN WHICH LINOLENIC ACID IS CONVERTED TO JASMONIC ACID, A POTENT ACTIVATOR OF DEFENSE GENE TRANSCRIPTION, INCLUDING PROTEINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peirce G., Strydom D., Johnson S., Ryan C.A.;
"A polypeptide from tomato leaves induces wound-inducible proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLUIAR LOCATION: Cytoplasmic.
TISSUB SPECIFICTTY: ALL ORCANS EXCEPT THE ROOTS. TRANSPORTED OUT OF WOUNDS TO DISTAL TISSUBS.
INDUCTION: By wounding; in leaves.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lycopersicon esculentum (Tomato).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, lamiids, Solanales, Solanaceae, Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The systemin signaling pathway: differential activation of plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McGurl B., Pearce G., Orozco-Cardenas M., Ryan C.A.; "Structure, expression, and antisense inhibition of the systemin
                                                                                                                                                                          39;
                                                                                                                                                                        77; Indels
                                                                                                           1251 AA; 143741 MW; 54BA51C7404AC572 CRC64;
                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 AA
                                                                                                                                         Query Match 9.6%; Score 86.5; D
Best Local Similarity 22.8%; Pred. No. 84;
Matches 46; Conservative 40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     145 OKSDSTKDVTATVLD--KNNIS 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20175266; PubMed=10708853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=92196587; PubMed=1549783;
                                                                Malaria; Receptor; Membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 255:1570-1573(1992)
                                            EMBL; M88098; AAA29744.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inhibitor proteins.";
Science 253:895-898(1991),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                            1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 179-196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Systemin precursor.
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NON TER
SEQUENCE
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           between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 YIIK------IEGDDDA------QEKLKVEYEEEFYKKKIVEKETPS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KIVVK-----DFARNTTVKEFILNKDTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 KIIEKETPSQDINNKDTISSYVLRDDTQEIPKME-H-----EEGGYVKEKIVEKETISQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 PVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKE---EENKPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pyrococcus kodakaraensis.
Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97316461; PubMed=9172372;
Adul Rahman R.N.Z., Jongsareejit B., Fujiwara S., Imanaka T.;
Adul Rahman R.N.Z., Jongsareejit B., Fujiwara S., Imanaka T.;
"Characterization of recombinant glutamine synthetase from the
hyperthermophilic archaeon Pyroccus sp. strain KOD1.";
Appl. Environ. Microbiol. 63:2472-2476(1997).
-i- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 FDVSKKKDN----PQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDK 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                    Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                  FA251D94BAA9C5A9 CRC64;
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13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      9.6%; Score 86;
21.5%; Pred. No.
                                                                                                                                                                                                                                       SYSTEMIN
                                                                                                                                                                                                                                                                                                                                                                    22999 MW;
                                                                                                                                          EMBL; M84800; AAA34182.1; -. EMBL; M84801; AAA34184.1; -. PIR; T07149; T07149.
                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 21.5
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                                                                                                                                                                                                                                                                                                                                                                  200 AA;
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                                                                                                                                                                                                      Hormone, Repeat
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008467;
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102 DPRGILKRVLERLEKEGLKAHIGPEPEFYIFKKNGTWELHIPDSGGYFDLVGLDKAREIR 161
                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Penicillin-binding protein 1A/1B (PBP1) [Includes: Penicillin-insensitive transglycosylase (EC 2.4.2.-) (Peptidoglycan TGase);
Penicillin-sensitive transpeptidase (EC 3.4.2.-) (DD-transpeptidase)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Sequence analysis of the Bacillus subtilis chromosome region between the serA and kdg loci cloned in a yeast artificial chromosome."; Microbiology 142:2005-2016(1996).
                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98044033; PubMed=9384377;
Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
                                                                                                                                                                                                                                                                                                               -----NPQVNHSQLNESHRKEDLQREEHSQKSD---STXDVTATVLD 159
                                                                                                                                                                                                                                                                                                                           162 REIALYMPYLGLKPEVLHHEVGKAQHEIDFRYDEALRTADNIVSFKHVVKAVAE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=168 / Marburg;
MEDLINE=96349105; PubMed=8760912;
Sorokin A.V., Azevedo V., Zumstein E., Galleron N., Ehrlich S.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Popham D.L., Setlow P.; "Cloning, nucleotide sequence, and mutagenesis of the Bacillus subtilis pond operon, which codes for penicillin-binding protein (PBP) 1 and a PBP-related factor.";
                                                                                                                                                                                                 72;
                                                                                                                                 (UNDER CONDITIONS OF ABUNDANT FAMINE) (BY SIMILARITY).
                                                                                                                                                                             DB 1; Length 443;
                                                                                                                                                                                                  46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                           GLUTAMINE) (BY SIMILARITY) 443 AA; 50259 MW; 9426DCCFEEF18168 CRC64;
                                                                                                                                                                                                                        58 YKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFI----
                                                                                                                                                                                                                                                                   95 --KPVFKKIEEKKEEEN-----KPTFDVSKKKD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE OF 499-515.
                                                                                                                                                                            Query Match
9.6%; Score 86; DB 1
Best Local Similarity 17.8%; Pred. No. 30;
Matches 31; Conservative 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           914 AA
                  InterPro; IPR001691; GLN synth.
InterPro; IPR001899; GLNA.
InterPro; IPR001809; GLNA.
Etam; PP00120; gln-synt, I.
Pfam; PP03951; gln-synt, I.
ProDom; PD001057; gln-synt, C;
I.IGRFAMS; TIGR00653; Gln synt, C;
PROSITE; PS00180; GLNA. I; I.
PROSITE; PS00181; GLNA.ATP; I.
                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95113769; PubMed=7814321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Bacteriol. 177:326-335(1995).
BAA20530.1; -.
                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=168 / Marbu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                 362
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                                                                                                                        Ligase.
BINDING
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PBPA BACSU
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Deniar R. Collega J.J. Comercon I.C. Terraria E. Prolage D. P. T. Rentian K. D. Elamerson P. T. R. Britich S. D. Elamerson P. T. R. Britich S. D. Elamerson P. T. R. Britich S. D. Elamerson P. T. R. Britich S. D. Elamerson P. T. R. Britich S. D. Elamerson P. T. R. Adisport S. H. Pebber C. F. Prolage D. S. Candi G. O. W. J. R. Adisport S. Elamentan J. R. Gandi G. O. W. J. L. Haga R. Malchen J. Harwood C. R. Henaut A. D. Deris B. W. Ramerson D. M. Branch G. O. W. B. J. Haga R. Malchen J. Harwood C. R. Henaut A. D. Deris B. W. Ramerson D. M. Ramerson D. M. Ramerson D. M. Ramerson D. M. Ramerson D. M. Ramerson D. M. Ramerson D. M. Ramerson D. M. Ramerson D. M. Ramerson D. M. Ramerson D. M. Ramerson D. M. Levine A. Liu H. Masada S. Mauch C. Median W. Reliado R. P. Millon M. P. Lander S. Handlon R. J. Millon M. P. Lander G. Markin S. Malchen C. M. Ramerson D. Park R. M. M. Ramerson D. M. Ramerson D. M. Ramerson D. M. Ramerson D. M. Ramerson D. M. Ramerson D. M. Ramerson D. M. Ramerson D. M. Ramerson D. M. Ramerson D. M. Ramerson D. M. Ramerson D. M. Ramerson D. M. Ramerson D. M. Ramerson D. M. Ramerson D. M. Ramerson D. M. Ramerson D. M. Ramerson D. M. Maria S. Mandlon R. M. Ramerson D. M. Ramerson D. M. Ramerson D. M. Ramerson D. M. Maria S. Mandlon R. M. Ramerson D. M. Mandlon R. M. Ramerson D. M. Mandlon R. M. Ramerson D. M. Mandlon R. M. Ramerson D. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M. Mandlon R. M.
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 ISGFEGKKDA--GYVINLSKDTFIKPVFKKIEEKKEEENK--------- 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 ----PTFDVSKKKDNPQVNHSQLN-----ESHRKEDLQREEHSQKSDSTKDVTA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 VKEFILNKDTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptidoglycan synthesis; Cell wall; Transferase; Glycosyltransferase;
Hydrolase; Multifunctional enzyme; Transmembrane; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
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ACYLATED BY PENICILLIN (BY SIMILARITY)
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Garbarino J.E., Gibbons I.R.; "Expression and genomic analysis of midasin, a novel and highly conserved AAA protein distantly related to dynein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 9.6%; Score 86; DB 1; Length 914; Best Local Similarity 23.0%; Pred. No. 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL)
TRANSGLYCOSYLASE.
TRANSPEPTIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6978E33DFE2423E6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   resistance; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                     EMBL, L47838; AAB384591;
EMBL, 299115; CAB14148.1;
PIR; I40529; 140529.
Subtilist: BG10954; ponA.
InterPro; IPR001361; FN III.
InterPro; IPR001264; Glyco_trans_51.
InterPro; IPR001460; Transpeptdse.
Pfam, PP00901; Transpeptidse.
Pfam; PP00901; Transpeptidse.
ProDom; PD00185; Transpeptidse.
ProDom; P000185; Glyco_trans_51; I.
ProDom; P000185; Glyco_trans_51; I.
SNART; SM00060; FN3; I.
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77 246 TRA
329 662 TRA
706 784 FII
390 390 ACI
914 AA, 99562 MW, 6
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Mammalia; Eutheria; Primates;
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                                                                                                                                      EMBL; U11883; AAA64947.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58
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TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=12102729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibiotic
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ACT SITE
SEQUENCE
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                                                                                                                                                                          TISSUE=Brain;
MEDLINE=97349984; PubMed=9205841;
Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,
Nagases T., Tankawa K.-I., Nakajima D., Ohira M., Seki N.,
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. VII.
The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";
DNA Res. 4:141-150(1997).
-!- FUNCTION: May function as a nuclear chaperone and be involved in the assembly/disassembly of macromolecular complexes in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                        Iracey A.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO: 0005634; C: nucleus; NAS.
GO; GO: 00016887; F: ATPase activity; NAS.
GO; GO: 00016887; F: ATPase activity; NAS.
GO; GO: 0006461; P: protein complex assembly; NAS.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003593; WWF_A.
Ffam; PR00004; AAA; 1.
SWART; SW00382; AAA; 7.
SWART; SW00382; WWF, 1.
Chaperone; ATP-binding; Repeat; Nuclear protein.
NP_BIND 329 336 ATP.
                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 4.6e+02;
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                                            SEQUENCE OF 1255-2356 AND 3550-5596 FROM N.A.
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P (POTENTIAL).
P (POTENTIAL).
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9.6%; Score 86;
Best Local Similarity 23.4%; Pred. No. 4
Matches 30; Conservative 27; Mismatch
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                                                                                                                                                        SEQUENCE OF 3550-5596 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5596 AA; 632802
BMC Genomics 3:18-18(2002).
[2]
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                                                                   rissum=Testis;
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                                                                                                                                                                                                                                                                                                                                                                             Miosga T., Zimmermann F.K.; Region of Saccharomyces cerevisiae on "Sequence analysis of the CEN12 region of Saccharomyces cerevisiae on a 43.7 kb fragment of chromosome XII including an open reading frame homologous to the human cystic fibrosis transmembrane conductance regulator protein CFTR.";
                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; NCBI_TaxID=4932;
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDILINE-93087480; Valueda-1454790;
Ripmaster T.L., Vanghn G.P., Woolford J.L. Jr.;
"A putative ATP-dependent RNA helicase involved in Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 387:87-90(1597).

-I FUNCTION: PROBABLE HELICASE INVOLVED IN RIBOSOME ASSEMBLY.
-I SUBCELLULAR LOCATION: Nuclear.
-I SUBLERITY: BELONGS TO THE DEAD BOX HELICASE FAMILY.
                                                                                                                                                                                                                                                                                                 cerevisiae ribosome assembly.";
Proc. Natl. Acad. Sci. U.S.A. 89:11131-11135(1992)
                                                                                                                                           update)
                                                                                         752 AA
                                                                                                               01-OCT-1993 (Rel. 27, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Probable ATP-dependent RNA helicase DRSI.
DRSI OR YLL008W OR L1345.
                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S. or send an email to license@isb-sib.ch).
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MEDLINE=96405918; PubMed=8810043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   box.
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InterPro; IPR001650; Helicase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X91488; CAA62783.1; -. EMBL; Z73113; CAA97452.1; -. PIR; S64750. S64750. S6750. S6750. SGD; S0003931; DRS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L00683; AAA34666.1; -.
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                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                              (east 12:693-708(1996)
                       4747 EDDEKSDS 4754
142 EHSQKSDS 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                         YEAST
                                                              RESULT 33
DRS1_YEAST
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70 ----GWEI--SGFEGKKDAGYVINLSKDIFIKPVFKK-----IEEKKEEENKPIFD 114
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                                                                                                                                                                                           DEAD BOX.
MVVGTKKYSNLDFVPT1SDSEDDVP1LDSSDDEKVEAKKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=97344368; PubMed=9200815; Voss H., Benes V., Andrade M.A., Valencia A., Rechmann S., Teodoru C., Schwager C., Paces V., Sander C., Ansorge W.; "). "DNA sequencing and analysis of 130 kb from yeast chromosome XV.";
                                                                                                                                                                                                                                   KKRKGKNNKKKVSEGDNLDEDVHEDLD -> MTKKSRLRRL
RRSGRVRITRKRLVRGITSMRMFMRTWT (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96239492; PubMed=8657111;
Chen G.-C., Zheng L., Chan C.S.M.;
"The LIM domain-containing DbmI GTPase-activating protein is required for normal cellular morphogenesis in Saccharomyces cerevisiae.";
Mol. Cell. Biol. 16:1376-1390(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                   26 ILDSSDDEKVEAKK---TTKKRKGKN-NKKKVSEGDNLDEDVHEDLDAGFKFDLDADDTT
                                                                                                                                                                                                                                                                                                                                                                                           17 ILINKDIGEVSELKPHRVIVIIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFD----
                                                                                                                                                                                                                                                                                                                                                        Gaps
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SEQUENCE FROM N.A.
STRAIN=S288C / FY1679;
STRAIN=S298C / FY1679;
Wiemann S., Rechmann S., Benes V., Voss H., Schwager C., Vlcek C., Stegemann J., Zimmermann J., Erfle H., Paces V., Ansorge W.;
"Sequencing and analysis of 51 kb on the right arm of chromosome XV acquering scerevisiae reveals 30 open reading frames.";
Yeast 12:281-288(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=S288c;
MEDLINE=96101594; PubMed=7498791;
Stevenson B.J., Ferguson B., de Virgilio C., Bi E., Pringle J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RGA1_YEAST STANDARD; PRT; 1007 AA.
P39033; P39934;
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Rho-type GTPase-activating protein 1.
RGA1 OR DBMI OR THEI OR YOR127W OR 03290 OR YOR3290W.
Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSKKKDN------PQVNHSQLNESHRKEDLQREEHSQKSDSTKDVT
                                                                                                                                                                                                                                                                                                                                                        43;
                                                                                                                                                                                                                                                                                                                  Length 752;
                                                                                                                                                                                                                                                                                                                                                        64; Indels
Pfam; PF00270; DEAD; 1.

R Pfam; PF00271; helicase C; 1.

R SMART; SM00487; DEXDC; 1.

R SMART; SM00487; DEXDC; 1.

R SMART; SM00489; DEAD ATP HELICASE; 1.

R PROSITE; PS00039; DEAD ATP HELICASE; 1.

TO ATP-binding; RNA-binding; Helicase; Nuclear protein.

ATP-binding; RNA-binding; Helicase; Nuclear protein.

ATP-DIAG. ATP (POTENTIAL).

ATP (POTENTIAL).
                                                                                                                                                                                                                                                                           60747607A6E5E4A8 CRC64;
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                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                9.5%; Score 85.5; DE
21.8%; Pred. No. 57;
tive 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND MUTAGENESIS.
                                                                                                                                                                                                                                                                           84843 MW;
                                                                                                                                                                                                                                                                                                                                                          38; Conservative
                                                                                                                                                    190
282
388
68
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                                                                                                                                                                                                                                                                             752 AA;
                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4932;
                                                                                                                                                    DOMAIN
NP BIND
SITE
CONFLICT
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                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                    Query Match
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RESULT 35
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GO; GO: 00005100; F:Rho Grpase activator activity; IPI.

RG; GO: 00005100; F:Rho Grpase activator activity; IPI.

RG; GO: 000011; F: signal transducer activity; IPI.

RG; GO: 0000118; P:apical bud growth; IPI.

RG; GO: 00007129; P:setablishment of cell polarity (sensu Sacch. . ; IPI. RG; GO: 00007124; P:setablishment of cell polarity (sensu Sacch. . ; IPI. RG; GO: 00007124; P:setablishment of cell polarity (sensu Sacch. . ; IPI. RG; GO: 00007124; P:setablishment of cell polarity (sensu Sacch. . ; IPI. RG; GO: 00007124; P:setablishment of cell polarity (sensu Sacch. . ; IPI. RG; GO: 00007124; P:setablishment of cell polarity (sensu Sacch. . ; IPI. RG; GO: 00007124; P:setablishment of cell polarity (sensu Sacch. . ; IPI. RG; GO: 00007124; P:setablishment of cell polarity (sensu Sacch. . ; IPI. RG; GO: 00007124; P:setablishment of cell polarity (sensu Sacch. . ; IPI. RG; GO: 00007124; P:setablishment of cell polarity (sensu Sacch. . ; IPI. READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; READ; RE
                                                                                                                            STRAIN-SNY243;

MEDLINE-91087574;

PRAME SNY 243;

MEDLINE-91087574;

Ramer S.W., Elledge S.J., Davis R.W.;

Ramer S.W., Elledge S.J., Davis R.W.;

Ramer S.W., Elledge S.J., Davis R.W.;

a strong inducible promoter.";

Proc. Natl. Acad. Sci. U.S.A. 89:11589-11593 (1992).

Proc. Natl. Acad. Sci. U.S.A. 89:11589-11593 (1992).

MECATIVE REGILATOR OF THE PHEROMONE-RESPONSE PATHWAY THROUGH THE STEED PROTEIN KINASE, ACTS AT A STEP BETWEEN THE GPROTEIN AND THE MAP KINASE MODULE. DOMINANT SUPPRESSOR OF BUD EMBREGENCE DEFECT CAUSED BY DELETION OF IPL2/BEM2. INVOLVED IN THE CONTROL OF POLARIZED CELL GROWTH AND PROPERS BUD SITE SELECTION.

COLUMN STEP SELECTION.

C. -: SIMILARITY: Contains 1 Rho-GAP domain.
                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Ammerer G., Sprague G.F. Jr.;
"Mutation of RGA1, which encodes a putative GTPase-activating protein for the polarity-establishment protein Cdc42p, activates the pheromone-response pathway in the yeast Saccharomyces cerevisiae."; Genes Dev. 9:2949-2963(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTPase activation; Repeat; LIM domain; Metal-binding; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V -> A.

K -> R.

C -> S.

C -> S. BIPOLAR BUDDING.

C->S: BIPOLAR BUDDING.

C->S: BIPOLAR BUDDING.

C-> S: BIPOLAR BUDDING.

C-> S: C -> S.

D -> E (IN REF. 4).

T -> P (IN REF. 4).

I MW; C805411B57553791 CRC64;
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LIM 2.
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EMBL, X90518; CAA62108.1; --
EMBL, X94345; CAA64046.1; --
EMBL, Z75035; CAA99326.1; --
EMBL; X90950; CAA62445.1; --
EMBL; L02617; AAA3553.1; --
PIR; $48535; $48535.
                                                                                                                SEQUENCE OF 570-639 FROM N.A.
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37
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DOMAIN 13
DOMAIN 70
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866
898
926
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CONFLICT
SEQUENCE
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VARIANT
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MUTAGEN
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408
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                                                                                                                                                                                                                                                                                                                                                                    409 SGKGRKISRSLSRRSKDLMI------NLKSRATGKQDSNVKLSPASKVTSRR 454
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MEDLINB=97405699; PubMed=9260743;

MAD., Nothias F., Boyne L.J., Fischer I.;

Ma D., Nothias F., Boyne L.J., Fischer I.;

"Differential regulation of microtubule-associated protein 1B (MAP1B)
in rat CNS and PNS during development.";

J. Neurosci. Res. 49:319-32(1997)

-!- FUNCTION: The function of brain MAPS is essentially unknown.

Phosphorylated MAP1B may play a role in the cytoskeletal changes that accompany neurite extension. Possibly MAP1B Binds to at least two tubulin subunits in the polymer, and this bridging of subunits might be involved in nucleating microtubule polymerization and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         stabilizing microtubules.
SUBUNIT: 3 different light chains, LC1, LC2 and LC3, can associate with MAP1A and MAP1B proteins.
                                                                                                                                                                                                     21 DIGEVSELKPHRVTVTIQNGKEMSSTI-----VSEEDFILPVYKGELEKGYQFDGWEIS
                                                                                                                                                                                                                                                                                                   75 GFEGKKDAGYVINLSKOTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAPB RAT STANDARD; PRT; 2459 AA.
P15205; Q62958; Q9ER21; Q9QW92;
01-APR-1990 (Rel. 14, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Microtubule-associated protein 1B (MAP 1B) (Neuraxin) [Contains: MAP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1541-2459 FROM N.A., AND TISSUE SPECIFICITY.
TISSUE-Spinal cord;
MEDLINE=90059871; PubMed=2555150;
Reinitz A., Grenningloh G., Hermans-Borgmeyer I., Kirsch J.,
Littauer U.Z., Prior P., Gundelfinger E.D., Schmitt B., Betz H.;
"Neuraxin, a novel putative structural protein of the rat central nervous system that is immunologically related to microtubule-
                                                                                         25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the rat microtubule-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zauner W., Kratz J., Staunton J., Feick P., Wiche G.; "Identification of two distinct microtubule binding domains on recombinant rat MAP 1B.";
Eur. J. Cell Biol. 57:66-74(1992).
                         DB 1; Length 1007;
                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | | : | | : : | | | 455 SODLMRDNDSHTGLDTPNSNSTSLDILVNNQKSLNYKRFTDN 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [2]
SEQUENCE OF 96-2459 FROM N.A., DOMAIN, AND INDUCTION.
STRAIN-Sprague-Dawley; TISSUE-Brain, and Glial tumor;
MEDLINE-92347374; PubMed=1639992;
Teairk P., Wiche G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                            135 KEDLOREEHSOKSDSTKDVTATVLD----KNNISSKSTTNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Isolation and sequencing of the 5' end of tassociated protein (MAPIB) encoding cDNA."; Gene 172:307-308(1996).
                                                     ; Pred. No. 78;
34; Mismatches
                     9.5%; Score 85.5; I
21.0%; Pred. No. 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-142 FROM N.A.
STRAIN-Sprague-Dawley; TISSUB=Testis;
MEDLINE-9625/242; PubMed=8666295;
Liu D., Fischer I.;
Query Match
Best Local Similarity 21.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              associated protein 5.";
EMBO J. 8:2879-2888(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               light chain LC1].
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                                                                                                                                                                                                                                                                                                                                                                                            noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              583 EKVIVKKÜKPGKVESKPSVTEKEVPSKEEQS-------PV-KAEVA-----EK 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 SGFEGKKDAGYVINLSKDTFIKPVFK-KIEEKKEEENKPTFDVSKKKDNPQVNHSQLNES 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 KEFILNKDTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEI 73
                                                               nerve levels are high early in development but decrease during postnaral development and are low in adults. In dorsal root ganglia levels remain high throughout development.

INDUCTION: By nerve growth factor.

INDUCTION: By nerve growth factor is region with many copies of the sequence KKEE and KKEI/V, repeated but not at fixed intervals, which is responsible for the binding of MAPIB to microtubules.

WHY. LCI is coexpressed with MAPIB. It is a polypeptide generated from WAPIB by proteolytic processing. It is free to associate with both MAPIB and MAPIB. It interacts with the amino-terminal region
TISSUE SPECIFICITY: Nervous system (spinal cord, brain stem, cerebellum and cerebrum). Not expressed in liver, spleen, kidney,
                                                                                                                                                                                                                                                                               CAUTION: A C-terminal fragment of this protein (residues 1597 to 2459) was originally described as neuraxin in Ref.3.
                                               DEVELOPMENTAL STAGE: In cerebral cortex, spinal cord and sciatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HIGHLY BASIC, CONTAINS MANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.5%; Score 85.5; DB 1; Length 2459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               623 AATESKP-----KVTKDKVVKKEIKTKPEEKKEE--KPKKEVAKKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HRKEDLOREEHSOKSDSTKDVTATVL--DKNNISSKSTTNNPNK 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --KTPLKKDEKPKKEEAKKEIKKEIKKEEKKELKKETPLK 704
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T -> S (IN REF. 1).
L -> K (IN REF. 3).
L -> I (IN REF. 3).
MW; 2E3F6872DEDBBBA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKEE AND KKEI/V REPEATS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Microtubules, Repeat, Phosphorylation.
CHAIN ? 2459 MAP1 LIGHT CHAIN LC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               llarity 24.4%; Pred. No. 2e+02; Conservative 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement ((or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAP1B 10.
GLU-RICH.
LYS-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LYS-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAPIB 3.
MAPIB 4.
MAPIB 5.
MAPIB 6.
MAPIB 7.
MAPIB 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000102; MAPIB neuraxin.
Pfam; PF00414; MAPIB neuraxin; 10.
PROSITE; PS00230; MAPIB NEURAXIN; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAP1B
MAP1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X16623; CAA34620.1; ALT_SEQ.
                                                                                                                                                                                                                                   of MAP1B (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U52950; AAB17068.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X60370; CAC16162.1;
                                                                                                                                                                                                                                                  PIM: Phosphorylated. SIMILARITY: TO MAPIA.
 TISSUE SPECIFICITY:
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2112
2169
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2169 216
2459 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A56577; A56577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is in no way
| for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 DFGDSKTVSLCVKRLIYTNDNGEIVKGVCSNFLCDLKPGSEVVLTGPVGKEMLMPKDPNA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---VPTSSSLLYK 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 TIV--SEEDFILP----VYKGELEK--GYOFDG--WEISGFEGKKDAGYVINLSKDTFIK 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00371; FPNCR.
Oxidoreductase; Flavoprotein; NADP; FAD; Chloroplast; Transit peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 DFARNTT----VKEFILNKDTGEV-----SELKP-HRVTVTIQNGKEM-----SS
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Michalowski C.B., Schmitt J.M., Bohnert H.J.;

Michalowski C.B., Schmitt J.M., Bohnert H.J.;

Expression during salt stress and nucleotide sequence of cDNA for ferredoxin-NADP+ reductase from Mesembryanthemum crystallinum.";

Plant Physiol. 18:817-822(1989).

-!- FUNCTION: MAY PLAY A KEY ROLE IN REGULATING THE RELATIVE AMOUNTS

OF CYCLIC AND NON-CYCLIC ELECTRON FLOW TO MEST THE DEMANDS OF THE PLANT FOR ATP AND REDUCING POWER.

-!- CATALYTIC ACTIVITY: Reduced ferredoxin + NADP(+) = oxidized ferredoxin + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- COFACTOR: FAD.
-!- COFACTOR: FAD.
-!- PATHWAY: FINAL STEP IN LINEAR PHOTOSYNTHETIC ELECTRON TRANSPORT
CHAIN; IT HAS ALSO BEEN IMPLICATED IN CYCLIC ELECTRON FLOW AROUND
PHOTOSYSTEM I, ITS ROLE BEING TO RETURN ELECTRONS FROM FERREDOXIN
TO THE CYTOCHROME B-F COMPLEX.
-!- SUBGELLULAR LOCATION: CHLOROPELAST; STROMAL SIDE OF THE THYLAKOID
AND FRINGE PORTION OF THE MEMBRANE.
-!- SIMILARITY: WITH OTHER SPECIES FUR.
                                                                                             Ferredoxin--NADP reductase, chloroplast precursor (EC 1.18.1.2) (FNR)
                                                                                                                                                    Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Aizoaceae; Mesembryanthemum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NADP (RIBOSE PART) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.5%; Score 85; DB 1; Length 365;
28.1%; Pred. No. 28;
iive 20; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Electron transport; Photosynthesis; Thylakoid; Membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHLOROPLAST (POTENTIAL). FERREDOXIN--NADP REDUCTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02A10BFB66EC15FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mesembryanthemum crystallinum (Common ice plant)
                                                        (Rel. 31, Last sequence update) (Rel. 41, Last annotation update)
365 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P00455; 1FNC.
InterPro; IPR001709; FPN_cyt_redctse.
InterPro; IPR001433; Oxred_FAD/NAD(P)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       binding_1; 1.
                                      (Rel. 31, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41063 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M25528; AAA33029.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41; Conservative
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00175; NAD_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                   NCBI_TaxID=3544;
                                                                                                                   PETH OR FNRA
                                    01-FEB-1995
01-FEB-1995
                                                                             28-FEB-2003
  FENR MESCR
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98 IDGGNTHFPDTMRRNAELADSGINFIGTGVSGGEKGALLGPSMMPGGOKEA----Y 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91
                                                                                                                                                                                                                                                  Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K., Weissenbach J., Ehrlich S.D., Sorokin A.; "The complete genome sequence of the lactic acid bacterium Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KDFARNTTVKEFILNKDTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVY-KGEL-
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                                                                                                                                                Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                        lactis ssp. lactis IL1403.";
Genome Res. 11:731-753(2001).
-!- CATALYTIC ACTIVITY: 6-phospho-D-gluconate + NADP(+) = D-ribulose
5-phosphate + CO(2) + NADPH.
-!- PATHWAY: Haxose monophosphate shunt.
-!- PATHWAY: BELONGS TO THE 6-PHOSPHOGLUCONATE DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00461; 6PGD; 1.
Gluconate utilization; Oxidoreductase; Pentose shunt; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 9.5%; Score 85; DB 1; Length 472; Local Similarity 22.9%; Pred. No. 37; nes 32; Conservative 23; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6EF4F504F217E55F CRC64;
                                                                                                     5-OCT-2001 (Rel. 40, Last sequence update)
3-FEB-2003 (Rel. 41, Last annotation update)
phosphogluconate dehydrogenase (EC 1.1.1.44)
                                                                472 AA
265 EEFEKMKEKAPENFRLDFAVSREQTN 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR00618; 6PGD.
Interpro; IPR006114; 6PGD C.
Interpro; IPR006113; 6PGD_decarbox.
Interpro; IPR006115; 6PGD NAD.
Interpro; IPR006184; 6PGD NAD.
                                                                PRT;
                                                                                                                                                                                                                         STRAIN=1L1403;
MEDLINE=21235186; Pubmed=11337471;
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150 DLVAPIFEQIAAKAPQDGKP 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF03446; NAD binding 2; 1. PRINTS; PR00076; 6PGDHDKGNASE. TIGREAMS; TIGRO0873; gnd; 1.
                                                                                        (Rel. 40, Created)
(Rel. 40, Last seq
(Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE006295; AAK04720.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           472 AA; 52424 MW;
                                                                STANDARD;
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Pfam; PF03446; NAD bin
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                                                                                                                                                                                                              SEQUENCE FROM N.A.
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SEQUENCE 472 AA
                                                                                                    16-OCT-2001
28-FEB-2003
                                                                                         16-OCT-2001
                                                               LACLA
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Matches
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RESULT 38

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------WEISGFEGKKDAGYVINL---SKDTFIKPVFKKIEEKKE------- 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      439 GYEFLIDPVFWKTTQSQGKSMATNMTNLKRLSSDDTNTKKALKEVSTHKNGSDKDGIIGK 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----EBNKPTFDV-SKKKDNPQVNHSQLNESHRKEDL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     499 YSNLLTKKSTTVTAVAQKSMTDNNSGTEQKKNLSEVDTKKKEKESKGKTQSNGQDSGQQN 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 RNTTVKEFILNKD-----TGEVSELKPHRVTVTIQNGKEM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                     'Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 24:4420-4449(1996).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81; Indels 110;
                                                                                                                                                                                                                      Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
                                                                     01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical lipoprotein MG040 homolog precursor (D09_orf657).
MPN052 OR MP102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL LIPOPROTEIN MG040 N-ACYL DIGLYCERIDE (POTENTIAL). 6147B1A5673606A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                              Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.5%; Score 85; DB 1; Length 657; 16.7%; Pred. No. 53; ative 38; Mismatches 81; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -------SSTIVSEEDFILPVYKGELEKGYQFDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE, PS00013; PROKAR LIPOPROTEIN; 1.
Hypothetical protein; Lipoprotein, Membrane, Signal;
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; PubMed=8948633;
Himmelreich R., Hilbert H., Plagens H., Pirkl E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 QREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPN 173
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  657 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              719 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Potential).
-!- SIMILARITY: SOME, TO T.PALLIDIUM TMPC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE000012; AAB95750.1; -.
                                                         01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 27 N
657 AA; 71671 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S73428; S73428.
InterPro; IPR003760; Bmp.
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  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26
657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF02608; Bmp; 1.
                                                                                                                                                                                                  Mycoplasma pneumoniae.
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les 46; Conserv
                                                                                                                                                                                                                                                NCBI_TaxID=2104;
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ID YBLE SCHPO
AC Q10342; Q9URU8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Potential)
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Y040 MYCPN
P75062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pneumoniae.
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580 ELVDRMTELASQSILTPNDLKK 601
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                                                                                                                                                                                                                                                                                                                        Mood V., Gwilliam R., Relaidspasson, A good V., Gwilliam R., Hayles J., Baker S., Basham D., Bowman S., Boouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Bouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Rollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Holroyd S., Hornboy T., Howarth S., Hornboy D., Hodgson G., Holroyd S., Hornboy T., Howarth S., McDonald S., McLean J., Jagels K., James K., Jones L., Jones M., Lather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Sauros R., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Starp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Hothert D., Whitchead S., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Wolckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mulbert H., Meltjens I., Vanstreels E., Rieger M., Schaefer M., Mulbert H., Mahlert H., Mettjens I., Weller H., Manbutt R., Purnelle B., Cychen W., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Loras M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Dominguez A., Revuelta J.L., McCombie W., Panlsen I., Potashkin J., Ashayors P., Shayors S.L., King S., Mimenez J., Sanchez M., del Rey F., Benitto J., Shayors R., Her genome sequence of Schizosaccharomyces pombe.";

Nature 415:871-880 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics and the EMBL outstation.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 WEIS-GFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 EFILNKDTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGEL----EKGYQFDG 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-GLU.
93864D55B86BD1D6 CRC64;
                                                                                                                                       Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
18-ERB-2003 (Rel. 41, Last annotation update)
Hypothetical protein C106.14c in chromosome II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34; Conservative 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59;
                                                                                                                   Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                              MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: TO YEAST YGR245C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AL110295; CAB53730.1; -. PIR; T39271; T39271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81250 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GeneDB SPombe; SPBC106.14c;
Pfam; PF05285; SDA1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
                                                                                                                                                                                        Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               719 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                 NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAINSANCE 12228;
Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
Chen Z., Wen Y., 2002) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: One of the essential components for the initiation of
protein synthesis. Protects formylmethionyl-tRNA from spontaneous
hydrolysis and promotes its binding to the 30S ribosomal subunits.
Also involved in the hydrolysis of GTP during the formation of the
70S ribosomal complex (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE IF-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Initiation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G-DOMAIN.
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
                                                                                                                                                                                               Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales; Staphylococcus
                                                                               Last sequence update)
Last annotation update)
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720 AA
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                                                                                                                                          Translation initiation factor IF-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGREAMS, TIGRO0487; IF-2; 1.
TIGREAMS, TIGRO0231; small GTP; 1.
PROSITE; PSO1176; IF2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE016747; AA004542.1; -.
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Pfam; PF05009; GTP EFTU; 1.
Pfam; PF03144; GTP EFTU D2; 1.
Pfam; PF04760; IF2 N; 2.
ProDom; PD186100; ĪF2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79343 MW;
                                                       (Rel. 42, Created)
(Rel. 42, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23; Conservative
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334
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                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                          NCBI_TaxID=1282;
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                                                       15-SEP-2003
                                                                               15-SEP-2003
15-SEP-2003
STAEP
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                          QBCST4;
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February 10, 2004, 10:48:44; Search time 35.0346 Seconds (without alignments) 697.707 Million cell updates/sec
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1 DTGEVSELKPHRVTVTIQNG.....ATVLDKNNISSKSTTNNPNK 154
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:
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:- /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.]
:: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                     1107863 segs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
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SIDS1/gcgdata/geneseq/
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                                                                                           - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                           Perfect score:
                                                                                           OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                       Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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		46			SUMMARIES	
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
	799	100.0	:	22	AAB48343	S. pneumoniae Sp
7	799	100.0		21	AAY81710	. Streptococcus pr
٣	799	100.0	2140	24	ABU01020	S. pneumoniae ty
4	615	77.0		19	AAW55096	
'n	615	77.0		23	ABP54590	S. preumoniae SP
9	118	14.8		22	AAG81779	S. epidermidis o
7	118	14.8	778	23	ABP39023	Staphylococcus e
60	107.5	13.5		21	AAG47777	Arabidopsis thal
6	105	13.1		21	AAB18278	Plasmodium falci

pl3 neu Npe Npe neu p04 ope epi lia

Drosophila melanog	Staphylococcus lug	falcip	Arabidopsis thalia		œ	Novel human diagno	Human ORFX ORF2661	Human cell cycle r	Human colon cancer	Staphylococcus epi	Pathogen specific	Staphylococcus epi	Drosophila melanog	S. aureus trigger	Chlamydia pneumoni	S. aureus trigger	Drosophila melanog	Pathogen specific	Drosophila melanog	Shrimp white spot	Candida albicans e	proteir	proteir	Human protein SEQ	Candida albicans e	secrete	Human protein SEQ	protein	Human secretory po	Arabidopsis thalia	Human polypeptide	Plasmodium falcipa	Staphylococcus epi	re B	Salmonella typhi c	
22 ABB61977		•	21 AAG37134	AAG3713	•					·			·			20 AAY03189	·	24 ABJ18979		•		•	•	22 AAM79319		•	22 AAM80268	•	Ť	21 AAG47057 .	•			AAG850	22 AAU38439	
564	2060						. 209									525																	~	922	m	
12.7	12.1	٠	٠		٠	11.6	•	11.3	•	•	•	11.3	11.3		•		11.2	11.1	11.1	11.1	•	٠	•	11.0	11.0	11.0	11.0	11.0	11.0	10.9			•	•		
101.5	96.5	96	ന	e	3	2	90.5	o	0	06	90	06	06	σ	8	89.5	σ	89	88.5	ø	88	88	88	88	_	87.5	7	7	7	87	87	87	87	87	86.5	
10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	. 33	34	35	36	37	38	39	40	. 41	42	43	44	45	

ALIGNMENTS

Immunogenic; Sp128; Sp130; pneumococcal; otitis media; nasopharyngeal; bronchial; lung; blood; infection; immune response; immunotherapy; antibacterial; auditory; vaccine. AAB48343 standard; Protein; 773 AA. S. pneumoniae Sp130 polypeptide. 09-JUN-2000; 2000WO-US15925. 10-JUN-1999; 99US-0138453. 20-APR-2001 (first entry) Streptococcus pneumoniae. (MEDI-) MED IMMUNE INC Choi GH; WPI; 2001-112197/12. N-PSDB; AAC84742. WO200076540-A2. 21-DEC-2000. Adamou JE, AAB48343; RESULT 1

New vaccines comprising Sp128 or Sp130 polypeptides, for treating and

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Claim 2; Page 41-42; 76pp; English.
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                                                                                                                                                                                                                                                                                                                  The invention relates to novel immunogenic polypeptides, Sp128 and Sp130 from S. pneumoniae. Vaccines comprising the polypeptides are useful for the treatment and prevention of pneumococcal infections, particularly infections caused by Streptococcus. The antigens are used as immunogenic agents to stimulate an immune response. The antisers and antibodies may also be used in diagnosing and treating pneumococcal infections may also be used in diagnosing and treating pneumococcal infections of antibodies serve as a mechanism for stimulating production of antibodies for use in passive immunotherapy, diagnostic reagents, and as reagents in other processes such as affinity chromatography. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKK
umococcal infections, particularly infections caused by e.g. otitis media, nasopharyngeal, bronchial, lung or
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100.0%; Pred. No. 2.3e-71;
ive 0; Mismatches 0;
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     preventing pneumococcal infections,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY81710 standard; Protein; 2120 AA
                                                                                                                                                                                                                         Claim 8; Page 51-54; 54pp; English.
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Best Local Similarity
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                                                                  Streptococcus, e
blood infections
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This sequence represents a Streptococcus pneumoniae protein of the invention. The proteins (or their homologues, derivatives and/or fragments) are useful as immunogens or antigens. Immunogenic or antigenic compositions comprising the proteins are useful as vaccines and also in diagnostic assays. The sequences are useful for the detection or diagnostic assays. The sequences are useful for the detection or the function or expression of the protein or pophylaxis or interfering with the function or expression of the protein or pophylaxis of S. pneumoniae infection. As the sequences can be used to treat S. pneumoniae infection, the elderly, and in patients which has high rates in they can be used to treat bacterial pneumonia, which has high rates in they can be used to treat bacterial pneumonia, which has high rates in they can be used to treat section, they can be used to treat section, they can be used to treat section with immunosuppressive disorders, allowed to the used to treat because of the protein or with immunosuppressive disorders, especially AIDS. They can also be used to treat pneumococcal septicaemia, otitis media, sinusitis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1933 DIGEVSELKPHRVIVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKK 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DAGYVINLSKOTFIKPVFKKIEEKKEEENKPTFDVSKKKONPQVNHSQLNESHRKEDLQR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 799; DB 21; Length 2120; 100.0%; Pred. No. 9.3e-71; ive 0; Mismatches 0; Indels 0;

    pneumoniae type 4 strain protein from coding region #590.

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(GENO-) INST GENOMIC RES.
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                                                          The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS56454. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the nucleic acid cited above or fragments between nucleotides at 100 of a sequence contained within a Streptococcus nucleic acid sequence, where the first primer is substantially complementary to the target sequence and the second primer is substantially complementary to the target sequence and the second primer is substantially complementary to the complement of the target. Sequence and the second primer is substantially complementary to the complement of the target. Sequence is and where the parts of the primers having substantial complementarity define the termini of the target sequence to be amplified, assay comprising contacting a test compound with the protein, and determining whether the test compound binds to the protein and a Streptococcus pneumoniae bacterium, where one or more genes encoding the proteins has been rendered inactive. The proteins, medicaments for treating or preventing a disease or infection due to streptococcus bacteria, particularly S. pneumoniae, such as pneumonia, sepsis, otitis media or ear infection. They are also useful for identifying immunodominant proteins. The methods are useful for the the 2469 proteins expressed by the identified coding regions from the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae, antigen; vaccine, infection; diagnosis; detection; pneumonia; otitis media; meningitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 799; DB 24;
100.0%; Pred. No. 9.4e-71;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae SP0043 protein.
                                  Claim 1; SEQ ID No 1180; 56pp; English.
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Best Local Similarity 100.
Matches 154; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2140 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomic sequence.
 or ear infection
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The present sequence represents a protein from Streptococcus pneumoniae.

The nucleic acid sequence encoding the Streptococcus preumoniae protein
can be useful in vaccines for inducing protective antibodies against
Streptococcus pneumonia, for treatment or prevention of infection e.g.
pneumonia, oritis media or meningitis. Probes based on the nucleic acid
are used to detect Streptococcus infection (by usual hybridisation or
amplification methods), also for isolating Streptococcus genes or their
allelic variants. The protein can be used similarly to detect specific
antibodies in standard immunoassays, especially for diagnosing or
monitoring infections. Antibodies which bind the protein are used to
detect corresponding antigens, to purify the protein and for passive
cimmunisation (optionally coupled to a toxin). Vaccines are administered,
e.g. by injection, orally or through the skin, typically at 0.01-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 KKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 YKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSK
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                                                                                                                                                                                                                                                                Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or thair epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77.0%; Score 615; DB 19; Length 117; 100.0%; Pred. No. 5.2e-54; tive 0; Mismatches 0; Indels 0
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                                                                                                                                                Kunsch CA;
                                                                                                                                                Choi GH, Hromockyj A, Johnson LS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP54590 standard; Protein; 117 AA
                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 62; 118pp; English.
                                                                                          (HUMA-) HUMAN GENOME SCI INC
                                              96US-0029960.
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  97WO-US19422.
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(KUNS/) KUNSCH C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 AA;
                                                                                                                                                                                                                         N-PSDB; AAV27357
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                                              31-OCT-1996;
30-OCT-1997;
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ABP54590
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|: ||| : |||||| : || ||| DSVNAQSLKP----ITIGNGKQIKQQSVKSGTKVLPHSKVMLMTDGELTMP-DMTGWTKE 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            641 DVLAFEDLTKLKVSTKGNGFVTNQSISKGOIK-------NKDKIEVSLSAEDT 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus epidermidis; open reading frame; ORF; bacterial infection; antibacterial; gene therapy.
                                                                                                                                (II) given in AGBB145 to AGBB120, from Staphylococcus spidermidis.

(I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55991 to
                                                                                                                                                                                                                                                                                                                                                                                                                                    in the examplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4465 to 4472,
                                                                                                                                                                                                                                                                                                                                                                                                               AAH55098 represent oligonucleotide sequences and primers which are used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EISGFE----GKKDAGYVIN--LSKDTFIKPVFKKIEEKKEEENKPTFDVS----KK
                                                                                                               AAH51970 represent nucleic acids (I) encoding polypeptide in AAG81454 to AAG83120, from Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYK-----GELEKGYQFDGW---
Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNN 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3868.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.8%; Score 118; DB 22; 27.2%; Pred. No. 0.0063; iive 23; Mismatches 57;
                                                                    Claim 18; Page 208; 2188pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP39023 standard; Protein; 778 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-064964P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0134001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-055779P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 27.29
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      746 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US6380370-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-APR-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP39023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38 YKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae antigens given in ABP44557 to ABP54669.
The S. pneumoniae antigens have antibacterial activity and can be used in vaccines. The S. pneumoniae antigens can also be used to prevent or attenuate a Streptococcal infection in an animal. The polynucleotides encoding the S. pneumoniae antigens can be used to detect Streptococcus nucleic acids. AB084905 to AB085130 represent primers used in the cloning of S. pneumoniae ORFS (open reading frames) which are used in an example from the present invention.
                                                                                                                                         Fannon MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                            New Streptococcus pneumoniae antigens, useful for detecting Streptococcus and for preventing or attenuating disease caused by Streptococcus infection -

    epidermidis open reading frame protein sequence SEQ ID NO:652.

                                                                                                                                                                                                                                                                                                                                                                                                                    ABQ84792 to ABQ84904 represents nucleic acids which encode the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 77.0%; Score 615; DB 23; Length 117; Best Local Similarity 100.0%; Pred. No. 5.2e-54; Matches 117; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epidermidis SR1 strain; infection; diagnosis;
                                                                                                                                         Dougherty B,
                                                                                                                                         Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG81779 standard; Protein; 746 AA
                                                                                                                                         Barash SC,
                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 29; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0164258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-NOV-2000; 2000WO-US30782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccination; endocarditis
  BARASH S C.
DILLON P J.
DOUGHERTY B.
FANNON M R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-316495/33.
N-PSDB; AAH52629.
                                                                                                                                         Kunsch CA,
                                                                                                                                                                                                            2002-479261/51
                                                                                               ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 AA;
                                                                                                                                                                                                              WPI; 2002-479261,
N-PSDB; ABQ84825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200134809-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GLAX ) GLAXO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-MAY-2001
                                                                                                                                                               Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                    (FANN/)
(ROSE/)
    (BARA/)
(DILL/)
(DOUG/)
                                                                                                                                         Choi GH,
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RESULT 6 AAG81779

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8

g

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Gaps

46;

Length 746; Indels

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990S-01320487.
990S-0132407.
990S-0132484.
990S-0132485.
990S-0132486.
                                                                                                                                        990S - 0134256
990S - 0134218
990S - 01342219
990S - 0134370
990S - 0134370
990S - 0135124
990S - 013524
990S - 0135629
990S - 0135629
990S - 0137222
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990S - 0.138847
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99US-0144325.
99US-0144332.
99US-0144332.
99US-0144333.
99US-0144334.
                                                         30-APR-1999
04-MAY-1999
                                                                                                                                                          14-MAY-1999
14-MAY-1999
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                                                                                                                                                                                                                                 .9-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP315124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

N. B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site.
                                                                                                                                                                                                                                                                                                                                                                           1 DTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYK------GELEKGYQFDGW--- 51
                                                                                                                                                                                                                                                                                                                                                                                                                                    52 EISGFE-----GKKDAGYVIN--LSKDTFIKPVPKKIEEKKEEENKPTFDVS----KK 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein identification, signal transduction pathway, metabolic pathway, hybridisation assay, genetic mapping, gene expression control, promoter;
                                        Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             720 DDDQEKTDEDSSDNKSKKDKADEDHSNTSSSTKN-----DKSNADSKNDSDD 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KONPOVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNN 151
                                                                                                                                                                                                                                                                                                                  14.8%; Score 118; DB 23; Length 778; 27.2%; Pred. No. 0.0067; tive 23; Mismatches 57; Indels 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana protein fragment SEQ ID NO: 60255.
                                                                                  Disclosure; SEQ ID 3868; 267pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG47777 standard; Protein; 484 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0121825.
99US-0123180.
99US-012548.
99US-0125788.
99US-012624.
99US-0127462.
99US-0128234.
99US-0128234.
99US-0128234.
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                                                                                                                                                                                                                                                                                                                            Local Similarity 27.2% nes 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           termination sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana.
WPI; 2002-381255/41.
N-PSDB; ABN91568.
                                                                                                                                                                                                                                                                                     778 AA;
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
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19-APR-1999
                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66
                                                                                                                                                                                                                                                                                                                     Query Match
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PR 20-70L-1999; 9908-0144884.

PR 21-70L-1999; 9908-0144884.

PR 22-70L-1999; 9908-0144884.

PR 22-70L-1999; 9908-0144884.

PR 22-70L-1999; 9908-0145086.

PR 22-70L-1999; 9908-0145081.

PR 22-70L-1999; 9908-0145081.

PR 22-70L-1999; 9908-0145081.

PR 22-70L-1999; 9908-0145191.

PR 22-70L-1999; 9908-0145191.

PR 23-70L-1999; 9908-0145191.

PR 24-70L-1999; 9908-0145191.

PR 24-70L-1999; 9908-0145191.

PR 24-70L-1999; 9908-0145191.

PR 02-70L-1999; 9908-0145191.

PR 03-70L-1999; 9908-014919.

PR 03-70L-1999; 9908-014919.

PR 03-70L-1999; 9908-014919.

PR 11-70L-1999; 9908-014919.

PR 11-70L-1999; 9908-014919.

PR 21-70L-1999; 9908-015919.

PR 21-70L-19
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                                                                                                                                                                                                                                                                                                                                                       .---- 101
                                                                                                                                                                                                                                                                                                                                                                                                                 204 PMENRDQVRQTESAEKSHRKENVTKSEKPRDQEGVKKTEAKDKDKNKEKKEEKTESINK 262
                                                                                                                                                                                                                                                                                                          9 KPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFE-----GKK 60
                                                                                                                                                                                                                                                                                                                                                                                                   102 PQVNHSQLNE----SHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide.
                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium falciparum chromosome 2 related protein SEQ ID NO:135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proteins encoded by chromosome 2 of the human malarial parasite,
                                                                                                                                                                                                                                                                                      45;
                                                                                                                                                                                                                                                            13.5%; Score 107.5; DB 21; Length 484; 20.1%; Pred. No. 0.039; Live 32; Mismatches 66; Indels 45;
                                                                                                                                                                                                                                                                                                                                                      61 DAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter JC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB18278 standard; Protein; 665 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gardner M,
                                                                             99US-0160814.
99US-0160815.
99US-0160980.
99US-0160981.
99US-0161404.
99US-0161405.
                                                                                                                                                          990S-0161406
990S-0161359
990S-0161350
990S-0161361
990S-0161920
990S-0161993
990S-0161993
99US-0159637.
99US-0159638.
99US-0159584.
99US-0160741.
                                             99US-0160767.
99US-0160768.
99US-0160770.
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                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 20.1%
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-NOV-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-365347/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HOFF/) HOFFMAN S.
(CARU/) CARUCCI D.
(GARD/) GARDNER M.
(VENT/) VENTER J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200025728-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-NOV-1999;
           14-OCT-1999;
18-OCT-1999;
21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
                                                                                        21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
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28-OCT-1999;
29-OCT-1999;
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26-OCT-1999
                                                                                                                                                                                              26-0CT-1999
                                                                                                                                                                                                         28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB18278;
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AAB18278
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Guss B,
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Peptide
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                                                                                                 Also described are: (1) mucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).

(I) and (II) are useful for the development of vaccines against P. falciparum infection. (I) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in infection, or they can be used to identify drug resistance in subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasite lifecycle, and provide new targets for complexity of the parasite lifecycle, and provide new targets for resistance to insecticides have led to a resurgence of malaria in many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                      parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 GKKDAGYVINLSKDTFIKPVFKKIEEKKE------EENKPTFD----VSKKKDNPQ 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 NKKD------VKEGVKELEEKKKEEKISDDHKVEENKKSDDHKVEENKKSDDHK 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DTGEVSELKPHRVT-VTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEI--SGFE
                                                                                          Plasmodium falciparum
Plasmodium falciparum, useful as antimalarial vaccines and in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 VNHSQLNESHRKEDLQR-EEHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----DKKEKKSENKNKDENK 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21; Length 665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster polypeptide SEQ ID NO 12723
                                                                                         2 of the human malarial parasite,
                                                                                                                                                                                                                                                                                                                                                                                                                                                13.1%; Score 105; DB 2 24.4%; Pred. No. 0.11; iive 34; Mismatches
                                           Disclosure; Page 321-322; 577pp; English
              diagnosis of P.falciparum infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | :: :: | : :: | | | : : : | VEENKKSDDHKIEEVKKVEEHEEDEEE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB61977 standard; Protein; 564 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 24.48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                   665 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200171042-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB61977
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EDLDTPLSESRFSK--VPDGWVDEHRDEHDGHDVQEPSGEALDDHDEHDDHDDHEDEDEE 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 PVFKKIEEKKEEENKPT-----PDVSKKKDNPQVNHSQLNESHRKEDLOREEHSQKSDS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |: ::||: || :|| :|| | ::|
|136 PLTEELEBERLEBEREEPTEEDEPAADEEYEEDEDEENNA -- GENITAEDAEEEEEEEEDNDD 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---NLSKDTFIK 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                            capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Von Willebrand factor binding protein; vWb; immunogen; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Mature von Willebrand factor binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                              insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus lugdunensis von Willebrand factor binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25;
                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 12723; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 EDFILPVYKGELEKGYQFDGW-----EISGFEGKKDAGYVI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Frykberg L, Jacobsson K, Ahlen J, Nilsson M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.7%; Score 101.5; DB 22;
Similarity 24.5%; Pred. No. 0.19;
34; Conservative 29; Mismatches 51; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE20967 standard; Protein; 2060 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 TKDVTATVLDKNNISSKST 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 EGTVEATVEATTEAT 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-APR-2001; 2001WO-SE00766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-OCT-2000; 2000SE-0003573.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48..2060
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WPI; 2001-656860/75.
N-PSDB; ABL06080.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine; infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     564 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200228892-A1.
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (I) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).

CC (I) and (II) are useful for the development of vaccines against CC intibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of infection with P. falciparum. Furthermore, (I) falciparum. Sequencing of the Plasmodium chromosome 2 and the infaction, or they can be used to identify drug resistance in falciparum. Sequencing of the Plasmodium chromosome 2 and the complexity of the parasite biology, a process hampered by the complexity of the parasite biology, a process hampered by the complexity of the parasite biology, a process hampered by the complexity of the parasite biology, a process hampered by the complexity of the parasite biology, a process hampered by the parasite of insecticides have led to a resurgence of malaria in many cresistance to insecticides have led to a resurgence of malaria in many drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide conditional with the present invention, but which are not process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2173 KPYKIT---ENNKK-----NEGNEILKKYSIENEEKANYDKEQNENCILDKDIQCNVNT 2223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 -----SKDTFIKPVFKKIBEKKEBENKPTFDVSKKKDNPQVNHSQLNE----SHRKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 KPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINL
                                                                                                                                                                                                                                                                                                                                                                                                                                                            32;
                                                                                                                                                                                                                                                                                                                                                                                                                       12.0%; Score 96; DB 21; Length 2500; 26.1%; Pred. No. 5.5; ive 30; Mismatches 54; Indels 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana protein fragment SEQ ID NO: 45610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2281 LEEEE---KSDDKRD-----DKKNDNTREKNNLDNK 2308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOREEHSOKSDSTKDVTATVLDKNNISSKSTTNNPNK 154
                                                                                                                                                                                                                                                                                                                                                        specifically mentioned within the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG37134 standard; Protein; 408
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990S-0126264-
990S-0126785-
990S-0127462-
990S-012834-
990S-0129845-
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99US-0123548
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 26.1 les 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                            2500 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP1033405-A2
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29-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG3713
            g
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                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to von Willebrand factor binding protein or polypeptide (vWb) from Staphylococci. The vWb and immunogens of vwb are useful in vaccines to combat infections caused by Staphylococci. The invention is also useful for detection of Staphylococcal infection and purifying von Willebrand factor from a complex solution. The present sequence is Staphylococcus lugdunensis vWbl protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DAGYVINLSKDTFIKPVFKKIEE-----KKEEENKPTFDVSKKKDNPQVNHSQLNESH 113
                                                                                                                                                                                                                                                                                                                                                                                          4 EVSELKPHRVTVTIQ-NGKEMSSTIVSEEDFILPVYKGELEKGYQFDG--WEISGFEGKK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide.
                                                                                New von Willebrand factor binding protein from Staphylococci, useful for determining and treating staphylococcal infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum chromosome 2 related protein SEQ ID NO:129
                                                                                                                                                                                                                                                                                                                                                          39;
                                                                                                                                                                                                                                                                                                                      y Match 12.1%; Score 96.5; DB 23; Length 2060; Local Similarity 25.7%; Pred. No. 3.8; hes 39; Conservative 25; Mismatches 49; Indels 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 RKE--DLQREEHSQKSDSTKDVTATVLDKNNI 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 302-309; 577pp; English
                                                                                                                                  Claim 3; Page 35-41; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gardner M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB18272 standard; Protein; 2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US26796.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carucci D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum.
                              WPI; 2002-304928/34.
N-PSDB; AAD33371.
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CARUCCI D.
GARDNER M.
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                                                                                                                                                                                                                      4 EVSELKP-HRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDA 62
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                                                                                                                                                                                         11.7%; Score 93.5; DB 21; Length 408; 25.0%; Pred. No. 0.79; ive 28; Mismatches 58; Indels 31
                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana protein fragment SEQ ID NO: 45609.
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99US-0161359
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09-WAR-1999;
03-MAR-1999;
25-MAR-1999;
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01-ARR-1999;
06-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                       62
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99US-013428.
99US-0134219.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags continued to the control of (II) or to treat disease therapy techniques to restore normal activity of (II) or to treat disease states involving to restore normal activity of (II) or to treat disease states involving to restore normal activity of (II) or to treat disease states involving a cod supplement. (II) and it issue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical inspirate and polymicleotide sequences have applications in disgnostics, for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences and products dependent on DNA and amino acid sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 LSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQRE----E 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvilsant; osteopathic; antiarthritic; immunosupperssant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; burne damage; cartilage damage; antiinflammatory disease; coagulation;
                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 11.6%; Score 92.5; DB 22; Length 2519; Local Similarity 31.0%; Pred. No. 13; nes 22; Conservative 19; Mismatches 17; Indels 13;
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                                                                                                                                    Claim 20; SEQ ID No 46995; 103pp; English.
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Best Local Similarity 25.0%; Pred. No. 0.98;
Matches 39; Conservative 28; Mismatches 58; Indels 31; Gaps
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food supplement; medical imaging; diagnostic; genetic disorder.
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23-AUG-2000; 2000US-0649167
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CECRP-5; cell cycle regulation protein-5; cell proliferation; cell proliferative disease; cancer; atherosclerosis; cirrhosis; hepatitis; poriasis; immune system disorder; allergy; asthma; acquired immune deficiency syndrome; Crohn's disease; Blast method; rheumatoid arthritis; gene therapy; chromosomal mapping.
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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatocropic; vulnerary; antipsoriatic; antipornian; notropic; neuroprotective; osteopathic; anticonvulsant; antiathritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; antimusouspressive; antidiabetic; hypotensive; dermatological; antimusouspressive; antithromatory; antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating or treating conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, conditions and nucleic acids may be used to treat cancers, graft vs host disease, cardiovascular disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            erythematogus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids and peptides derived from open reading frame X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.3%; Score 90.5; DB 21; Length 209; 28.1%; Pred. No. 0.62; tive 17; Mismatches 56; Indels 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 NPQVNH-----SQLNESHRKEDLQREEHSQKSD--STKDVTATVLDK 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 KEFVRHKEKIKQAKEA-VKENLKKFSDSVKSTFRHFKDTTKNIFDE 166
                                                                                                                                                                                                                                                                                                                                                                                                                    useful for treating e.g. cancers, proliferative disorde
neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 4497-4498; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY44364 standard; protein; 757 AA.
                                                                                                                            31-WAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                                                                                      31-MAR-2000; 2000WO-US08621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAR-2000 (first entry)
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                                                                                                                                                                                                                                                                                       Leach M;
                                                                                                                                                                                                                                            CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                WPI; 2000-602362/57.
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Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  209 AA;
                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAC77106
  WO200058473-A2
                                                                                                                                                                                                                                                                                       Shimkets RA,
                                             05-OCT-2000
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Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cytostatic; cardioactive; neuroprotective; vulnerary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antinifective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder.

Human colon cancer antigen protein sequence SEQ ID NO:859.

(first entry)

09-MAR-2001

AAB53319;

AAB53319 standard; Protein; 758 AA.

AAB53319

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The present sequence is cell cycle regulation protein-5 (CECRP-5). Blast analytical method was used to identify this protein. CECRPs are activators of cell proliferation or inhibitors of cellular processes that modulate proliferation. They are used to treat or prevent cell proliferative diseases like cancers, atherosclerosis, cirrhosis, hepatitis, psoriasis, immune system disorders (e.g. acquired immune deficiency syndrome, allergy, asthma, Crohn's disease, rheumatoid arthritis). Antibodies are raised to screen for specific binding agents. The corresponding nucleic acid is used in gene therapy, chromosomal mapping and isolation of related sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel regulatory proteins, for diagnosis, treatment and prevention of cell proliferative and immune system diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baughn MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.3%; Score 90.5; DB 21; Length 757; 28.1%; Pred. No. 3.7; ive 17; Mismatches 56; Indels 47;
                                           note= "Potential phosphorylation site"
                                                                                                    note= "Potential phosphorylation site"
                                                                                                                                                               note= "Potential phosphorylation site"
               note= "Potential phosphorylation site"
                                                                                                                                                                                                                                                                                   /note= "Potential phosphorylation site"
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                                                                        note= "Potential phosphorylation
                                                                                                                                                                                           note= "Potential phosphorylation
                                                                                                                                                                                                                        note= "Potential phosphorylation
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730
                                                                                                                                   note= "Potential phosphorylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 70-71; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang YT,
                                                                                                                                                                                                                                                                                                                                                                        99WO-US12906.
                                                                                                                                                                                                                                                                                                                                                                                                     98US-0088695
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Best Local Similarity 28.1<sup>§</sup>
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000-105887/09.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                757 AA;
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N-PSDB; AAZ29484.
Modified-site
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(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Ruben SM; WPI; 2000-587534/55.

N-PSDB; AAC98076.

08-MAR-2000; 2000WO-US05883.

WO200055351-A1.

Homo

21-SEP-2000

99US-0124270.

12-MAR-1999;

Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon disorders such as colon cancer

Claim 11; Page 1408-1411; 2104pp; English.

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AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular; neuroprotective, immunomodulatory, gynacecological, gastrointestinal, vulnerary, nephrotropic, antilnfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polymucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polymucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, immune system disorders, muscular disorders, reproductive disorders, immune diseases, and cardiovascular disorders, and cardiovascular disorders, and cardiovascular disorders, and cardiovascular disorders, exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----ISGFEGKKDAG----YVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKD 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       454 VEAKDONGKOGTDGKKKGGRGSHRAKNKSKETFLGSV-------KETFDAMKNST 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47;
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28.1%; Pred. No. 3.8;
Live 17; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             758 AA;
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Local Sim-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 -----ISGFECKKDAG----YVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKD 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 453 VEAKDQNGKQGTDGKKKGGRGSHRAKNKSKETFLGSV------KETFDAMKNST 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 GEVSELKPHRVTVTIQNGKEMSSTIVSE--EDFILPVYKGELEKGYQF----DGWE---
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25

101 NPOVNH-----SQLNESHRKEDLOREEHSOKSD--STKDVTATVLDK 140

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                                                                                                                                                                                             Staphylococcus epidermidis; open reading frame; ORF; bacterial infection; antibacterial; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABB35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---GYQFDGWEISG--FEGKKDAGYVINLSKDTFIKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 SIDHSLSHLAEMVVKEDGAVENGDTVNIDFSG-SVDGEFFDGGQAEGYDLEIGSGSFIPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DTGEVSELKPHRVTVT-IQNGKE--MSSTIVSEEDFILPVYKG-ELEK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                 Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3033.
502 KEFVRHHKEKIKQAKEA-VKENLKKFSDSVKSTFRHFKDTTKNIFDE 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 23; Length 442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----SHRKEDLOREEHSOKSDSTKDVTATVLDKNNISSKSTTN 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269 SDAENVDEYKENLRKRLSEQKATEAENT-----EKEBAINKATEN 308
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                                                                           ABP38188 standard; Protein; 442
                                                                                                                                                                                                                                                                                                                                                                                97US-064964P.
                                                                                                                                                                                                                                                                                                                                                                                                                (GENO-) GENOME THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                    98US-0134001
                                                                                                                                                                                                                                                                                                                                                                  97US-055779P
                                                                                                                                                                                                                                                                                                                                                                                                                                            Bush D;
                                                                                                                                                                                                                                              Staphylococcus epidermidis
                                                                                                                                     (first entry)
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Matches 49; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               442 AA;
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                                                                                                                                                                                                                                                                          US6380370-B1
                                                                                                                                                                                                                                                                                                                                      13-AUG-1998;
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                                                                                                                                      24-JUL-2002
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                                                                                                       ABP38188;
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                                               RESULT 20
                                                              ABP38188
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producing hyperimune serum-reactive antigens from a pathogen, cumour, a listue or host prome to auto-immunity, where the antigens are used in a vaccine, comprises providing antibody preparation from a plasma pool of a type of animal, or individual sera with antibodies against the specific pathogen, tumour, allergen, tissue or host prome to auto-immunity. The hyperimune serum-reactive antigens comprising any of the 62 sequences of 53-261 amino acids fully defined in the specification, or their hyperimune fragments are useful for the manufacture of a pharmaceutical preparation, particularly a vaccine or epidermidis. The preparation of antibodies is useful for the manufacture of a medicament for treating or preventing staphylococcal infections or colonisation against S. aureus or S. colonisation against S. aureus or S. colonisation against S. aureus or S. epidermidis. The antibody preparations may also be used for diagnostic and imaging purposes. Other conditions that can be treated include cancer, autoimmune diseases or infections caused by viral (e.g. HIV, hepatitis A, B or C); fungal or protozoan pathogens. This sequence represents a staphylococcal protein relating to the method for identifying and producing pathogen specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   341 KMTDLQDTKYVVYESVENNESMMDTFVKH-----PIKTGMLNGKKYMVMETTNDDYWKDF 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- DAGYVINL-SKDTFI 74
                                                                                                                                                                                                                                                                                                                Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV; hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen; auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
                                                                                                                                                                                                                                  Pathogen specific antigen related staphylococcal protein SEQ ID No 414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel method for identifying, isolating and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 EVSELKPHRVTV--TIQNGKEMSSTIVSEEDFILPVYKGELE-KGYQF-----DGWEIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, for preparing vaccine or medicament for treating or preventing e.g. staphylococcal infections, comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zauner W;
Hafner M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Meinke A, Nagy E, Von Ahsen U, Klade C, Henics T,
Minh DB, Vytvytska O, Btz H, Dryla A, Weichhart T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 90; DB;
Pred. No. 3.4;
32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 7; Page 220; 252pp; English.
ABJ19106 standard; Protein; 645 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                       autoimmune disease; HIV; hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              providing antibody preparation
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Best Local Similarity 21.4%;
Matches 45; Conservative 3
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                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus sp
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                                                                                                                                                            06-MAR-2003
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes an isolated antibody (I) that binds to a staphylococcal surface protein selected from any of the 12 sequences of 554-2283 amino acids given in ABP56875 to ABP56886. Also described:

(I) an isolated antisera (II) comprising (I); (2) a diagnostic kit (III) comprising (I) and means for detecting binding by (I); (3) diagnosing (MI) an infection of Staphylococcus aureus by adding (I) to a sample suspected of being infected with the infection, and determining if antibodies have bound to the sample; (4) a pharmaceutical composition (IV) for treating or preventing an infection of S. aureus comprising (I), and a vehicle, carrier or excipient; (5) treating (M2) or preventing an infection of S. aureus of a human or animal an immunogenic amount of the isolated surface protein; and isolated active fragment (V) from the A domain of the DsgA protein; and solated active fragment (V) from the A domain of the DsgA protein; and (R) a vaccine (VI) for treating or preventing an infection of S. aureus comprising the surface protein in an amount effective to elicit an immune response, and a vehicle, carrier or excipient. (I) has antiinflammatory, antibacterial, immunosuppressive and antiarthritic activities, and can be
KPVFKKIEEKKEEENKPTFDV----SKKKDNPQVNHSQLNESHRKEDLQ----REEHSQ 125
                                                      microbial surface component recognising adhesive matrix molecule; surface protein; infection; antibacterial; antiinflammatory; vaccine; immunosuppressive; antiarthritic; gene therapy; pneumonia; endocarditis; septic arthritis; biomaterial related infection.
                                                                                                                                                                                                                                                                                                Staphylococcus aureus; Staphylococcus epidermidis; MSCRAMM; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated antibody that binds to a staphylococcal surface protein, useful for treating or preventing Staphylococcus aureus infections, such as pneumonia, septic arthritis, endocarditis or biomaterial related infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hall A,
                                                                                                                                                                                                                                                                      Staphylococcus epidermidis KrkN protein SEQ ID NO:10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hutchins JT,
                                                                                                          126 KSDSTKDVT-ATVLDKNNISSKSTTNNPNK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INHI-) INHIBITEX INC.
(QUEE-) QUEEN ELIZABETH COLLEGE DUBLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 29-30; 122pp; English.
                                                                                                                                                                                        ABP56879 standard; Protein; 654 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Speziale P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patti JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JUN-2002; 2002WO-US19220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2001; 2001US-298098P
                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus epidermidis.
                                                                                                                                                                                                                                            (first entry)
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Patel P, Syribeys P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2003-167481/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYPA-) UNIV PAVIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABZ22903
                                                                                                                                                                                                                                                                                                                                                                                                         WO2002102829-A2.
                                                                                                                                                                                                                                            07-APR-2003
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                                                                                                                                                                                                                  ABP56879;
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher ewkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                      404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75 KPVFKKIEEKKEEENKPTFDV----SKKKDNPQVNHSQLNESHRKEDLQ----REEHSQ 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74
used in gene therapy. The antibody, composition and vaccine are useful for treating or preventing Staphylococcus aureus infection in a human or animal, such as pneumonia, septic arthritis, endocarditis or biomaterial related infections. The present sequence represents Staphylococcus epidermidis KrkN protein, which is used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                 350 KMIDLQDIKYVVVESVENNESMADIFVKH----PIKTGMLNGKKYMVMETTNDDYWKDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 EVSELKPHRVTV--TIQNGKEMSSTIVSEEDFILPVYKGELE-KGYQF-----DGWEIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GFEGKK-----DAGYVINL-SKDTFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     405 MVEGORVRTISKDAKNNTRTIIFPYVEGKTLYDAIVKVHVKTIDYDGQYHVRIVDKEAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                    99
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                                                                                                                                                                                                                                                                                                                       67; Indels
                                                                                                                                                                                                                                                                 DB 24; Length
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                                                                                                                                                                                                                                                           11.3%; Score 90; DB 2.
21.4%; Pred. No. 3.4;
:ive 32; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 KSDSTKDVT-ATVLDKNNISSKSTTNNPNK 154
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                               the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                        654 AA
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                                                                                                                                                                                                                                                                                                                    45;
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Best Local S
                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB58769;
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(GEST ) GENSET
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                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                     112
                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence is the Staphylococcus aureus trigger factor (tig) bolypeptides and polymucleotides are useful for diagnosing diseases related to over or underexpression of tig protein by identifying mutations in the tig gene, or determining tig polymeptide or mNA expression levels due to an infection of an organism with the tig gene. They can diagnose the stage and type of infection. Tig polypeptides are also useful for screening compounds which affect
                                                                                                                                                       69 SKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQ--- 125
                                                                                                                                                                                                   353 -----KPAEK--SKKEEKEDSTIKSKKEKADSPANNQKEQQIGVKKKISEPEDASNSHK 404
                                                                                                                                         9 KPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINL 68
                                                                                                                                                                                                                                                                                                                                                                                                          Trigger factor, tig, diagnosis, immune response, bacterial infection; S. aureus infection; otitis media, toxic shock syndrome; conjunctivitis;
 sequences (ABL01840-ABL16175) and the encoded proteins (ABB3737-ABB72072). (ABB37377-ABB72072). Sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Staphylococcus aureus trigger factor (tig) polypeptide and polynucleotide, useful as diagnostic reagents and for prevention and treatment of Staphylococci aureus infections
                                                                                                                  32;
                                                                                           DB 22; Length 1183;
                                                                                                                  54; Indels
(ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hodgson JE, Jaworski DD;
Traini CM, Wang M, Ward J;
                                                                                                                                                                                                                                                                                                                                                                                                                                 wound infection; impetigo; septic arthritis; therapy
                                                                                           Match
Local Similarity 24.7%; Pred. No. 7.8;
es 36; Conservative 24; Mismatches

    aureus trigger factor protein sequence.

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                                                                                                                                                                                                                                   ----KSDSTKDVTATVLDKNNISSKS 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                 AAY03190 standard; Protein; 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98EP-0306697.
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                                                                                                                                                                                                                                                                                                                                                              16-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosenberg M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-192663/17.
                                                                     1183 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAX28175.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burnham MKR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-AUG-1998;
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04-SEP-1997;
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Warren RL;
                                                                                                                                                                                                                                                                                                                                        AAY03190;
                                                                                            Query Match
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immunise and prevent disease. Diseases diagnosed, prevented or treated include: bacterial infections, especially Staphylococcus aureus infections which cause oritis media, toxic shock syndrome, conjunctivitis, wound infection, impetigo and septic arthritis etc. Tig polypeptides, polymucleorides and their (ant)agoniets can prevent adhesion of bacteria to matrix proteins, and are useful for use on wounds and body implants to prevent bacterial infection.
activity of the protein by measuring the binding to tig and observing the stimulation or inhibition of the polypeptide function. These can be used in treatment to inhibit or enhance tig activity, in addition to direct administration of tig polypeptide to treat conditions associated with a lack of tig polypeptide, or direct administration of antisense sequences to prevent expression. Tig polypeptides (administered directly, in a vector and as a vaccine) and antibodies induce an immune response to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 AIDHSLGHLAEMVVKEDGVVENGDTVNIDFSG-SVDGEEFEGGQAEGYDLEIGSGSFI-P 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 VFK-----KKIEEKKE-----EE---NKPTFDVS----KKKDNPQVNHSQLNE- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---GYQFDGWEISG--FEGKKDAGYVINLSKDTFIKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB .20; Length 402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIGEVSELKPHRVTVT-IQNGKE--MSSTIVSEEDFILPVYKG-ELEK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----SHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.2%; Score 89.5; Di
22.1%; Pred. No. 2;
ive 33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 975-976; Disclosure; 1912pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY35091 standard; Protein; 511 AA.
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97FR-0014673.
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                                                                                                                                                                                                                              ----VSKKKDNPQVNHSQLNESHRK 115
                                                                                                                                                                                                                                            This sequence is the Staphylococcus aureus trigger factor (tig) polypeptide of the invention. Tig polypeptides and polynucleotides are useful for diagnosing diseases related to over or underexpression of tig protein by identifying mutations in the tig gene, or determining tig polypeptide or mRNA expression levels due to an infection of an organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trigger factor; tig; diagnosis; immune response; bacterial infection; S. aureus infection; otitis media; toxic shock syndrome; conjunctivitis; wound infection; impetigo; septic arthritis; therapy.
         frames in the complete genome (see AAX91990) of Chlamydia pneumoniae.
C. pneumoniae causes respiratory disease such as pneumonia and disease, sarcoidosis, sinusitis, purulent otitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
 AAY34584-Y35879 represent the proteins encoded by all the open reading
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Staphylococcus aureus trigger factor (tig) polypeptide and polynucleotide, useful as diagnostic reagents and for prevention and treatment of Staphylococci aureus infections
                                                                                                                                                                                                     21;
                                                                                                                                                                            11.2%; Score 89.5; DB 20; Length 511; 24.5%; Pred. No. 2.7;
                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hodgson JE, Jaworski DD;
Traini CM, Wang M, Ward J;
                                                                                                                                                                                                     33;
                                                                                                                                                                                                                                                                                               155 GDLDRVGHDSNEDSTEDSRS---EGGEPSSKSSS 185
                                                                                                                                                                                                                                                                               116 EDLQREEHSQKSDSTKDVTATVLDKNNISSKSTT 149
                                                                                                                                                                                                     17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 S. aureus trigger factor protein sequence.
                                                                                                                                                                                                                              74 IKPVFKKIEEKKEEENKPTFD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Traini CM,
                                                                                                                                                                                                                                                                                                                                                                      AAY03189 standard; Protein; 525 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 14; Page 6; 31pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                     23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lawlor EJ, Rosenberg M, Warren RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-192663/17.
N-PSDB; AAX28174.
                                                                                                                                                                                       Best Local Similarity
Matches 23; Conserva
                                                                                                                                                    511 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burnham MKR,
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                                                                                                                                                      Sequence
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polypeptides are also useful for screening compounds which affect
continuous are also useful for screening compounds which affect
continuous of the protein by measuring the binding to tig and observing the
stimulation or inhibition of the polypeptide function. These can be used
in treatment to inhibit or enhance tig activity, in addition to direct
administration of tig polypeptides to treat conditions associated with a
lack of tig polypeptide, or direct administration of antisense sequences
to prevent expression. Tig polypeptides (administered directly, in a
vector and as a vaccine) and antibodies induce an immune response to
immunise and prevent disease. Diseases diagnosed, prevented or treated
include: bacterial infections, especially Staphylococcus aureus
include: bacterial infection, impetigo and septic arthritis etc. Tig
polypeptides, polymucleotides and their (ant) agonists can prevent
and body implants to prevent bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 DETDIKPVAQPEVSVTQIEKGKDFIFEATVTVEPEVKLGDYKGLEIEKQETELSDDELQE 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 VFK-----KKKDNPQVNHSQLNE- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199 GPBEQLEGMKVDEEKDVVVTFPEBYHAEBLAGKEATFKTKVNBIKFKEVPBLTDEIANEL 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 20; Length 525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 -----SHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTN 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 DAEANTVDEYKENLRKRLAEQKATDAENV----EKEEAITKATDN 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIGEVSELKPHRVTVT-IQNGKE--MSSTIVSEEDFILPVXKG-ELEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
11.2%; Score 89.5; DI
Best Local Similarity 22.1%; Pred. No. 2.8;
Matches 50; Conservative 33; Mismatches
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             525 AA;
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RESULT 29
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                                                                                                                                                                                                                                                                                                             705 MESKEYSEPLAVKLGEDVSKSPSNESSDTKISEVKGEE--PKMNGELPKTGEOVKOPEKS 762
                                                                                                                                                                                                                                                                                                                                    ESHRK-EDLOREEHSOKSDSTKDVT-----ATVLDK 140
                                                                                                                                                                                                                                                                                                                                                   65
                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pathogen specific antigen related staphylococcal protein SEQ ID No 142.
                                                                                                                                                                                                                                             19 NGKE----MSSTIVSEEDF--ILPVYKGELEKGYQFDGWEISGFEGK--KDAGYV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen; auto-immunity; vaccine; staphylococcal infection; antibody; cancer; autoimmune disease; HIV; hepatitis.
                                                                                     insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zauner W;
Hafner M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying, isolating and producing hyperimmune serum-reactive
                                                                                                                                                                                                   Length 1408;
                     Disclosure; SEQ ID NO 2904; 21pp + Sequence Listing; English.
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Weichhart T,
                                                                                                                                                                                                   DB 22;
                                                                                                                                                                                                                        62;
                                                                                                                                                                                                 11.2%; Score 89.5; Dilarity 24.7%; Pred. No. 11; Conservative 23; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABJ18979 standard; Protein; 645 AA.
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                                                                                                                                                                                                                                                                                                                                                                                 NNISSKSTINNPNK 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Meinke A, Nagy E, Von
Minh DB, Vytvytska O,
Tempelmaier B;
                                                                                                                                                                                                           Local Similarity
Les 48; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-075410/07
                                                                                                                                                                             1408 AA;
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The invention relates to a novel method for identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, tumour, allergen, a tissue or host prone to auto-immunity, where the antigens a re used in a vaccine, comprises providing antibody preparation from a plasma pool of a type of animal, or individual sera with antibodies against the specific pathogen, tumour, allergen, tissue or host prone to auto-immunity. The hyperimmune serum-reactive antigens comprising any of the 62 sequences of 53-261 amino acids fully defined in the moutacture of a pharmaceutical preparation, particularly a vaccine anulacture of a pharmaceutical preparation, particularly a vaccine against staphylococcal infections or colonisation against S. aureus or S. epidermidis. The preparation of antibodies is useful for the manufacture of a medicament for treating or preventing staphylococcal infections or colonisation against S. aureus or S. epidermidis. The antibody preparations may also be used for diagnostic and imaging purposes. Other conditions that can be treated include cancer, autoimmune diseases or infections caused by viral (e.g. HIV, hepatitis A, B or C), fungal or protezing to the method for identifying and producing pathogen specific antigens of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           341 KMTDLQDTKYVVYESVENNESWMDTFVKH-----PIKTGMLNGKKXMVMETTNDDYWKDF 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75 KPVFKKIEEKKEEENKPTFDV----SKKKDNPQVNHSQLNESHRKEDLQ----REEHSQ 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 GFEGKK------DAGYVINL-SKDTFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                396 MVEGORVRIISKDAKNNTRIIIFPYVEGKTLYDAIVKVHVKTIDYDGOYHVRIVDKEAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 EVSELKPHRVTV--TIQNGKEMSSTIVSEEDFILPVYKGELE-KGYQF-----DGWEIS
antigens from a pathogen, for preparing vaccine or medicament for treating or preventing e.g. staphylococcal infections, comprises providing antibody preparation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila, developmental biology, cell signalling, insecticide, pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster polypeptide SEQ ID NO 21276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 KSDSTKDVT-ATVLDKNNISSKSTTNNPNK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              516 SSESGKGVTLATKPTKGEVESSSTT--PTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 89;
Pred. No.
                                                                                                                                                                         Claim 21; Page 168; 252pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB64828 standard; Protein; 281 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.1%;
21.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 21...
Best A5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         645 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200171042-A2
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Kodira

Shen Y,

Ye Y,

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He M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP73992 standard; Protein; 225 AA.
                                                                                                                                                                       Claim 1; Figure 3; 626pp; English.
Pham L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Воопе С,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-DEC-2000; 2000US-259128P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-FEB-2001; 2001US-0792024.
22-AUG-2001; 2001US-314050P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-DEC-2001; 2001WO-US49486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 11.1%
Best Local Similarity 23.3%
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 ISSKSTTNN 151
Не Ј,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Roemer T, Jiang B,
                                    2001-355877/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                    1141 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 SSSSSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Candida albicans
                                                       N-PSDB; AAH62788
Yang F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200253728-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP73992;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
χη X,
δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                         capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLiology expressed DNA sequences (ABLiology) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 NFEEFTINMITTOODLLKNIY-SLLDK------DNEGAITSKELGMVIRALGROPNESIA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KDTFIKPVFKKIEE-KKEEENKPTFDVSKKKDNPQVNHSQLNE----SHRKEDLQREEH 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 NGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVI-----NLS 69
                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shrimp white spot Bacilliform virus; WSBV; diagnosis; viral infection; antiviral agent; gene expression; antisense construct; transgenic viral resistant shrimp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                         invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23;
                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 21276; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shrimp white spot Bacilliform virus (WSBV) protein 99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.1%; Score 88.5; DB 22; 22.1%; Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PENY-) PE CORP NY.
(THIR-) THIRD INST OCEANOGRAPHY STATE OCEANI C A.
(SINO-) SINOGENOMAX CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31; Conservative 34; Mismatches
                                                         Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG85008 standard; Protein; 1141 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 SQKSDSTKDVTATVLDKNNI 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 IREYDLDQDNHINFEESNNM 268
                                                         Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-NOV-2000; 2000WO-US28888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          White spot syndrome virus.
                                                         Adams M,
                                                                                             WPI; 2001-656860/75.
N-PSDB; ABL08931.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 31; Conserv
                    CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                  (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  281 AA;
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                    (PEKE ) PE
                                                         Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG85008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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The invention provides the primary nucleotide sequence of the WSBV genome (AAH62689), predicted transcript sequences (AAH62689-AAH62839) and encoded proteins (AAG85101-AAG85051) and oligonucleotide sequences (AAH62840-63160) suitable for use as primare or probes. The nucleic acid molecules and proteins of the invention are useful for diagnosis and monitoring viral infection, in screens for antiviral agents and for monitoring viral gene expression or activity during a treatment regimen. The nucleic acid molecules are also useful as antisense constructs to control viral gene expression in infected cells and tissues and to create transgenic viral resistant shrimp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 EKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNN 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 STIVSEEDFILPVYKGELEKGYQFDGWEISGFEG--KKDAGYVINLSKDTFIKPVFKKIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
signal transduction; DNA replication; cell division; growth;
proliferation; Candida albicans; fungicide; antifungal.
Primary nucleotide sequence of the shrimp white spot Bacilliform (WSBV), useful for producing viral polypeptides that can be used screen for agents that are useful for treating WSBV infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                       25;
                                                                                                                                                                                                                                                                                                                                                                                                              Length 1141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohlsen KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Candida albicans essential protein SEQ ID NO 7829.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       43;
                                                                                                                                                                                                                                                                                                                                                                                                              DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              11.1%; Score 88.5; 123.3%; Pred. No. 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-566694/60.
N-PSDB; ABZ32542.
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82

09-JUN-2000; 2000JP-0241899.

(HELI-) HELIX RES INST

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The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying cone allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by insertion or replacement fragment with a heterologous promoter, so that expression of the second allele is regulated by the promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles modified are useful for identifying a gene that contributes. to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent, an antifungal agent that inhibits the growth of a diploid fungus contributes. (M1) is useful for identifying a compound which modulates the compound catabolism, blosynthetic, transporter, transcriptional, compound catabolism, blosynthetic, transporter, transcriptional, compound is signal transduction, DNA replication and cell division activity, or inhibit growth or proliferation of C. albicans cells and for translational infection by C. albicans need the invention. Note: The sequence data for this patent is not represented in the printed contribution to the European patent of the suronean patent of the suronean patent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 YDDDDDEFEGFESSNGAAKELNLSESQAIKEWKQRRDLEIEEREKLNSKKKEEIIEKAKS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YOFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKK----IEEKKEEENKPTFDVSKKK-- 99
          Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; primer; detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 -- DNPOVNHSQLNESHRKEDLQREEH--SQKSDSTKDVTATVLDKNN 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 44; SEQ ID NO 7829; 167pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 23; Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 11.0%; Score 88; DB 2
Best Local Similarity 28.0%; Pred. No. 1.2;
Matches 30; Conservative 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human protein sequence SEQ ID NO:15383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB94584 standard; Protein; 258 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99JP-0300253.
2000JP-0118776.
2000JP-0183767.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP1074617-A2.
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                  Constructing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUN-2001
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                                                                            expression
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The present invention describes primer sets for synthesising 5602

full-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-dT primer and an oligonucleotide complementary
to the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
cligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprises a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
polynucleotide which comprises a 1'-end sequence, where the
oligonucleotide which comprises a 1'-end sequence, where the
oligonucleotide which comprises a 1'-end sequence, the pacification. The primer sets can be used in antisense therapy and
in gene therapy. The primer sets can be used in antisense therapy and
in gene therapy. The primers are useful for synthesising polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
connection and/or diagnosis of the primers are also useful for the
connection and/or diagnosis of the primers are also useful for the
connection and/or diagnosis of the primers are also useful for the
connection and/or comprises of the primers and are also useful for the
connection and/or cliagnosis of the primers and are also useful set
connected by
the full-length cDNAs. The primers allow obtaining of the full-length
connected any specialised methods. AAH031629 to AAH13632
ceptreent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 YKGELEKGYQFDGWEISGFEGKKDAGY--VINLSKDTFIKPVFKKIEEKKEEENKPTFDV 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 SKKKDNPQ-----VNHSQLNESHRKEDLQREEHSQKSDSTKDVTATV--LDKNNISSK 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
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                                                                                                                                              Saito K, Ya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; SEQ ID 15383; 2537pp + CD ROM; English
                                                                                                                                          hikawa T, Hayashi K, S
Wakamatsu A, Nagai K,
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                                                                                                                                      sogai T, Nishikawa T,
Sugiyama T, Wakamatsı
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                                                                                                                                                                                                                                                            WPI; 2001-318749/34.
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                                                                                                                                                  Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200157190-A2
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                                                                                                                                                                                     Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM79318;
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AAM79318
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WPI; 2001-476283/51.
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Best Local Similarity
Matches 33; Conserv
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                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAK52452
                                                           WO200157190-A2.
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                                                                                  09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148
                                                                                                                                                                                                                                                                                                                                  The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256 WKQDTPKSKAGYVQEEHKKQETPKLWPVQLQKBQ-DPKKQTPKSWTPSMQSEQNTTKSWT 314
                                                                                                                                                                                                                                                                                                                                                                 production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity infinity in activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
                                                                                                                                                                                   Ma Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: Macros for SEQ ID NO 2110 (AAX52581), 2111 (AAX52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 GELEKGYOFDGWEISG--FEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 -KKDNPQVNHSQLNESHRKED------LQREEHSQKSDSTKDVTATVLDKNNISSKST
                                                                                                                                                                                                                                                                       Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                                                                                                                                                 Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW; Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 11.0%; Score 88; DB 22; Length 817; Local Similarity 27.3%; Pred. No. 7.4; He 33; Conservative 21; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                           Claim 20; Page 215; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM79319 standard; Protein; 817 AA.
                                            03-FEB-2000; 2000US-0496914.
27-AFR-2000; 2000US-0560875.
20-UJN-2000; 2000US-0598075.
19-JJL-2000; 2000US-0620325.
01-SEP-2000; 2000US-0654936.
15-SEP-2000; 2000US-063325.
20-CT-2000; 2000US-063325.
30-NOV-2000; 2000US-0728422.
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                        05-FEB-2001; 2001WO-US04098
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                                                                                                                                                                                                                                  WPI; 2001-476283/51.
N-PSDB; AAK52451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       817 AA;
                                                                                                                                                          (HYSE-) HYSEQ INC
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09-AUG-2001
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Zhao QA,
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                                                                                                                                                                                                           Xue AJ,
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Matches
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM89302) that exhibit activity elating to erytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymerleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treatment of cancer, leukaemia, nervous system disorders, arthritis and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C, Cao Y,
Wang 2W;
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tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu (
Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R,
Xue AJ, Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Page 215; 6221pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                               03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
20-UNN-2000; 2000US-05298075.
19-JJL-2000; 2000US-06298075.
15-SEP-2000; 2000US-0654936.
15-SEP-2000; 2000US-0653561.
20-OCT-2000; 2000US-063325.
                                                                                                                                                                                                                                                                                                                                                05-FEB-2001; 2001WO-US04098
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126 LEIPEFVDEDTYDL-YMIEIKEYESKMKEERARREKERKEREKRDLEEKKKKQQQQQKS 184

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The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying cone allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by insertions or promoter. So that expression of the second allele by the promoter. So that expression of the second allele is regulated by the promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles modified are useful for identifying a gene that contributes to the survival or growth of a fungus, a gene that is sesential to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent that inhibits the growth of a fungus to an antifungal agent that inhibits the growth of a diploid fungus of disease. (M1) is useful for identifying a compound which modulates the activity of a gene product, preferably enzymatic activity, carbon compound catabolism, blosynthetic, transporter, transcriptional, compound stabolism, blosynthetic, transporter, transcriptional, compound to inhibit growth or proliferation of C. albicans cells and for translational, signal transduction, DNA replication and cell division activity. The method is useful for identifying a compound having the ability to inhibit growth or proliferation of C. albicans cells and for transitication but is based on sequence information supplied to Derwent by parament of the pronent by the propersure of the propertion of the pronent by the propertion of the pronent by the propertion of the propertion of the pronent by the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional
                                                                                                                                 strain; biosynthesis;
                                                                                                                         Fungus; yeast; tetracyclin; promoter; GRACE strain; blosynthe
signal transduction; DNA replication; cell division; growth;
proliferation; Candida albicans; fungicide; antifungal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 44; SEQ ID NO 7046; 167pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bussey H, Ohlsen KL;
                                                                        Candida albicans essential protein SEQ ID NO 7046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boone C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-FEB-2001; 2001US-0792024.
22-AUG-2001; 2001US-314050P.
                                                                                                                                                                                                                                                                                                                                                                                                                                               29-DEC-2000; 2000US-259128P.
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                          30-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roemer T, Jiang B,
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                                                                                                                                                                                                                                     Candida albicans
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                                                                                   4 EVSELKPH---RVTVTIQNGKEM----SSTIVSEEDFILPVYKGELEKGYQFDGW--- 51
                                          21; Gaps
Length 635;
                                            Indels
                                            68;
  DB 23;
Ouery Match
11.0%; Score 87.5; DE
Best Local Similarity 22.1%; Pred. No. 5.9;
Matches 36; Conservative 38; Mismatches
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Sequence

70 KMKKFKPSPWTRMPFTPKQGIBLNHWVKGSKBLIEQQEF----EEDGTPKPYFFEKYNVQ 125 -EISGF--EGKKDAGYVINLSK-DTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHS 107

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Sequences ABB10381-ABB12330 represent 1350 novel human polypeptides, and sequences ABB0825-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a comprising and nuclectide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of identifying compounds which chind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby collypeptides of the invention have homology to known proteins, thereby collypeptides of the invention have homology to known proteins, thereby collypeptides of the invention and polypeptides of the invention may contain an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities, seem cell growth factor activity; haematopoiesis regulatory activity; tissue growth activities; chemotactic or chemokinetic activities; haemacetaic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis.

Depending on their biological activities, polypeptides and nucleotides of
                                                                                                                                                                                                                                                                                                                     Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopolesis regulation; tissue growth; immunomodulator; activin; inhibin; ofmentaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumnour; haematopoletic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; atherosclerosis; coronary heart disease; arterial ischemia; bone disorder; osteoporosis; vascular growth disorder; issue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiantlammatory; antiathmatic; antiathritic; haemostatic; antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic, osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
                      Human secreted protein homologue, SEQ ID NO:2651.
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                                                                                                                                                    ABB12281 standard; peptide; 2515 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang YT, Liu C, Drmanac RT;
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                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                ABB12281;
                                                                                                         RESULT 36
                                                                                                                                  ABB1228
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conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammantory conditions (e.g., archima or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal conscious growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound repair (or nucleic acids encoding them) may be used to promote wound crepair (or nucleic acids encoding them) may be used to promote wound corporation and ulcers), while those with commondiatory activities may be used in the treatment of viral, chacterial and fungal infections in addition to immune disorders. Comprome cell growth factor activity may be used in cell cultures to promote cell growth factor activity may be used to neuroepithelial cells that can be used to augment or replace cells damaged by illness, cutoimmune disease or accidental damage. The polypeptides and nucleotides caucimmune disease or accidental damage. The polypeptides and in drug screening techniques. The present sequence represents a novel human companies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2352 IAELOREPLLVNESLNVENSGFRTNEEIHSESYNKGEISSGRKDNAEAISGHSVEADP-- 2409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 VINLSKOTFIKPVFKKIEEKKEEENKPTFDVSKKK------DNPQVNHSQLNESH 113
invention are useful for preventing, treating or ameliorating medical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22; Length 2515;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.0%; Score 87.5; DB 22; 24.2%; Pred. No. 40; Live 29; Mismatches 55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human protein SEQ ID NO 3914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUL 2000; 2000US-0620325.
01-SEP-2000; 2000US-0654936.
15-SEP-2000; 2000US-0653561.
20-OCT-2000; 2000US-0693325.
30-NOV-2000; 2000US-0728422.
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20-JUN-2000; 2000US-0598075
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Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            2515 AA;
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::||: : | | | : | | | 352 IAELQREPLIVNESLINVENGERTHEEIHSESYNKGEISSGRKDNAEAISGHSVEADP-- 2409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAW78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymetides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, esg. stem cell growth factor activity, hammanomodulatory activity and activity, issue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
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                                                                                                                                                                                                                            Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
      u P, Xu C, Cao Y,
Chen R, Wang ZW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2515;
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      Zhou P,
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Drmanac RT, Asundi V, Zhou
Wang J, Zhang J, Ren F,
Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.0%; Score 87.5; DE
24.2%; Pred. No. 40;
tive 29; Mismatches
                                                                                                                                                                                                                                                                                                                                  Claim 20; Page 465-466; 6221pp; English.
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2000US-0560875.
2000US-0598075.
2000US-0620325.
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Matches 38; Conservative
                                                                                                                                       WPI; 2001-476283/51.
   Liu C, I
Wang D,
Yang Y, I
                                                                                                                                                                   N-PSDB; AAK53401
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27-APR-2000; 2
20-JUN-2000; 2
19-JUL-2000; 2
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      Tang YT,
Zhao QA,
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Chinn J; Amshey SR; ld Y, Gerstin EH;

2001US-280067P. 2001US-280068P. 2001US-291280P.

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New human secretory proteins and polynucleotides, useful for diagnosing, treating or preventing autoimmune/inflammatory disorders (e.g. AIDS), neurological disorders (e.g. Alzheimer's), or cell proliferations or cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin F
Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
                                                                                                                                                                                                                                                                                                                        17-MAY-2001; 2001US-291849P.
19-JUN-2001; 2001US-299428P.
20-JUN-2001; 2001US-299776P.
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                                                                                                                                              27-MAR-2002; 2002WO-US09921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INCY-) INCYTE GENOMICS INC
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                        WO200283876-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynetides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity activity and activity and activity and activity and activity activity and activity of activity and activity of activity and activinihibin activity and activity and activity activity and activity activity and activity activity and activity activity and activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activity activi
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                                                                                                                                                                                                            Ma Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inflammation.

Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
(AAW80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy .
                                                                                                                                                                                                            Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35;
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                                                                                                                                                                                                      Drmanac RT, Asundi V, Zhou P, Xu C, Ca
Wang J, Zhang J, Ren F, Chen R, Wang
Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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24.2%; Pred. No. 40;
ive 29; Mismatches 55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; Page 466-467; 6221pp; English.
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                        15-SEP-2000; 2000US-0663561.
20-OCT-2000; 2000US-0693325.
30-NOV-2000; 2000US-0728422.
01-SEP-2000; 2000US-0654936
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                                                                                                                                                                                                         Liu C, D
Wang D,
Yang Y, W
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                                                                                                                                                 (HYSE-) HYSEQ INC
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                                                                                                                                                                                                      Tang YT,
Zhao QA,
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The invention relates to a secretory polynucleotide (designated sptm)

comprising any of 567 polynucleotide sequences (ABZ15837-ABZ3643), a

maturally occurring polynucleotide sequence at least 90 % identical to

the polynucleotide sequence, a polynucleotide complementary to them or an

RNA equivalent of them. The polypeptide or polynucleotide are useful for

treating, preventing or diagnosing a disease or condition associated with

the expression of functional SPTM. These are particularly useful for

the expression of functional SPTM. These are particularly useful for

diagnosing, treating or preventing autoimmune/inflammatory disorders

(e.g. acquired immunodeficiency syndrome, anaemia, asthma or Crohn's

disease), neurological disorders (e.g. epilepsy, Huntington's disease,

multiple sclerosis, cerebral palsy, Parkinson's disease, anxiety,

schizophrenia or amnesia), or cell proliferative disorders (e.g.

psoriasis, polycythemia vera, or cancers including adenocarcinoma,

checkins of the invention (ABPF1584-ABPF5962).

proteins of the invention (ABPF1584-ABPF5962).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2671 IAELOREPLLVNESLNVENSGFRTNEEIHSESYNKGEISSGRKDNAEAISGHSVEADP-- 2728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 VINLSKOTFIKPVFKKIEEKKEEENKPTFDVSKKK------DNPQVNHSQLNESH 113
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Claim 27; SEQ ID NO 1057; 458pp + Sequence Listing; English.
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25.4%; Pred. No. 52;
tive 22; Mismatches
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ftp.wipo.int/pub/published_pct_sequences
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Matches 43; Conservative
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990S-0139459-990S-0139460-990S-01394610-990S-01394610-990S-01394610-990S-01394610-990S-01394610-990S-01394610-990S-01394610-990S-0139462-990S-0139462-990S-0139462-990S-014632-990S-014632-990S-014632-990S-014632-990S-014632-990S-014632-990S-014632-990S-014632-990S-014632-990S-014632-990S-014632-990S-014632-990S-014632-990S-014632-990S-014632-990S-014632-990S-014632-990S-014632-990S-014632-990S-014632-990S-014632-990S-014633-990S-014633-990S-014633-990S-014633-990S-014633-990S-014633-990S-014633-990S-014633-990S-014633-990S-014733-990S-014733-990S-014733-990S-014733-990S-014733-990S-014733-990S-014733-990S-014733-990S-014733-990S-014733-990S-014733-990S-014733-990S-014933-990S-014933-990S-014933-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014932-0-990S-014942-0-990S-014942-0-990S-014942-0-990S-014942-0-990S-014942-0-990S-014942-0-990S-014942-0
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-AUG-1999
                                                                                                                                                                Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 59270.
                                             AAG47057 standard; Protein; 313 AA.
                                                                                                                                                                                                                                                                                                                                                 99US-0121825.
99US-0123180.
99US-0123548.
99US-0125788.
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99US-0132484.
99US-0132485.
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99US-0132863.
99US-0134256.
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99US-0139456.
99US-0139457.
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                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0126785
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99US-0134219
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                                                                                                       18-OCT-2000 (first entry)
                                                                                                                                                                                                                             Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                         06-SEP-2000
                                                                         AAG47057;
                 RESULT 40
AAG47057
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Search completed: February 10, 2004, 10:53:55 Job time: 37.1775 secs

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99US-0151066.
99US-0151080.
99US-0151303.
                                                   99US-0151930.
99US-0152363.
99US-0153070.
                                                                                         99US-0153758
                         30-AUG-1999;
31-AUG-1999;
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9 65 VINLSKOTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHS 124 6 SELKPHRVTVTIONGKEMSSTIVSEEDFILPVYKGELEKGYOFDGWEISG-FEGKKDAGY 64 46; Indels 34; Gaps Query Match
10.9%; Score 87; DB 21; Length 313;
Best Local Similarity 25.4%; Pred. No. 2.5;
Matches 36; Conservative 26; Mismatches 46; Indels 3 a a

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:||: | : | : | : | 142 KKSNKKKMDMTSKKENKIEEE 163 125 OKSDSTKDVTATVLDKNNISSK 146

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NCBI_TaxID=1313;
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                                                                                                   February 10, 2004, 10:48:44; Search time 29.0366 Seconds (without alignments) 1457.493 Million cell updates/sec
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848
1 TTVKEFILNKDTGEVSELKP......ATVLDKNNISSKSTTNNPNK 164
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RIES	Description	Q9aht5 streptococc	Q97ry6 streptococc	Q8dqp7 streptococc	Q984m8 streptococc	Q8cpk8 staphylococ	Q95pi5 plasmodium	Q9u6c4 plasmodium	Q9u0g0 plasmodium	Q25995 plasmodium	Q8ij55 plasmodium	Q25706 plasmodium	Q90784 gallus gall	Q25705 plasmodium	. Q8i5f3 plasmodium	Q8i2k8 plasmodium	שיייים שוויים וושכט
SUMMARIES	Ü	Q9AHTS	Q97RY6	08DQP7	Q9S4M8	OBCPKB	095PIS	Q9U6C4	Q9U0G0	025995	081355	025706	090784	025705	QBISF3	QBI2KB	026019
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12.9 12.7 12.5	12.3 540 10 12.3 540 10 12.2 325 5 12.1 2081 10	12.1 238 5 12.0 312 16 12.0 382 5 12.0 556 5	12.0 948 5 12.0 1377 5 11.9 1373 5 11.8 375 4	11.8 622 16 0980A1 11.8 1130 5 081524 11.8 3127 5 0810A0 11.7 385 5 0913424 11.7 4524 5 081349 11.7 211 5 P91488	11.7 11.7 11.7 11.7
17 109 18 108.5 19 107.5 20 106		26 102.5 27 101.5 28 101.5 29 101.5	2000	35 100 36 100 37 100 38 99.5 39 99.5	41 42 43 44 45 99 99

ALIGNMENTS

Choi G.H., Barash S.C., Rosen C.A., Masure H.R., Tuomanen E.,
Gayle A., Brewah Y.Y., Walsh W., Barren P., Lathigra R., Hanson M.,
Langermann S., Johnson S., Koenig S.,
"Use of a Whole Genome Approach To Identify Vaccine Molecules
Affording Protection against Streptococcus pneumoniae Infection.";
Infect. Immun. 69:1893-1898 (2001).
I- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
MANIDE BOND (BY SIMILARITY).
HSSP, P00782; 2SBT. Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Created) Last sequence update) Last annotation update) PRT; 2119 AA Pfam; PF00082; Peptidase S8; 2. PRINTS; PR00723; SUBTILISIN. TIGRFAMs; TIGR01167; LPXTG_anchor; 1. InterPro; IPR001899; Gram pos_anchor.interPro; IPR006192; LPXTG. InterPro; IPR001209; Peptidase_S8. InterPro; IPR001680; WD40. STRAIN=N4; MEDLINE=21116976; PubMed=11179332; Interpro; IPR001680; WD40.
Pfam; PF00746; Gram pos_anchor; 1.
Pfam; PF02225; PA; 1. 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-MAR-2003 (TrEMBLrel. 23, Serine protease (Fragment) Streptococcus pneumoniae. nterPro; IPR003137; PA. PRELIMINARY; SEQUENCE FROM N.A. MEROPS; S08.064;

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121
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                    SEQUENCE
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Q8DQP7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1982 WEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLN 2041
                                                                                                                                                                                                                                                                                                                                                                                                                                     61 WEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLN 120
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                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                         Length 2119;
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                            2119 AA; 238226 MW; 517F9B7F6B960A6A CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                    ; Score 848; DB 2;
; Pred. No. 9.6e-53;
0; Mismatches 0;
R PROSITE; PS50840; PA; 1.
R PROSITE; PS50840; PA; 1.
R PROSITE; PS00137; SUBTILASE HIS; 1.
R PROSITE; PS00138; SUBTILASE SER; 1.
C PROSITE; PS00678; WD.REPEATS_1; 1.
C PLI wall; Peptidoglycan-anchor; Protease.
NON_TER 1 1 1.
SEQUENCE 2119 AB.
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Pfam, PF00225; PA; 1.
Pfam, PF00022; Peptidase S8; 2.
PRINTS; PR00723; SUBTILISIN.
PROSTE; PS0047; GRAM POS_ANCHORING; 1.
PROSTIE; PS0840; PA; 1.
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InterPro; IPR001892; LPXTG.
InterPro; IPR003137; PA.
InterPro; IPR0010209; Peptidase_S8.
InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1-OCT-2001 (TrEMBLrel. 18, Created)
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PROSITE; PS00138; SUBTILASE SER; 1.
PROSITE; PS00678; WD_REPEATS_1; 1.
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01-MAR-2003 (TrEMBLrel. 23, Last ar
Serine protease, subtilase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21357209; PubMed=11463916;
                                                                                                                                                                                                                                    Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 164; Conservative 0
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EMBL; AE007373; AAK74791.1;
MEROPS; SO8.064; -.
TIGR; SP0641; -.
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NCBI_TaxID=1313;
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Q97RY6
                      STREETS
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2003 WEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLN 2062
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                                                                                                                                                                                                                                   1943 TTVKEFILNKDTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDG 2002
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                                                                                                                                                                                                                                                                                                                               61 WEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLN 120
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Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S., Benskins J., Alborn W.E. Jr., Fritz L., Fu D.-J., Fuller W., Geringer C., DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C., Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E., LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P., McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I., Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P., Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G., Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P.L.,
                                                                                                                                 Gaps
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"Genome of the bacterium Streptococcus pneumoniae strain R6.";
"Genome of the bacterium Streptococcus pneumoniae strain R6.";
J. Bacteriol. 183:5709-5717(2001).
EMBL; AE006434; AAK99365.1; -.
Hydrolase; Complete proteome.
SEQUENCE 2144 AA; 240436 MW; 8C1B4B1DBCS03A0C CRC64;
                                                                Length 2140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ol-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Cell wall-associated serine proteinase PrtA (EC 3.4.21.-).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 164
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                                                                                                                                 Indels
240426 MW; FA44AD8E2938B334 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9S4M8 PRELIMINARY; PRT; 2144 AA. Q9S4M8; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
                                                                Query Match 100.0%; Score 848; DB 16; Best Local Similarity 100.0%; Pred. No. 9.7e-53; Matches 164; Conservative 0; Mismatches 0;
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Matches 163; Conservative
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      2140 AA;
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01-MAR-2003
01-MAR-2003
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--NISSKSTTNN 161
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                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=5833;
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                                                                                                                   Bethe G., ten Thoren E., Bongaerts R.J.M., Heinz H.+P., Zysk G.; "Cloning and sequencing of a novel surface protease of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   CELL WALL-ASSOCIATED SERINE PROTEINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.
                                                                                                                                                     Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN AN AMIDE BOND (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2144;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.5%; Score 844; DB 2; Length 21 98.8%; Pred. No. 1.9e-52; ive 2; Mismatches 0; Indels
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2144 AA; 240724 MW; 2052511470741331 CRC64;
                                    Streptococcus pneumoniae.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Cell wall-associated serine proteinase PrtA precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Penicillin-binding protein 1.
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Bacteria; Firmicutes; Bacillales; Staphylococcus
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                                                                                                                                                                                                                        InterPro; 1PR001999; Gram pos_anchor.
InterPro; 1PR001999; Gram pos_anchor.
InterPro; 1PR001929; LEXTG.
InterPro; 1PR0010137; PA.
InterPro; 1PR0010209; Peptidase_SB.
InterPro; 1PR001680; WH90.
Pfam; PF001046; Gram pos_anchor; 1.
Pfam; PF00225; PA; 1.
Pfam; PF00129; Paptidase_SB; 2.
Pfam; PF00123; SUBTILISIN.
TIGRPAMS; TIGR01167; LEXTG anchor; 1.
PROSITE; PS50847; GRAM POS_ANCHORING; 1.
PROSITE; PS50840; PA; 1.
PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00137; SUBTILASE SER; 1.
PROSITE; PS00138; WD REPEATS_1; 1.
Cell wall; Peptidoglycan-anchor; Signal.
SIGNAL
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                                                                                                                                                                                         EMBL; AF127143; AAD48399.1; -. HSSP; P00782; 2SBT.
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Matches 162; Conservative
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STRAIN=ATCC 12228;
                                                                                             SEQUENCE FROM N.A.
                                                           Streptococcus.
NCBL_TaxID=1313;
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                                                                                                                                                                                                                                                                                                                                                                   62 -EISGFE-----GKKDAGYVIN--LSKDTFIKPVFKKIEEKKEEENKPTFDVS----K 107
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                                                                                                                                                                                                                                                                                             10 KDTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYK-----GELEKGYQFDGW--
                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TDDDQEKTDEDSSDNKSKKDKADEDHSNTSSSTKN-----DKSNADSKNDSDD 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 KKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNN 161
                                                                                                                                                                                                           46;
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                                                                                                                                                     14.0%; Score 119; DB 16; Length 775; 27.0%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum.
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium
                                                                                                                                                                                                           57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55; Indels
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Chen 2., Wen Y.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AR016746; AA004453.1; -.
COMDLete proteome.
SEQUENCE 775 AA; 86354 MW; 4A00563A7BB8777C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monkeys.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY044180; AAK94780.1; -.
NON TER 361 361
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361 AA; 41163 MW; 6127A3041587BA74 CRC64;
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Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 13.3%; Score 112.5; DB 5; Best Local Similarity , 22.4%; Pred. No. 1.4; Matches 43; Conservative 33; Mismatches 55;
                                                                                                                                                        Query Match 14.0%; Score 119; DB Best Local Similarity 27.0%; Pred. No. 1.1; Matches 47; Conservative 24; Mismatches
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[2]
SEQUENCE FROM N.A.
STRAIN=NF54;
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                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                            01-NOV-1996
01-NOV-1996
                                                                                                                                                                              STRAIN=NF54;
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                                                                                                                                                                                                                                                                         229 PEHKKEENMLSHLYVSSKDKENISKENDDVLDE-KEERAREBEELEERANEEETESSIS 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GWEISGF--EGKKDAG----YVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNP 112
                                                                                                                                                                                                                                                                                                            67 -EGKKDAG-----YVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                257 ETTESEINEDEEGEEEEEEEKEEENDNKKKEQAKEQSNDQKEDMEAQNLISKNQNNN 312
                                                                                                                                                                                                                                                        19 KPHRVTVTIQNGKEMSSTIVSEEDF-----ILPVYKGELEKGYOFD-GWEISGF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 QVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATV-----LDKNNISSKSTTNN 161
                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                             288 EDEEEEEEEEEKKKEEDEKKKEQSKENNDQKKDMEA----QNLISKNQNNN 336
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                                                                                                                                                                                                                                39;
                                                                                                               Li X.R., Yu X.B., Luo S.H., Shan Z.X., Fang J.M., Xu J., "Sequence of Plasmodium falciparum secreted polymorphic antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | || || :: || ::| TKTKEYAQKAKAYEKAKAAYGKANQAVLKAKEASS-----YNYIL-----
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                                                                                                                                                                                                         Length 379;
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                                               Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium reichenowi.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5854;
                                                                                                                                                                                                                                 Indels
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                                                                                                                                                   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF188190; AAF04099.1; -.
SEQUENCE 379 AA; 43316 MW; C152A54E1F9D5F25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  346 AA; 39127 MW; A804B96BDFAFA010 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Okenu D.M.W., Thomas A.W., Conway D.J.,
"Allelic lineages of the merozoite surface protein 3
Plasmodium reichenowi and Plasmodium falciparum.";
Mol. Biochem. Parasitol. 109:185-188 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                 29;
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                                                                                                                                                                                                         DB 5;
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13.3%; Score 112.5; D
Best Local Similarity 23.6%; Pred. No. 1.5;
Matches 41; Conservative 35; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2002 (TrEMBLrel. 22,
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                                    Plasmodium falciparum
              Polymorphic antigen.
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                                                                                       SEQUENCE FROM N.A.
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                                                                                                      STRAIN=FCC1/HN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDILINE=22255705; PubMed=12368864;
MEDILINE=22255705; PubMed=12368864;
Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TTVKEFILLN-KDTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFD
                                                                                                                                                                                                                                                                                          MEDLINE=95198774; PubMed=7891748; Mn J.F., Favaloro J.M., MCCOll D.J., Silva A., Foley M., Kun J.F., Favaloro J.M., Thompson J.K., Marshall V.M., Coppel R.L., Kemp D.J., Anders R.F.; "Molacular variation in a novel polymorphic antigen associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McColl D.J., Anders R.F.;
"Conservation of structural motifs and antigenic diversity in the Plasmodium falciparum merozoite surface protein-3 (MSP-3).";
Mol. Biochem. Parasitol. 90:21-31(1997).
EMBL; L28825; AAC09377.1; -.
SEQUENCE 354 AA; 40119 MW; 3A7256152F48B527 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.1%; Score 111.5; DB 5; Length 354; 22.5%; Pred. No. 1.7;
                                                                                                                                                                 Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBL_TaxID=5843;
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Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Merozoite surface protein 3.
                                                                                               Last annotation update)
                                                                     Last sequence update)
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354 AA
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Mol. Biochem. Parasitol. 68:53-67(1994).
                                                Created)
                                                                                                                                               (isolate NF54)
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  PRELIMINARY;
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                    67 -EGKKDAG-----YVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLN 120
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Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McRadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Vener J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------ESHRKEDLOREEHSOKSDSTKDVTATVLDKNNISSKSTTNN 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McColl D.J., Anders R.F.;
"Conservation of structural motifs and antigenic diversity in the Pasmodium falciparum merozoite surface protein-3 (MSP-3).";
MOI. Biochem. Parasitol. 90:21-31(1997).
EMBL: U08852; AAC47832.1; -.
                                                                                                                                                     45;
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                                                                                                                               DB 5; Length 354;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polymorphic antigen.
Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                         "Genome sequence of the human malaria parasite Plasmodium falciparum.",
                                                                                                                           Query Match 13.1%; Score 111.5; DB 5; Length Best Local Similarity 22.5%; Pred. No. 1.7; Matches 41; Conservative 34; Mismatches 62; Indels
                                                                                                                                                                                            Nature 419:498-511(2002).
EMBL; AE014834; AAN35542.1; -.
SEQUENCE 354 AA; 40119 MW; 3A7256152F48B527 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      379 AA; 43302 MW; ABF9D54E1ED91A24 CRC64;
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(TrEMBLrel. 01, Last sequence update)
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STRAIN-cs12;
MEDLINE-98156743; Pubmed-9497029;
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01-OCT-2002
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Q25706;
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                                                                                                                                                Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burg M.A., Cole G.J.;
"Claustrin, an antiadhesive neural keratan sulfate proteoglycan, is structurally related to MAPIB.";
"Un Neurobiol. 25:1-22(1994).
EMBL; X67778; CAA47988.1;
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"Conservation of structural motifs and antigenic diversity in the Plasmodium falciparum merozoite surface protein-3 (MSP-3).";
MOI. Biochem. Parasitol. 90:21-31(1997).
EMBL; U08851; AAC478111; -.
SEQUENCE 379 AA; 43344 MW; DC7AF106887C8AAO CRC64;
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NCBI_TaxID=5833;
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1038 AA; 117112 MW; 213D694A5B510927 CRC64;
                                                                                                                                                                                                                                                                                                                                                      Cole G.J.; Submitted (OCT-1992) to the EMBL/GenBank/DDBJ databases
                              Last sequence update)
Last annotation update)
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plasmodi... for antigen.
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MEDLINE=94157526; PubMed=7906711;
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01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2002 (TrEMBLrel. 22,
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Gallus gallus (Chicken)
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TISSUE=Brain;
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Last annotation update)

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                                                                                                    -----FD---GWEISGF--EGKKDAG----YVINLSKDTFIKPVFKKIEEKKEEEN
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
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                     DTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQ--
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829 AA; 98816 MW; EF2675E301B2CE93 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                         147 VLDKNNISSKSTTNN 161
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Q812K8
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114 KIILNRKTGNVYSSEIYKL---FHNKNEMFDPITHDKISKEDFIVLQDPLNNKTSYVASH 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5; Length 609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                               Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McColl D.J., Anders R.F.; "Conservation of structural motifs and antigenic diversity Plasmodium falciparum merozoite surface protein-3 (MSP-3)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        CAD51984.1; -. 8CDF86E85FF9A021 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 109.5; D
Pred. No. 4.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           380 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36; Mismatches
                                    307)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95198774; PubMed=7891748;
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Large cyclophilin-like protein.
PFI1490C.
                                    (isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polymorphic antigen precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 23.99
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 419:527-531(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                              Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AL929358; CAL
SECUENCE 609 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                   NCBI_TaxID=36329;
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01-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              026019;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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SEQUENCE
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Best Local (
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                                                                                                                                                                                                                                                                                                                      224
                                                                                                                                                                                                                                                                                                                                                                       63 ISGF--EGKKDAG-----YVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVN 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
Croin A., Davis R., Davis P., Dear P., Dearden F., Dogget J.,
Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
Krights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
A. Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
A. Alandream M.A., Rutter S., Ruttherford K.M., Sanders M., Simmonds M.,
Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
Sulston J.E., Craig A., Newbold C., Barrell B.G;
By Sulston J.E., Craig A., Newbold C., Barrell B.G;
By Level B. S., Mooney B., Charles B., Sulston J.E., Craig A., Newbold C., Barrell B.G;
By Level B. S., School C., Barrell B.G;
By Level B. S., School C., Barrell B.G;
By Level B. S., School C., Barrell B.G;
By L. Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stander B., Stande
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                                                                                                                                                                                                                                                                                                                                                                                                      225 FGGVPEHKKEENMLSHLYVSSKDKENISKENDDVLDE-KEEEREETEEEELEEKNEEET 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 HSQLN------ESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNN 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 TGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVY-----KGELEKGYQFD-GWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pain A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5; Length 3008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    главтослит falciparum (isolate 3D7).
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
VCBI_ТахID=36329;
                                                                                                                                                                         Length 380;
                                                                                                                                                                                                                     67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Devlin K., Baker S., Davies P., Mungal K., Berriman M.,
Devlin N., Bowman S., Churcher C., Quail M., Barrell B.,
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3008 AA; 356023 MW; 60BCBBE15C599B4 CRC64;
                                                                       25 POTENTIAL.
380 POLYMORPHIC ANTIGEN.
43290 MW; 0986CA1393094CA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                         DB 5;
                                                                                                                                                                    12.9%; Score 109; DB 5.
Larity 23.5%; Pred. No. 2.7;
Conservative 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.4%; Pred. No. 26; ive 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 3008 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26;
Mol. Biochem. Parasitol. 90:21-31(1997).
EMBL; L07944; AAC09378.1; -.
Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22255708; PubMed=12368867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AL929351; CAD51431.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 32.4 nes 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
                                                                                              26 3
                                                                                                                                                                                             Best Local Similarity
Matches 42; Conserv
                                                                                                                        SEQUENCE
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                                                                                                                                                                         Query Match
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Q81436;
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Matches
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60 ILGFEDDILYEYCISQLKQSKEKK---DGEEDKYLNAKKLKINLTGFIGNKKSDIFIEEL 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 E-----DVTATVLDKNNISSKSTTN 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37 IVSEEDFILPVY----KGELEKGYQFDGWEISGFEGKK----DAGYVINLSKDTFIKPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          de l'ARFOGLI8.1.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE 99376085; PubMed=10448855;
Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
Churcher C.M., Craig A., Davies R.W, Devlin K., Feltwell T.,
Churcher S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Hornsby
Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S.,
Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,
Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,
Whitehead S., Woodward J.R., Newbold C., Barrell B.G.,
"The complete nucleotide sequence of chromosome 3 of Plassmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61;
                              88 FKKI--EEKKEE-----ENKPIFDVSK-KKDNPQVNHSQLNE----
---STINNPNK 164
                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l protein.
600 AA; 71663 MW; 57EAB42565CAD64C CRC64;
                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Last Sequence update)
1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical 71.7 kDa protein.
PFC0465C, MAL3P4.20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47;
127 DLQREEH----SQKSDSTKDVTATVLDKNNISSK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.8%; Score 108.5; D
29.3%; Pred. No. 4.9;
tive 22; Mismatches
                                                                                                                                                                                                                                         (TrEMBLrel. 08, Created)
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EMBL; AL008970; CAA15610.2;
InterPro; IPR002483; PWI.
Pfam; PF01480; PWI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54; Conservative
                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 NPNK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235 KTNK 238
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STRAIN=7G8;
                                                                                        128
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                                                                                                                                                                                                                                                                 82 RENRYIDIVQNNSNGESK------YVQDLARRIRYDB-EATGSQSAQRIDHPNQK 129
                                                                                                                                                                                                                                                                                                                             : | ::: | : ::: | 130 NVGITEKAFENSPIEETSHRVDDNKRINNQKNFTAAKSSENAVSRVSFGADHKRAEVMGK 189
                                                                                                                                                                                                                                                                                                                                                                                          PMENRDQVRQTESAEKSHRKENVTKSEKPRDQEGVKKTEAKDKNKEKKEKKEKTESINK 248
                                                                                                                                                                                                                                              19 KPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFE-----GKK 70
                                                                                                                                                                                                                                                                                                                                                                        POVNHSQLNE-----SHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=2255705; PubMed=12368864; Milte O., Berriman M., Hyman R.W., Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nene V., Shallom S.J., Sub B., Peterson J., Angiuoli S., Pertea M., Allen J., Selangut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McFadden G.I., Cummings L.M., Subramanian G.M., Mingall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
                                                                                                                                                                                                                   Gaps
                                                                      "Structural analysis of Arabidopsis thaliana chromosome 5. VII.
Sequence features of the regions of 1,013,767 bp covered by sixteen physically assigned R1 and TAC clones.";
DNA Res. 5:297-308(1998)
BMBL; AB015468; BAB10694.1; -.
SEQUENCE 470 AA; 53758 MW; 6D686CE72E35AC54 CRC64;
            STRAIN=COlumbia;
MEDLINE=99081489; PubMed=9872454;
Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99021743; PubMed=9804551; Gardner M.J., Tettelin H., Carucci D.J., Cummings L.M., Aravind L., Koonin E.V., Shallom S., Mason T., Yu K., Fujii C., Pederson J., Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Pertea M., Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O. Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.; "Chromosome 2 sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                 45;
                                                                                                                                                                                    DB 10; Length 470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
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"Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                             71 DAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDN-----
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EMBL, ABO01410; AAC71925.2; -.
Hypothetical protein:
SEQUENCE 951 AA; 112486 MW; AC8D889358A84F4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                 12.7%; Score 107.5; D 20.1%; Pred. No. 4.4;
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                                                                                                                                                                               Query Match
Best Local Similarity 20.1*
Matches 36; Conservative
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EEKNKINKSDLHRONELNLOSGK-----NEQDI-----NKNEKGKO----DISNSNA 170
                                                                                                                                                                                EGKKDAGYVINLSKDTFIKPVFKKIEEKKE------EENKPTFD----VSKKKDNP 112
                                                                                                                                                                                                          60 GWEISGF--EGKKDAG----YVINLSKDTFIKPVFKKIEEKKEBENKPTFDVSKKKDNP 112
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                                                                                         10 KDTGEVSELKPHRVT-VTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEI--SGF 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                               Gaps
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                                                                                                                                                                                                                                                                                                 113 OVNHSQLNESHRKEDLOR-EEHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 164
                                               26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Okenu D.M.N., Thomas A.W., Conway D.J.;
"Allelic lineages of the merozoite surface protein 3 gene in Plasmodium relichenowi and Plasmodium falciparum.";
Mol. Biochem. Parasitol. 109:185-188(2000).
EMBL; AJZ52287; CAB85901.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum (isolate 7G8).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
  DB 5; Length 951;
                                               40; Indels
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Last annotation update)
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12.5%; Score 106; DB 24.3%; Pred. No. 12; ive 35; Mismatches
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24.3%; Pred. No. 4.9;
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01-OCT-2000 (TrEMBLrel. 15, Last seque
01-OCT-2002 (TrEMBLrel. 22, Last annot
Merozoite surface protein 3 (Fragment)
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Query Match
Best Local Similarity 24.34
Matches 42, Conservative
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NCBI_TaxID=57266;
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InterPro; IPR001251; CRAL_TRIO
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01-JUN-1998
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                       Colorant K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Colorant K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Tang C., Toriumi M., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kaniya A., Karlin-Neumann G., Kawai J., Kosema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Sarou M., Saki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; Shinited (MAY-2001) to the EMBL/GenBank/DDBJ databases.

RMBL; AV035162; AAK59666.1; -REMBL/GenBank/DDBJ databases.

RICEPPO; IPRO01071; Retablind/tocTrans.

REMBL; AV035162; AAK59666.1; -REMBL/GenBank/DDBJ Cardabases.

RICEPPO; CREININIDHBP.

REMBL; SMO0180; CREININIDHBP.

REMBL; SMO0180; CREININIDHBP.

REMBL; SMO0180; CREININIDHBP.

REMBL; SMO0180; CREININIDHBP.

REMBL; SMO0180; CREININIDHBP.

REMBL; SMO0180; CREININIDHBP.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
Quach H.L., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
Yu G., Yuan S., Chen H., Cheuk R., Jones T., Kim C.J., Nguyen M.,
Balm G.J., Shinn P., Southwick A., Tripp M.G., Wu T., Davis R.W.,
Ecker J.R., Theologis A.;
"Arabidopsis Open Reading Frame (ORF) Clones.";
Submitted (CGT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC007060; AAD257561; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=cv. Columbia;
Vysocskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Li J., Kremenetskaia I., Luros J., Ngan I., Gonzalez A., Altafi H.,
Araujo R., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.,
Huizar L., Kim C., Palm C., Rowley D., Shinn P., Walker M.,
Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.,
"Arabidopsis thaliana chromosome 1 BAC T518 sequence.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
               Chung M.K.,
Yu G.,
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nes 40; Conservative
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               SEQUENCE FROM N.A.
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61 WEISGFEGKKDAGYVINLSKDTFIKPVFKK---IEEKKEEENKPTFDVSKKKDNPQVNHS 117
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                                                                                                                                                                                                                           Length 540;
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                Pfam; PF00650; CRAL_TRIO; 1.
PFfam; PF03765; CRAL_TRIO; 1.
PRINTS; PR00180; CRETINALDHBP.
SMART; SM00516; SEC14; 1.
PROSITE; PS50191; CRAL_TRIO; 1.
Hypothetical protein.
SEQUENCE 540 AA; 61189 MW; 0C2590D518ACFBS8 CRC64;
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Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 QLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISS 155
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                      12.3%; Score 104; DB 10;
25.3%; Pred. No. 9.2;
ative 28; Mismatches 64;
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23.8%; Pred. No. 5.7;
tive 25; Mismatches
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PR001071; RetBind/tocTrans
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Query Match
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Q9PPL5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGFEGKKD-----AGYVINLSKDTFIKPVFKKIEEKKEEENKP--TFDVSK-KKD 110
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A MEDLINE=22255708; PubMed=12368867;
A MIJI N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
A Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
A Chillingworth T., Christodoulou Z., Clark E., Clark R., Corton C.,
Cronin A., Davies R., Davis P., Dearten F., Doggett J.,
A Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
A Harper D., Hauers H., Hornsby T., Holroyd S., Horrocks P.,
A Harper D., Hauers H., Hornsby T., Money P., Moule S., Murphy L.,
A Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
A Line A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,
Oliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch E.,
A Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
Seeger K., Sharp S., Smith R., Squares S., Stevens K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 ILNKDTGEVSELK---PHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEI 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakamura Y., "Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the regions of 4,251,695 bp covered by ninety Pl,
                                                                                                                                                 Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots, Rosidae;
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 NPQVNHSQLNESHRKEDLQ----REEHSQKSDSTKDVTATVLDKNNISSKSTTNNPN
                                                                                                                                                                                                                                                                                                                               STRAIN=Columbia;
Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.1%; Score 103; DB 10; Length 2081; 26.0%; Pred. No. 47; 1. 17; Indels 30. 13ve 29; Mismatches 72; Indels 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AP002057; BAB03174.1; -. SEQUENCE 2081 AA; 232851 MW; D3603E1F85EFFF29 CRC64;
                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 12, Last annotation update)
Genomic DNA, chromosome 3, BAC clone: T19NB.
Arabidopsis thaliana (Mouse-ear cress).
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PRT; 2081 AA.
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MEDLINE=20363099; PubMed=10907853;
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PRELIMINARY;
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DNA Res. 7:217-221(2000)
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92 ESKKKATSRKKIKKINFKIKKNNLİEKVIKK---KAFLEAKNTVFPSLKKYNTVPHISNN 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 EEYESKHTKKSNIYLKED---LINVKLEEKQSLAKKIFSKWKERRKEENKKTKKNFLFSR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 KKDNP----QVNHSQLNESHRKEDLQREEHSQKSDSTKDV--TATVLDKNNISSK--STT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 EGKKDA-----GYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDN--PQV--N 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                             38 KEKEKTQETKKHD-----ENNKSNNNVVNSSENF-MKIYKNILKQNYHVEKFKKQNENIE
                                                                                                                                                                                                                                                                                                                                               10 KDTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISG---F
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                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20150912; PubMed=10688204; Retley J.M., Churcher C., Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C., Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S., Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W., Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M., Whitchead S., Barrell B.G.; Whitchead S., Barrell B.G.; The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervariable sequences.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 H--SQLNESHRKED----LQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPN 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 HNISQNDHNKKKQDKNIKLIEKSNKDDNN-----NINNKKNNNQKCDTKNLN 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Sulston J.E., Tivey A., Unwin L., Whitehead S., Woodward J., Sulston J.E., Craig A., Newbold C., Barrell B.G; "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13."; Nature 419:827-511(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31;
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                                                                                                                                                                                                                                             DB 5; Length 238;
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                                                                                                                                EMBL; AL929356; CAD51839.1; -.
Hypothetical protein.
SEQUENCE 238 Aa; 28481 MW; DA175A2B5A109B49 CRC64;
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Last annotation update)
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Pred. No. 7.6;
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; Pred. No. 4.8;
26; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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EMBL; AL139076; CAB72966.1; -.
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28.0%;
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25.0%;
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SEQUENCE 312 AA;
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78 EDLOTPLSESRFSK--VFDGWVDEHRDEHDDGPSGEALDDHDEHDDHEDEDEE 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 EDFILPVYKGELEKGYQFDGW-----EISGFEGKKDAGYVI-----NLSKDTFIK 85
                                                                     Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith B., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20564328; PubMed=10956665;
Dinchuk J.E., Henderson N.L., Burn T.C., Huber R., Ho S.P., Link J.,
O'Neil K.T., Focht R.J., Scully M.S., Hollis J.M., Hollis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Aspartyl beta -Hydroxylase (Asph) and an Evolutionarily Conserved Isoform of Asph Missing the Catalytic Domain Share Exons with Junctin.";
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MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endoptera; Arthropoda; Hexapoda; Insecta; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5; Length 382;
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"Sequencing of Drosophila melanogaster genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                           FlyBase;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biol. Chem. 275:39543-39554(2000).

EMBL; AE003808; AAF58063.2; --

EMBL; AF289494; AAG40807.1; -.

Flybase; Fsgm0034075; Asph.

SEQUENCE 382 AA; 43287 MW; 60E5C03AEBFC6E8B CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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24.5%; Pred. No. 9.5;
tive 29; Mismatches
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ASPH OR CG8421 OR CG18658.
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Flybase; FBgn0034075; Asph. SEQUENCE 556 AA; 63144 MW; B420980CBD6C357A CRC64;

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RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Brauton G.G., Wortman D.R., Yandell M.D., Zhang O., Chen L.X., Bratton G.G., Wortman D.R., Yandell M.D., Zhang O., Chen L.X., Brandon R.C., Rakter E.G., Helt G., Champe M., Pfeiffer B.D., And H.-J., Andrews-Pfannacch C., Baldwin D., Ballew R.M., Basu A., An H.-J., Andrews-Pfannacch C., Baldwin D., Ballew R.M., Basu A., Baxwalale J., Bayraktarcglu L., Badalwin D., Ballew R.W., Basu A., Baxwalale J., Bayraktarcglu L., Badalwin D., Ballew R.W., Basu A., Baxwalale J., Bayraktarcglu L., Badalwin D., Ballew R.W., Bacchan M.R., Bouck J., Broketein P., Brotchan W., Bouck J., Broketein P., Brotchan J., Bandler H., Cadieu E., Center A., Chandra I., R. Borkey S., Dahlke C., Davenport L.B., Davies P., R.A. Deng Z., Mays A.D., Dew I., Dietz S.W., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., R.A. Doup L.S., Downes M., Deng T., Gary N.S., Gelbart W.M., Glasser K., Forsler C., Gabriellan A.E., Gary N.S., Gelbart W.M., Glasser K., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Houston K.A., Howland T.J., Wall, M.-H., Ibeewam C., Alalli M., Kalush F., Karpen G.H., Kez Z., Kenison J.A., Hostin D., Houston K.A., Howland T.J., Wall, M.-H., Ibeewam C., Alalli M., Kalush F., Karpen G.H., Kez Z., Kenison J.A., Markluo G., Milshina N.V., Mobarry C., Mortis J., Moshrefi A., Morthorson D., Rak Mount S.M., Mol M., Whoshers R.D., Purl Y., Purl Y., Recebe M.G., Milshina N.V., Nobarry C., Mortis J., Morth P., Smith T., Shine B.C., Siden-Kiamos I., Simpson M., Stupski M.P., Smith T., Shine B.C., Siden-Kiamos I., Simpson M., Stupski M.P., Smith H.O., R. Shine B.C., Siden-Kiamos I., Simpson M., Stupski M.P., Smith H.O., R. Shine B. Shoriska R., Wenselenger T., Worler S., Changer S., Changer S., Changer S., Changer S., Changer S., Changer S., Changer S., Changer S., Changer S., Changer S., Changer S., Changer S., Changer S., Changer S., Changer S., Changer S., Changer S., Changer S., Changer S., Changer S., Changer S., Changer S., Changer S., Chan
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A Evans C.A., Gocayre J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Parfan D.,

Rerriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

I Degwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,

Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

Supmitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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S.E., Gibbs R.A., Rubin G.M., Venter C.J.; to the EMBL/GenBank/DDBJ databases.

Adams M.D., Celniker Submitted (MAR-2000)

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AE003808; AAF58064.2; -.

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86 PVFKKIEEKKEEENKPT----FDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDS 139
                                                                                                                                                                                                        MEDLINE=20196006; PubMed=10731132; Adams C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holt R.A., Eshburner M., Henderson S.N., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandell M.D., Zhang Q., Chen L.X., Abbardell M.D., Zhang Q., Chen L.X., Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Besaley E.M., Ballew R.M., Bauson P., Helt G., Nelson C.R., Miklos G.L.G., Ballew R.M., Borchan M.R., Bouck J. Brokatein P., Brottier P., Borkova D., Botchan M.R., Bouck J., Brokatein P., Brottier P., Borkova D., Botchan M.R., Bouck J., Davhadari D., Bolshakov S., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Danke C., Davenport L.B., Davies P., Danne P., Herris P., Davies P., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Horris N.L., Harrey D., Heiman T.J., Wei M., Glasser K., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K., Alalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Hostin M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Lei Y., Mattei B.E., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Non Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
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                                                                                         41 EDFILPVYKGELEKGYQFDGW-----EISGFECKKDAGYVI------NLSKDTFIK
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MEDLINE=20564328; PubMed=10956665;
Dinchuk J.B., Henderson N.L., Burn T.C., Huber R., Ho S.P., Link J.,
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
    DB 5; Length 556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                Indels
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Aspartyl beta-hydroxylase variant 1 (CG8421-PA).
                                                                                                                                                                                                                                                                                                                                                                                                                              785 AA.
12.0%; Score 101.5;
24.5%; Pred. No. 14;
cive 29; Mismatches
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194 EGTVEATVEATTEAT 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASPH OR CG8421 OR CG18658.
                                                  34; Conservative
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                       Best Local Similarity
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RESULT 31

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78 EDLDTPLSESRFSK--VFDGWVDEHRDEHDGHDVQEPSGEALDDHDEHDDHDDHEDEDEE 135
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                                                                                                                                                                                                                                                                                                                                                       Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
A Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
A Carlson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
A Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
A pacleb J., Paragas V., Park S., Prii H. S., Pfeiffer B.,
A phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K. Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 12.0%; Score 101.5; DB 5; Length 785; Best Local Similarity 24.5%; Pred. No. 21; Matches 34; Conservative 29; Mismatches 51; Indels 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to the EMBL/GenBank/DDBJ databases
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InterPro; IPR001440; TR.
InterPro; IPR006025; Zn WTpeptdse.
PROSITE; PS00142; ZINC PROTEASE; 1.
SEQUENCE 785 As; 89843 MW; 30A8DFCD6836F7F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 TKDVTATVLDKNNISSKST 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF289493; AAG40806.1; -. EMBL; AE003808; AAM70947.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 F-----LQREEHSQK--- 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=2255705; PubMed=12368864;
Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
WcRaden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 FILNKDTGEVSEL------KPHRVTVTIQNGKEMSSTIVSEEDFILPVY-----KG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               619 SLAINMSIDHY----FSHMKDNLRVICEPGRYMVAASSTLAVKIIGKR-----RPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 -----SDST-----SDST------SDST-NNIS-SKSTTNNPN 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     726 GNIMNDLIITSTNDSTNKKNDHSSSQVIQNVSCTIRDKEGDNIKINTHTINNPN 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Eukaryotic translation initiation factor 3 subunit 10, putative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89;
                                                                                                                                                                                                                                                                Birkholtz L., Joubert F., Neitz A.W.H., Louw A.I.;
"Molecular characterisation of Plasmodium falciparum ornithine
decarboxylase CDNA obtained by RACE.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF139900; AAF14518.1;
HSSP; P07805; IF3T.
InterPror; IFR00183; Decarbxylse2.
Pfam; PF02784; Orn Arg dec. N; 1.
Pfam; PF02784; Orn DAP_Arg_dec.; 1.
PRINTS; PR01179; ODADCREXLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
12.0%; Score 101.5; DB 5; Length 948;
Best Local Similarity 21.8%; Pred. No. 26;
Matches 51; Conservative 31; Mismatches 63; Indels 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI TaxID=36329;
                                                                                                                                                  Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                948 AA; 110350 MW; 43F103DB83F12835 CRC64;
                                                      Created)
Last sequence update)
Last annotation update)
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                                                      01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                  PRELIMINARY;
                                                                                                                Ornithine decarboxylase.
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                    STRAIN=FCUP1/RSA;
                                                                                                                                                                                        NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                      090406
Q9U4U6
ID Q9U4U6
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458 VGFTKQKEVISISTKKRPVPLLHYIYVYDSVXLVMDEKNKFYSSAFKEIYVKIREKQEAN 517
                                                                          NKPTFDVSKKKDNPQVNHSQLNESH-RKEDLQREEHSQKSDSTKDVTATVLDKNNISSKS 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 VEAKDQNGKQGTDGKKKGGRGSHRVKNKSKGTFLGSV------KETFDAMKNST 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 NPQVNHSQLNESHRKEDLQREEHSQKSDST-----KDVTATVLD-KNNISSKSTTNNP 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 KEFVRHKEKIKQAKEDV-KENLKKFSDSVKSTFRHFKDTTKNIFDEKGNKRFNATKEAA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 GELQQLSGSQL----HGKSDSPNVYTEKKEIAILRERLTELERKLTFEQQRSDLWERLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 GEVSBLKPHRVTVTIQNGKEMSSTIVSE--EDFILPVYKGELEKGYQF----DGWE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48;
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Bacteria, Firmicutes, Mollicutes, Mycoplasmataceae, Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=98043401; PubMed=9383053;
Edwards M.C., Liegeois N., Horecka J., DePinho R.A., Sprague (
Edwards M.C., Liegeois N., Horecka J., DePinho R.A., Sprague (
Tyers M., Elledge S.J.;
"Human CPR (cell cycle progression restoration) genes impart i
phenotype on yeast cells.";
Genetics 147:1063-1076(1997).
EMBL; AF011794; ABB63314.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.8%; Score 100; DB 4; Length 375; 28.0%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44320 MW; OC261BF68AAEF7AD CRC64;
                                                                                                             01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell cycle progression restoration 8 protein.
CPR8.
                                                                                                                                                                                                                                                                                                                                                                   375 A.A.
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18,
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01-OCT-2001 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF02987; LEA; 1
SEQUENCE 375 AA; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens (Human).
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                                                                                                                                                                                                                                     572
                                                                                                                                                                                   158 TTNN 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NK 164
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01-OCT-2002 (
LIPOPROTEIN.
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Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D., Mungall K., Bownan S., Atkin R., Baker S., Barron A., Brooks K., Buckee C.O., Burrows C., Cherwach I., Chillingworth C., Cheristodoulou Z., Clark L., Clark R., Corton C., Croin A., Davis R., Dear P., Dearden F., Deogett J., Harper D., Hauser H., Hornsby T., Holroyd S., Harrocks P., Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P., Minghtes A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N., Line A., Maddison M., Mclean J., Monney P., Moule S., Murphy L., Aline R., Ormond D., Price C., Quail M.A., Rabbinowitsch E., Sandra M.A., Ruter S., Smith R., Squares S., Stevens K., Staylor K., Tivey A., Unwin L., Whitehead S., Woodward J., Stevens K., Sulston J.B., Woodward J., Seeger K., Sharp S., Smith R., Squares S., Moodward J., Seeger K., Sharp S., Smith R., Squares S., Woodward J., Stevens K., Sulston J.B., Sharp S., Santh R., Squares S., Woodward J., Seeger K., Sharp S., Mathin L., Whitehead S., Woodward J., Stevens K., Sulston J.B., Smith R., Squares S., Barrell B.G., Santh R., Squares S., Stevens K., Sulston J.B., Sharp S., Santh R., Squares S., Stevens K., Sulston J.B., Sharp S., Santh R., Squares S., Stevens K., Sulston J.B., Sharp S., Santh R., Squares S., Stevens K., Squares S., Stevens K., Squares S., Stevens K., Squares S., Stevens K., Squares S., Stevens K., Squares S., Stevens K., Squares S., Stevens K., Squares S., Stevens K., Squares S., Stevens K., Squares S., Stevens K., Squares S., Stevens K., Squares S., Stevens K., Squares S., Stevens K., Squares S., Stevens K., Squares S., Stevens K., Squares S., Stevens K., Squares S., Stevens K., Squares S., Stevens K., Squares S., Stevens K., Squares S., Stevens K., Squares S., Stevens K., Squares S., Stevens K., Squares S., Stevens K., Squares S., Stevens K., Squares S., Squares S., Squares S., Squares S., Squares S., Squares S., Squares S., Squares S., Squares S., Squares S., Squares S., Squares S., Squares S., Squares S., Squares S., Squares S.
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                                                                                                                                                                                                                                                                                                                                                                                                                      ----DGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEK-----KEEENKPTFDVSK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----ESHRKEDLQR------EEHSQKSDSTKDVTAT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 FILNKDTGEVSE----LKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGW 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----EISGFEGKK-----DAGYVINLSKDTFIKPVFK----KIEEKKEEE 98
                                                                                                                                                                                                                                                                                                                3 VKEFILNKDIGEVSELKPHRVTVTIQNGKE--MSSTIVSEEDFILPVYKGELEKGYQF--
                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1373;
                                                                                                                                                                                                             Length 1377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata, Apicomplexa; Haemosporida, Plasmodium.
NCBI_TaxID=36329;
     Fraser C.M., Barrell B.; "Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                           587CF2E3F2C8FBE9 CRC64;
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I-MAR-2003 (TrEMBLrel. 23, Last sequence update)
I-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                             62;
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                                                                                                                                                                                                             DB 5;
                                                                                                                                                                                                        Query Match
12.0%; Score 101.5; I
Best Local Similarity 22.3%; Pred. No. 39;
Matches 43; Conservative 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicase with Zn-finger motif, putative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL929356; CAD51782.1; -.
                                                                                                        EMBL; AE014846; AAN36214.1; -.
Initiation factor.
SEQUENCE 1377 AA; 166059 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 KKDNPQVNHSQLN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 I---KKLCSTNTT 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 VLDKNNISSKSTT 159
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les 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                Nature 419:498-511 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                          falciparum."
                                                                                                                                                                                                                                                                                                                                                                                                                      59
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Matches
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STRAIN-BRISTOL N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jones S.J.M.;
                                                                Q8IDA0;
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thomas K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [2]
REVISIONS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101
                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                GC-BETA
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                                                   OBIDAO
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                       RESULT 37
Q8IDA0
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                                                                                                                                                                                                                                                      69 INSETKEIVKKE-----TILN------LSEDNIIFSLLNIENNAKFQLDEF----- 108
                                                                                                                                                                                                                                                                                 68 GKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKD----NPQVNHSQLNES- 122
                                                                                                                                                                                                                                                                                               109 -----VSKDEKFRIKFQEINFSQTEQ-KITDNISSKEDEKNKDPKDNENSNNNSS 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 SGFEGKKDAGYV--INLSKOTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNE 121
                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22255705; PubMed=12368864;
Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M.-S., Nene V., Shallon S.J., Suh B., Peterson J., Angluoli S.,
Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
                                                                                                                                                                                                                             8 LNKDTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       568 SFLSGSNDSYRIDRIYLSPDNYFSYSSNRNRNNINDENVEVIQVEETRSDYNESHDETNE
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                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 SHRKEDLOREEHSOKS------DSTKDVTATVLDKN-NISSKSTTNNPNK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis.";
Nucleic Acids Res. 29:2145-2153(2001).
EMBL, AL445564; CAC13338.1; -
MypuList; MYPU 4650; -
Complete proceome.
SEQUENCE 622 AA; 73762 MW; 42BD88930861960D CRC64;
                          Galisson
                                                                                                                                                                                                  38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53; Indels 14;
                       Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galis
Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
Blanchard A.;
                                                                                                                                                                        DB 16; Length 622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 5; Length 1130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                      123 -HRKEDLQREEHSQKSDSTKDVTATVLDKN-NISSKSTTNNPNK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                     DQKNDELQKNNSDKLNDNVQDEKANKENSNSNDSKEKNDENTNK 201
                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE014829; AAN35244.1; -.
Hypothetical protein.
SEQUENCE 1130 AA; 131697 MW; FEGAAFE08C4CCDB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                 31; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 11.8%; Score 100; DB Local Similarity 26.1%; Pred. No. 40; nes 30; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  $
                                                                                                                                                                      Query Match 11.8%; Score 100; Di
Best Local Similarity 24.4%; Pred. No. 21;
Matches 40; Conservative 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1130
           MEDLINE=21267165; PubMed=11353084;
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 419:498-511 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=36329;
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                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 36
Q81JZ4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---DVSKKKDNPQVNHSQL-----NESHRK---EDLQR 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Harris B., Lennard N., Clark L., Line A., Barron A., Corton C.,
Harris B., Lennard N., Hall N., Atkin R., Chillingworth C., Doggett J.,
Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AL844509; CAD52725.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 KEFILINKDIGEVSELKPHRVTVTIQNG-----KEMSSTIVSEEDFILPVYKGELEKGYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1969 KKF--KRNTSYVLESPLHLIGDIVDNNIKRKKKKKEIKTIVSDDMFTSPVNIKEYNYNEO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 FDGWEISG---FEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENK--------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1999 (TrEMBLrel. 09, Created)
01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical glycine-rich 37.0 kDa protein E02A10.2 in chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58;
                                                                                                                                                                                                                        Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 3127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3127 AA; 370597 MW; F0375C72B9007560 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
                                                            01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Guanylyl cyclase (EC 4.6.1.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2145 NEYPNYTSSSKDGVSYNFLSDSLFSSDNEYSSDNE 2179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 EEHSQKSDSTKD-VTATVLDKNNISSKSTTNNPNK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 100; DB 5;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WormPep; E02A10.2; CE09116.
InterPro; IPR002952; Eggshell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 11.8%;
Best Local Similarity 24.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; 281053; CAB02877.1;
HSSP; P10968; 2CWG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
PRELIMINARY;
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3812 TNESEVIKTEDKNIMNDVPVTQEEFDIKPEVVESNLIESNNNNNNKKSKNMNIVKNRSM 3871
                             44 ILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTF 103
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MEDLINE-22255708; PubMed=12368867;

MEDLINE-22255708; PubMed=12368867;

Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,

Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,

Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,

Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,

Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,

Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,

Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,

Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,

A. Maddison M., McLean J., Mooney P., Moule S., Wurphy L.,

Oliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch E.,

A Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,

Seeger K., Sharp S., Smith R., Squares S., Stevens K.,

A Sulston J. E., Craig A., Newbold C., Barrell B.G.

T. Wilston J. E., Craig A., Newbold C., Barrell B.G.

T. Willer D. J. Spandall J. H., Newbold C., Barrell B.G.
                                                                                                                                                                                                                     290 EEEPKKEEEKKEEVEKKE---EDEKKDE------EP--KKEEEKKEEEQKE--E 330
                                                                                                                                                                                                                                                              45 LPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFD 104
                                                                                                                                                                                                    2 TVKEFILINKD------TGEVSELKPHRVTVTIQ--NGKEMSSTIVSEEDFI 44
                                                                                                                                                                      43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Devlin K., Baker S.; Davies P., Mungal K., Berriman M., Pain A., Hall N., Bowman S., Churcher C., Quail M., Barrell B.; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                 POTENTIAL.
HYPOTHETICAL GLYCINE-RICH PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 11.7%; Score 99.5; DB 5; Length 4524; Best Local Similarity 24.3%; Pred. No. 2e+02; Matches 44; Conservative 27; Mismatches 81; Indels 29
                                                                                                                                     11.7%; Score 99.5; DB 5; Length 385; 27.7%; Pred. No. 13; ive 26; Mismatches 51; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum (isolate 3D7).
Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
                                                                                                                                                                                                                                                                                                                          105 VSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDK 150
                                                                                                                                                                                                                                                                                                                                          331 VEKKEE----EEKKDEEPKKEEEKKEEBEKKEDEVEEKSEKVEEK 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               525287 MW; 542206173C29567A CRC64;
                                                                                                          32AB25AE9B5073FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                  Hypothetical protein; Signal; Transmembrane.
SIGNAL
1 17 POTENTIAL.
                                                                                POTENTIAL.
                                                              E02A10.2
                                                                                              GLY-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 419:527-531(2002).
EMBL; AL929354; CAD51629.1; -.
                                                                                                          36963 MW;
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    PRINTS; PR01228; EGGSHELL.
                                                                                                                                    Query Match
Best Local Similarity 27.77
Matches 46; Conservative
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                                                                            104 DVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPN 163
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.7%; Score 99; DB 5; Length 211; 29.4%; Pred. No. 7.6;
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STRAIN=Bristol N2;
Maggi L., Le T.;
"The sequence of C. elegans cosmid T23B3.";
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; U88309; AAB42334.1; -.
WormPep; T23B3.5; CE14016.
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SEQUENCE 211 AA; 23955 MW; 11B16164AB7E5928 CRC64;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                      211 AA
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STRAIN-Bristol N2;
MEDLINE-99069613; Pubmed-9851916;
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SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Waterston R.;
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45	44	43	42	41	40	39	38	37	36	35	34	u u	32	31	30
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508	508	487	433	700	2401	1332	670	443	1087	253	650	1875	1202	688	1888
2	N	N	2	N	N	N	N	N	N	N	N	N	μ	N	N
C72074	B81594	T45982	A89951	867610	T28676	S41552	T28391	S66040	T30330	T32879	D90093	S38173	S05362	A47705	T39009
hypothetical prote	hypothetical prote	hypothetical prote	trigger factor (im	probable membrane	rhoptry protein -	probable transcrip	ORF MSV230 hypothe	serine-type D-Ala-	gelsolin-related p	hypothetical prote	heat shock protein	myosin-like protei	probable DNA-direc	triacylglycerol li	hypothetical prote

ALIGNMENTS

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on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.B. Science 293, 498-506, 2001

A; Authors: Loftus

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus A;Reference number: A95000; MUID:21357209; PMID:11463916 A;Accession: F95074

B.A.; Morrison, pneumoniae.

RESULT 1

R95074

R95074

Serine proteinase, subtilase family [imported] - Streptococcus pneumoniae (strain TIGR4)

C;Species: Streptococcus pneumoniae

C;Species: Streptococcus pneumoniae

C;Species: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001

C;Accession: F95074

R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid

R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, R.; Radune, D.; Holtzapple,

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RESULT 2
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-2140 <KUR>
A;Cross-references: GB:AE005672; PIDN:AAK74791.1; PID:g14972117; GSPDB:GN00164; TIGR:SP4
A;Experimental source: strain TIGR4
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                                                             ESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 2106
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D; Mismatches 0
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R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, e. R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, Y. P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.l A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6. A;Reference number: A97872; MUID:21429245; PMID:11544234

R.H.;

Jaskunas,

S.R.;

S.; DeHoff, , P.; McAhre

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McAhren,

metalloproteinase (EC 3.4.21.-) A [imported] - Streptococcus pneumoniae (st C;Species: Streptococcus pneumoniae C;Species: Streptococcus pneumoniae C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001 C;Accession: A97942

Streptococcus pneumoniae (strain

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A;Molecule type: mRNA
A;Residues: 1-1038 <BURI>
A;Cross-references: EMBL:X67778; NID:g406318; PIDN:CAA47988.1; PID:g406319
A;Cross-references: EMBL:X67778; NID:g406318; PIDN:CAA47988.1; PID:g406319
A;Cross-references: EMBL:X67778; NID:g406318; PIDN:CAA47988.1; PID:g406319
A;Cross-references: EMBL:X67778; NID:g406318; PIDN:CAA47988.1; PID:g406319
A;Accession: PC4334
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A;Status: preliminary
A;Molecule type: DNA
A;Residuss: 1-214 < KUR>
A;Cross-references: GB:AE007317; PIDN:AAK99365.1;
C;Genetics:
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N;Alternate names: keratan sulfate proteoglycan
C;Species: Gallus gallus (chicken)
C;Date: 07-Jul-1997 #sequence revision 12-Sep-1997 #text_change 21-Jul-2000
C;Accession: JC5497; PC4334; S37561
R;Burg, M.A.; Cole, G.J.
J. Neurobiol. 25, 1-22, 1994
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C;Keywords: hydrolase; serine proteinase
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                                                                                                                  VKKEVKAKPEEKKDEKEKPKKEVSKKEEKPLI--
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Pred. No. 1.8;
8; Mismatches 58
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Pred. No. 1.1e-53;
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RESULT 4

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hypothetical protein PFB0680w - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Stecies: Plasmodium falciparum C;Oate: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000 C;Accession: B71609
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; K.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falce, R; Reference number: A71600; MUID:99021743; PMID:9804551
A;Accession: B71609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Lawson, D.; Bowman, S.; Barrell,
submitted to the EMBL Data Library,
A;Reference number: Z18937
A;Accession: T18467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein C0465c - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan C;Accession: T18467 R;Lawson, D.; Bowman, S.; Barrell, B.
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A; Residues: 1-665 <GAR>
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A; Introns: 84/1;
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C;Genetics:
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A; Residues: 1-558 <LAW>
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                                                                                                                                                                                                          42;
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QVNHSQLNESHRKEDLQR-EEHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 164
                                                        ENKKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KINK
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                                                                                                                                EEKNKINKSDLHRONELNLOSGK-----NEQDI-----NKNEKGKO----DISNSNA 169
                                                                                                                                                                   KDTGEVSELKPHRVT-VTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEI--SGF 66
                                                                                             EGKKDAGYVINLSKDTFIKPVFKKIEBKKE----
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29.3%;
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                                                        VKEGVKELEEKKKEEKISDDHKVEENKKSDDHKVEENKKSDDH
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Pred. No. 2
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Pred. No. 1.1;
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                                                                                           EENKPTFD----VSKKKDNP 112
                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum
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R,Rieben Jr., W.K.; Gonzales, C.M.; Gonzales, S.T.; Pilkington, K.J.; Kiyosawa, Genetics 148, 1117-1125, 1998
A,Title: Dictyostelium discoideum nuclear plasmid Ddp5 is a chimera related to 1
A;Reference number: Z14684; MUID:98198836; PMID:9539429
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Nature 408, 816-620, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, T. Skano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Tile: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein G5 - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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                                                                                                                                                                                                                               A; Introns: 85/1
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C;Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                                                                                                                                                           A;Residues: 1-325 <RIE>
                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                        A; Accession: T18283
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Best Local
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                                                                                                                                            43;
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                                                                                                     HRVTVTIQNGKEMSSTIVSEEDFILPVYK-GEL--EKGYQFDGWEISGFEGK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WEISGFEGKKDAGYVINLSKDTFIKPVFKK---IEEKKEBENKPTFDVSKKKDNPQVNHS
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                                                              HRTITSIKN--RFSVKKIGDEEKLFRISKNGELIVLNELEFDNFHIK--EGKHLRKSKMF
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                       ---KDAGYV-----INLSKDTFIKPV-----FKK--
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                                                                                                                                                                                                                                                                      EMBL: U00796; NID: g2702254; PID: g2702258; PIDN: AAC18634
                                                                                                                                                                12.2%;
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                                                                                                                                                                  Score 103.5;
Pred. No. 1.
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Query Match
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A; PIOLECCE A. A; Residues: 1-622 < KUR>
A; Cross-references: GB: AL445566; PID: g14089879;
A; Cross-references: strain UAB CTIP
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                                                                                                                                                                                                                                           A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm. A;Reference number: A99512; MUID:21267165; PMID:11353084 A;Accession: A90570
                                                                                                                                                                                                                                                                                                                                                                C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001
C;Accession: A90570
                                             A; Gene: MYPU 4650
A; Genetic code: S
                                                                                                                                                                                                                                                                                                                                         R; Chambaud,
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                                                                                                                                                                                                                                                                                                                  I.; Heilig, R.; Ferris, S.; Barbe, ds Res. 29, 2145-2153, 2001
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DΒ
                                                                                                                                                                                                                                                                                                                                         V.; Samson, D.; Galisson, F.; Moszer,
                                                                                                                                               PIDN:CAC13638.1; GSPDB:GN00153
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Whitehead,
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A;Description: The sequence o
A;Reference number: Z20109
A;Accession: T25911
A;Status: preliminary; transl
A;Molecule type: DNA
A;Residues: 1-211 <MAG>
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A; Map posit
A; Introns:
                                                                                                                                                                                                                           hypothetical protein T23B3.5 - Caenorhabditis elegans C;Specites: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T25911 R;Maggi, L.; Le, T.
                                                                                                                                                                            R;Maggi, L; Le, T.
submitted to the EMBL Data Library, Februa
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A;Experimental source:
C;Genetics:
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A; Residues: 1-385 <WIL>
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A;Status: prelimina
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A;Reference number: Z19271
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   A;Map
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Best Local S
Matches 46
                   Gene: CESP:T23B3.5
                                       Genetics:
                                                      Cross-references: EMBL:U88309; PIDN:AAB42334.1; GSPDB:GN00019; CESP:T23B3;Experimental source: strain Bristol N2; clone T23B3
                                                                                                                             Status: preliminary; translated
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27.7%;
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; Pred. No. 4.1;
26; Mismatches
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1; Mismatches
                                                                                                                                 from GB/EMBL/DDBJ
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A; Experimental : C; Genetics: A; Gene: BH4017
                                                                                                                                                                                                                                                                   hypothetical protein BH4017 [imported] - Bacillus halodurans C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_chan C;Accession: A84152
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A;Reference number: A72200;
A;Accession: B72291
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein - Thermotoga maritima (strain c;Species: Thermotoga maritima (strain c;Species: Thermotoga maritima (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (richarder) (rich
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                                                                                                                                                                                                                                                             A;Status: preliminary
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C,Genetics:
A,Gene: TM1142
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                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-614 <STO>
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A; Residues: 1-219 < ARN>
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Best Local 9
                                                                                                                                                Cross-references: GB:AP001520; GB:BA000004; NID:g10176401; Experimental source: strain C-125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEPLIIEIF-KEDADFVLEKDENAVKVDTVPNEVRRDRIYVTDSPDVAKTLQEK 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEVFPKEDFQEI--LIPNFVFVELYATDEKTTLFAKE-----VLGEESVSYRDLFAGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKKDDKKDEKKDEKKDEKKEKSKKSKKSKKSKKSKKSK 170
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r: A72200; MUID:99287316; F
                                                                                                                                          strain
                                                                                                                                                                                                                                                                                                                                                                                                           K.; Takaki, Y.; Maeno,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.M.;
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11.5%;
27.3%;
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Pred. No.
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Pred. No. 2.3;
7; Mismatches 5
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   97.5;
No. 9.
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PMID:10360571
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                              <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                        Sasaki,
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                                                                                                                                                                                                                                                                                                                                                                                                           R.; Masui, N.; Fuji, F.;
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                                 614;
                                                                                                                                                                            PIDN:BAB07736.1;
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                                                                                                                                                                                                                                                                                                                                                     Bacillus
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Query Match Best Local Similarity

Score Pred.

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hypothetical protein T28D5.30 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 28-Jul-2000 C;Accession: T14188
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S46817
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A; Reference number: Z17931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, June 1994 A;Description: The sequence of S. cerevisiae A;Reference number: $46795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein YHR080c - yeast (Saccharomyces C;Species: Saccharomyces cerevisiae C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #
                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-988 <BEV>
                                                                                                                                                                                                                                                                                                                         R; Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 8R
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A; Residues: 1-1345 < FAV>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: S46817
                                                                                  A; Map position: 4
A; Introns: 162/3; 201/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: SGD: S0001122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:U10556; NID:g500825; PIDN:AAB68895.1; PID:g500838; MIPS:YHR080c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S46817
                                                                                                                                                                          A; Experimental source:
                                                                                                                                                                                                                                                               Accession: T14188;
                                                                                                                               Gene: ATSP:T28D5.30
                                                                                                                                                                                            Cross-references: EMBL:AL109819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Keywords: transmembrane protein
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KGELEKGYQFDGWEISGFEGKK-DAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKVIGIVDLGRKYHKGKEDLERRLSKSQIE 512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEPKPE--TYTLQTAIQM-TPIVNEYSPQTREEFL--
                                                                3; 201/3; 416/3; 438/3; 460/3; 482/3; 504/3; 519/3; 534/3; 559/3; 579/3; Arabidopsis thaliana hypothetical protein T21C14.40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164
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                                                                                                                                                                            cultivar
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                                                                                                                                                                                                                                                                                                     Sequence Database,
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  11.4%;
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                                                                                                                                                                          Columbia; BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GKIEEEKLQDKYNNYTFDFFKKEVVNVQSPIKSTSAL
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Pred. No. 24;
  Score 97;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -QKSSESRKSDDNKDILTHILDFVQNNFSSEIFMNKLLSP
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    DB 2;
18;
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                    Length 988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Arabidopsis thaliana (myll) C;Date: 23-Apr-1999 #text_change 23-Jul-1777 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1777 C;Accession: T05612 R;Bevan, M; Wedler, H.; Wedler, E.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F. R;Bevan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.
                                          A; Introns: 47/3;
                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-535 < LEI>
                                                                                                                                                                                                                                      A; Reference number: A; Accession: T37189
                                                                                                                                                                                                                                                        A; Description: The sequence A; Description in the sequence number: Z20523
                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, February 1996 A; Description: The sequence of C. elegans cosmid
                                                                                                                                                                                                                                                                                                                       C;Accession: T37189
R;Leimbac, D.; Minx
                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein C02H7.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #t
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A; Reference number: Z15419
A; Accession: T05612
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                                                                                     A; Gene: CESP: C02H7.1
                                                                                                                             A;Cross-references: EMBL:U49945; PIDN:AAC47924.1; GSPDB:GN00029; CESP:C02H7.1
A;Experimental source: strain Bristol N2; clone C02H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Introns: 110/3; 247/2; 282/3; 304/3; 361/3; 390/2; 418/3
A;Note: F9D16.270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F9D16.270 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999 C;Accession: T05612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-456 <BEV>
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  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 KDTGEVSELKP-HRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLOREEHSOKSDSTKDVTATVLDKWNISSKSTTWN--PWK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKDAGY--VINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSQKSDSTKDVT--ATVLDKNNISSKSTTNNPNK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEPVGDDVRSSGDMSPNPSAANNVREGPATFDIMESEDNPGRDNVAPMEDHIRSEVQLSP 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KNKKEKDPLKPKHPVSAFLVYANERRAALREENKSVVEVAK-----ITGEEWKNLSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKKAPYEKVAKKNKETYLQ-AMEEYKRTKEEE----ALSQKKE--
                                                                                                                                                                                                                                                                                                                             Minx, M.
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                                          100/3; 149/3; 304/2; 347/3; 458/3
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25.0%; Pred. No. 8.
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    Score 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIKKEKATKKKKNENVDPNK 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ed. No. 8.3;
Mismatches
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  DB 2;
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                                                                                                                                                                                                                                                                                                                                                                 #text_change
  Length 535;
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hypothetical protein PFB0650w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C;Accession: G71609
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin,
; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith,
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743; PMID:9804551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-2500 < CAR>
A; Cross-references: GB: AE001408;
A; Experimental source: clone 3D7
C; Genetics:
A; Map position: 3
A; Introns: 158/2; 329/3
A; Note: T209.90
                                                                                                                                                                 R;Nyakatura, G.; Fartmann, B.; Dav
submitted to the Protein Sequence
A;Reference number: Z24475
A;Accession: T47835
                                                                                                                                                                                                                                            hypothetical protein T2O9.90 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 C;Accession: T47835
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                                                                                                                              A;Status: preliminary A;Molecule type: DNA
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Best Local S
Matches 41
                                                                                                           Molecule type: DNA
Residues: 1-644 <NYA>
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                                                          Genetics:
                                                                          Experimental source:
                                                                                           Cross-references: EMBL:AL138658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINL
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26.1%;
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                                                                          Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30; Mismatches
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Pred. No.
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8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred.
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                                                                          BAC
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62;
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                                                                            T209
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2000
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A;Status: P---
A;Molecule type: DNA
A;Residues: 1-1397 <CHE>
A;Residues: 1-1397 < EMBL:X79345;
                                                                                                                                                                                       R;Cheesman, S.J.
submitted to the EMBL Data Library,
A;Reference number: Z17031
A;Accession: T10466
A;Status: preliminary; translated f:
                                                                                                                                                                                                                                                     DNA topoisomerase (ATP-hydrolyzing)
C;Species: Plasmodium falciparum
C;Date: 16-Jul-1999 #sequence_revis:
C;Accession: T10466
R;Cheesman, S.J.
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C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change
C;Accession: I37271; S52774
R;Hess, H.; Heid, H.; Zimbelmann, R.; Franke, W.W.
Exp. Cell Res. 218, 174-182, 1995
A;Title: The protein complexity of the cytoskeleton of bovine an A;Reference number: I37271; MUID:95255491; PMID:7737358
A;Accession: I37271
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                                                           A;Map position: 14
C;Superfamily: eukaryotic type
C;Keywords: ATP; DNA binding;
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A;Cross-references: EMB
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Best Local S
Matches 34
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              Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                   154 SSK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  257 SKDAKKDAKEIKKGKKDKKKPSSTDSDSKDDVKKE---SKKDATKDAKKVAKKDTEKESA 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 SK--KKDNPQVNHSQLN-----ESHRKEDLQREEHSQKSDSTKD---VTATVLDKNNI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 205 ESEGEKG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 KGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTF---DV
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 36;
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                                                                           type II DNA topoisomerase;
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 36;
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Score 95; DB
Pred. No. 38;
86; Mismatches
                                                                                                                                            NID: 9994807
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Pred. No.
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Pred. No. 14;
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   53,
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                               Length 1397;
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   26;
                                                                                topoisomerase
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RESULT 23
T27135
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                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNAA;Residues: 1-871 <WIL>
                                                                                                                                                                                                                                                                                      R; Kershaw, J.; Lennard, N. submitted to the EMBL Data A; Reference number: Z20316
                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein Y53C12B.3b - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein Y53C12B.3a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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                                                                                                                                                          A;Cross-references: EMBL:Z99278; PIDN:CAB16492.1; GSPDB:GN00020; CESP:Y53C12B.3b
A;Experimental source: clone Y53C12B
                                                                                                                                                                                                                                                               A; Reference number: A; Accession: T27135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Introns: 100/3; 177/3; 218/1; 423/3; 714/2; 864/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;Residues: 1-867 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Cross-references: EMBL:Z99278; PIDN:CAB16493.1; GSPDB:GN00020; CESP:Y53C12B.3a
;Experimental source: clone Y53C12B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :Gene: CESP:Y53C12B.3a
Query Match
Best Local Similarity
                                                                                                              Gene: CESP:Y53C12B.3b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                       Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                     100/3; 177/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YRCEHYQLPABEVSSHNIRKDNG------DLWCEHM-KKIKCGHCEATGEQGHHPLICP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---KGYOFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIE----EKKEEENKPTFDVS 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPKKDFKVDQEASIEATKTEISEENPK--TDDIQSKDDVTS------KSELHC 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTVKEFILNKDTG-----EVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELE- 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIEKVEEAIEFQRNVELSNREESNK--FKVARKQ-----GPSSMKKKKKKKKKLSSDEESE 1241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VFKKIEE-----KKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQ 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEEIIAGITVKDYDYLLSMPIFSLTLEK---VEDLLTQLKEKERELEILRNITVETMWLK 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGKEMSSTIVSEEDFIL--PVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKKDNPOVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKKEEERVAKSR--ESSQKPIDPQEISDDQDDTVPDVPDQIVEQDNQSHKSRHNSENR
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25.3%; Pred. No. 24;
                                                                     218/1; 423/3; 717/2; 867/3
    11.1%;
25.3%;
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    Score 94.5;
Pred. No. 24;
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                         DB
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                    Length
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RESULT
T18427
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A; Accession: T18427
A; Map position:
A; Introns: 30/2;
                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-210 <NEL>
                                                                                                                                                                                       A;Description: The sequence of C. elegans cosmid E03H12
A;Reference number: Z20520
A;Accession: T28771
                                                                                                                                                                                                                                                     R;Nelson, J.; Wohldmann, P.; Sanson submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                    hypothetical protein E03H12.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 25
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C;Date: 15-Oct-1999 #sequence_revision
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                                        A,Gene: CESP:E03H12.5
                                                                                  A; Experimental source: strain Bristol
                                                                                                      A;Cross-references: EMBL:AF000299; PIDN:AAC47980.1; GSPDB:GN00022; CESP:E03H12.5
                                                                                                                                                                                                                                                                                                    C;Accession: T28771
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A; Introns: 307/1; 1545/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:Z98547; NID:e1325376; PID:e1325379; PIDN:CAB11104.1
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                                                                                                                                                                                                                                                       J.; Wohldmann, P.; Sansone, J.
to the EMBL Data Library, June 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TKDVTATVLDKNNISSKSTTNNPNK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNH-SQLNESHRKEDLQREEHSQKSDS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HKIEQDIQDIHSIQTNICDENN-IEQINEENSKKGVRISGTDM---ENKND--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KKKEEERVAKSR--ESSOKPIDPQEISDDQDDTVPDVPDQIVEQDNQSHKSRHNSENR 808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPKKDFKVDQEASIEATKTEISEENPK--TDDIQSKDDVTS---
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  201/3
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; Pred. No. 1.2e+02;
30; Mismatches 50;
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Query Match Best Local Similarity

11.1%; 28.6%;

Score 94; Pred. No.

DB 2; 5.2;

Length

210;

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R;Resing, S.; Hofmann, C.J.B.
submitted to the EMBL Data Library, March 1993
A;Description: Smallest known eukaryotic genomes
A;Reference number: $42488
A;Accession: $42488
A;Molecule tvoc
                                                                                                                                                                                                                                                                                                                           RESULT 27
$42488 and the vestigial nucleomorph of a cukaryotic endosymbiont C; Accession: $42488; $45576 R; Resing, S.; Hofmann, C.J.B.

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A;Molecule type: DNA
A;Residues: 1-649 <RES>
A;Cross-references: EMBL:X72621; NID:g461335; PIDN:CAA51197.1;
R;Hofmann, C.J.B.; Rensing, S.A.; Haeuber, M.M.; Martin, W.F.;
Mol. Gen. Genet. 243, 600-604, 1994
A;Title: The smallest known eukaryotic genomes encode a protein
A;Reference number: S45576; MUID:94268506; PMID:8208251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Seki C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: E89883
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A;Molecule type: DNA
A;Residues: 1-645 <KUR>
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Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Accession: E89883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDLQ----REEHSQKSDSTKDVT-ATVLDKNNISSKSTTNNPNK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GQYHVRIVDKEAFTKANTDKSNKKEQQDNSAKKEATPATPSKPTPSPVEKESQKQDSQKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QF----DGWEISGFEGKK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAITEFONVOPTNEKMTDLODTKYVVYESVENNESMMDTFVKH-----PIKTGMLNGKKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLOREEHSOKSDSTKDVTATVLDKNNISSKSTTNNPNK 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 93.5;
Pred. No. 20;
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                                                                                           PID:g461336
Mueller, S.
                                 gene:
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                                                                                           S.B.; Couch,
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Sekimizu,
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A; Residues: 1-629 <STO>
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C;Accession: G96542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: hsp70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: F17J6.14
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                                       ANFQTQAPTGNDDAESDDPSEPVSHS---ETLNPPELEKKEVMRKDATERSVSADCQDKN
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Nature 408, 816-820, 2000
A;Authors: Hunter, J.I.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay A;Authors: Hunter, J.I.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malt C.A.; Li, J.H.; Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malt Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.I.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; S ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Description: involved in protein folding and assembling/disassembling of C;Superfamily: heat shock protein 70 C;Keywords: ATP; molecular chaperone; nucleomorph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein F17J6.14 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chin, C.W.; Chung, M.K.; Conn, L.; ansen, N.F.; Hughes, B.; Huizar, L.
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A; Residues: 1-24,'Q',26-91,'H',93-578 <HOF>
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A;Status: nucleic a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 HSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDK 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 SGFEGKKDA-----GYVINLS---KDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVN 115
                                                                                                          45 LPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 ILNKDTGEVSELKPHRVTVTIQNG---KEMSSTIVSEEDFILPVYKGELEKGYQFDGWEI 63
---EENKPTFDVSKKKDNPQ--VNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKN
                                                                                                                                                                                                                    TTVKEFILNKDTGEV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --LDKKLEAKNSLENYAYNIRNTVRD-----EKLKEKIQEEDKKSIEEKVKE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --VLEFIETNEDLEKEEYEEKEKELKNFANPIISK 615
                                                                                                                                                            TTAK---MSSSTAEVQLPAEKGVGKMDQKVSQEGMPHLETAKPTKDSAMEQTVEAEDVAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              GB:AE005173; NID:g11054631; PIDN:AAG27876.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J.R.; Palm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.0%;
                                                                                                                                                                                                                                                                                               11.0%; Score 93;
19.6%; Pred. No.
                                                                                                                                                                                                                                                                   39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 93.5;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.J.; Federspiel, N.A.; Kaul, S.; White, Conway, A.B.; Conway, A.R.; Creasy, T.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  shown
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21;
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                                                       AMNPIVEKAMSQIVEAEDAAINQAVD 501
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                                                                                                                                                                                                                                                                            73;
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                                                                                                                                                                                                                                                                                                                           Length
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Maiti, R.; Ma
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                                                                                                                                                                    1447
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war, K.,
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R;Gentles, S.; Churcher, R;Gentles, C.; Churcher, Submitted to the EMBL Data submitted to number: Z21815
                                                    A; Nolecule type: DNA
A; Residues: 1-1888 < GEN>
A; Cross-references: EMBL: 298531; PIDN
A; Cross-references: EMBL: 298531; PIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-2464 <NOB>
A;Cross-references: EMBL:X51396; NID:g52999; A;Cross-references: EMBL:X51396; NID:g52999; A;Cross-references: Badilla, R.; Paciucci, R.; Zab Arch. Biochem. Biophys. 310, 428-432, 1994 A;Title: Binding of heat-shock protein 70 (hs A;Reference number: S44387; MUID:94234720; PW A;Accession: S44387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 01-Sep-2000 C;Accession: S07549; S44387; A33645 R;Noble, M.; Lewis, S.A.; Cowan, N.J. Cell Biol. 109, 3367-3376, 1980 A;Title: The microtubule binding domain of microtubule-associated protein MAP1B A;Reference number: A33645; MUID:90094539; PMID:2480963 A;Accession: S07549
                                                                                                                                                                                                                                            hypothetical protein SPAC6B12.02c - fission yeast (Schizosaccharomyces pomb
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
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C;Keywords: microtubule binding; phosphoprotein; tandem repeat
F;589-786/Domain: microtubule binding #status experimental <MTB>
F;589-592,639-642,649-652,655-658,660-663,668-671,674-677,679-682,683-686,687-690,691-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein A; Residues: 653-663, 'IC' <SAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  microtubule-associated protein MAP1B -
A; Map position:
                                                                                                                              A;Status: preliminary; translated from
                                                                                                                                                      A;Accession: T39009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ,1861-2064/Region: 17-residue repeats
,91,116,351,888,1124,1153,1168,1208,1662,1877,1918,2003,2030,2054,2083/Binding site:
,147,969,1336,1562,1563,1702,1708,1990,2057,2063,2419/Binding site: phosphate (Thr)
                                      Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1953/Binding site: phosphate (Tyr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Mus musculus (house mouse)
                    Gene: SPDB:SPAC6B12.02c
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                                                                                                                                                                                                                                                                                                                                                                                                                         HRKEDLQRE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGFEGKKDAGYVINLSKDTFIKPVFK-KIEEKKEEENKPTFDVSKKKDNPQVNHSQLNES 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEFILNKDTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEI 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 93; DB:
Pred. No. 1e+0:
24; Mismatches
                                                        PIDN:CAB11064.1;
2h-; cosmid c6B12
                                                                                                                                                                                          August
                                                                                                                                                                                                                                                                                                                                                                                                                           -EHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  582
                                                                                                                                  GB/EMBL/DDBJ
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                                                                                                                                                                                          B.G.; Rajandream,
ust 1995
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Zabala, J.C.; Avila, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (hsp70) to tubulin. PMID:8179328
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                                                                          GSPDB:GN00066; SPDB:SPAC6B12.02c
                                                                                                                                                                                                                                                                                         (Schizosaccharomyces pombe)
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                    Genome:
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R;Farrell, A.M.; Foster, T.J.; Holland, K.T.
J. Gen. Microbiol. 139, 267-277, 1993
A;Title: Molecular analysis and expression of the lipase
A;Reference number: A47705; MUID:93171870; PMID:8436947
                                                           A; Molecule type: DNA
A; Residues: 1-1202 < KEM>
                                                                                                  A; Reference number: S05362; A; Accession: S05362
                                                                                                                                                                                                         C; Accession: S05362
                                                                                                                                                                                                                            C;Date: 10-Sep-1999 #sequence
                                                                                                                                                                                                                                                probable DNA-directed DNA polymerase (EC 2.7.7.7) -
C;Species: mitochondrion Ascobolus immersus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:M95577; NID:g153021; PIDN:AAA19729.1; A;Note: sequence extracted from NCBI backbone (NCBIN:125632, C;Superfamily: Staphylococcus triacylglycerol lipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA; p
A;Residues: 1-688 <FAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: Schizosaccharomyces hypothetical protein SPAC6B12.02c
                                         A; Cross-references:
                                                                                                                                              In organello replication and viral
mitochondrion
                                                                                                                                                               Genet. 218, 523-530,
                                                                                                                                                                                       F.; Meinhardt, F.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DWYSGKHELVQQSHSYKKPSDSKSVGGNIFSVNSKKHSVNINAKTAANN
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                                                                                                                                                                                                                                                                                                                                                                                                                  KEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKDAG-YVINLSKOTFIKPVFKKIE-EKKEEENKPTFDVSKKKDNPQV--NHSQLNESHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NKNVNEKSNVN-----SITENESLHNETPKNEDLI-----QQQKDSQNDNKSESVVEQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NKDTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NESHRKEDLOREEHSOKSDS-TKDVTATVLDKN-----NISSKSTTNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TSENPFOLNVAANAVSTIPVYRTTKTKMKKNRFKYVEVEKLPDLILESY---
                                                                                                                                                                                                                                                                                                                                                                               KQEDSQKENLSKQDTQSSKTTDLL-----RATAQNQSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lipase (EC 3.1.1.3) - Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                         EMBL:X15982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKKAPKFLRVFARSSSHIP--KMIRRKROMDSKKYFSFDKESDROVIDOVLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.9%; Score 92.5;
23.1%; Pred. No. 81
                                                                                                                        MUID:90066356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hydrolase
                                                                                                                                                                                       Esser,
                                                                                                                                                                                                                                 revision
                                                                                                                                                                   1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 92; DB:
Pred. No. 28;
28; Mismatches
                                       NID:g2933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-Nov-1994
                                                                                                                            PMID:2573
                                         PIDN: CAA34106.1;
                                                                                                                          affinity of
PMID:2573821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81;
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                                                                                                                                                                                                                                                                      fungus
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                                                                                                                                                                                                                                                                        (Ascobolus immersus)
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NCBIP:125633)
                                         PID:g1370212
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                                                                                                                                              extrachromosomal
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A;Molecule type: DNA
A;Residues: 1-1875 <BOU>
A;Residues: 1-1875 <BOU>
A;Residues: 1-1875 <BOU>
A;Cross-references: EMBL:X73541; NID:g450550; PIDN:CAA51948.1;
A;Experimental source: strain S288C
A;Experimental source: strain S288C
A;Experimental source: strain S288C
A;Experimental source: strain S288C
A;Experimental source: Exy; Botstein, D.
Mol. Gen. Genet. 237, 359-359, 1993
Mol. Gen. Genet. 237, 359-359, 1993
A;Title: A new yeast gene with a myosin-like heptad repeat stru
A;Reference number: S31207; MUID:93247549; PMID:8483450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-1875 <ABL>
A;Residues: 1-1875 <ABL>
A;Residues: 1-1875 <ABL>
A;Residues: 1-1875 <ABL>
A;Residues: 1-1875 <ABL>
A;Residues: 1-1875 <ABL>
A;Resperimental source: strain S288C
R;EOU, G.; Esteban, P.F.; Baladron, V.; Gonzalez, G.A.; Cantalejo, J.G.;
Yeast 9, 1349-1354, 1993
A;Title: The complete sequence of a 15 820 bp segment of Saccharomyces A;Reference number: S40644; MUID:94205265; PMID:8154186
                                       Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Saccharomyces cerevisiae C;Date: 03-May-1994 #sequence revisiae C;Accession: S38173; S40647; S31207 R;Baladron, V.; Ballesta, J.P.G.; Bc submitted to the Protein Sequence Day
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
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                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-300,'A',302-1875 <KOE>
A;Cross-references: EMBL:L01992; NID:g171958; PIDN:AAA34783.1; PID:g171959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               myosin-like protein MLP1 - yeast (Saccharomyces cerevisiae)
N;Alternate.names: protein YKR095w; protein YKR415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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                                                                                                                                                                             Matches
                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                             Gene: SGD:MLP1
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Matches
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Best Local
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  717
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                                          59
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                                                                                                                                                                             48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 FILNK----DTGEVSELKPHRVTVTIQNGKEMSSTI---VSEEDF--ILPVYKGELEK--
                                                                                                                                7 ILNKDTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDF----ILPVYKGE----LEKGYQF
                                                                                                                                                                                                    Similarity
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                                          DGWEISGFEGKKDA-----GYVINLSKDTFIKPVFKKIEEK------KEEENK 100
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                                                                                      LLNK---EIQDLYDSKSDISIKLGKEKSSRILAEERFKLLSNTLDLTKAENDQLRKRFDY
----LQNTILKQDSKTHETLNEYVSCKSKLSIVETELLNLKEEQKLRVHLEKNLKQELNK
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                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                           SGD:S0001803; MIPS:YKR095w
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                                                                                                                                                                             36;
                                                                                                                                                                                                  Score 92; DB
Pred. No. 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 92; DB 1;
Pred. No. 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bou, G.; del Rey, F.; Esteban, P.F.; Garcia-Cantalejo Database, March 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
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                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                         DB
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                                                                                                                                                                                                                       Length 1875
                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PID:g450554
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A; Molecule type: DNA
A; Residues: 1-253 <GAT>
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R;Gattung, S.; Scheet, P.
submitted to the EMBL Data Library, Januar
submitted to the sequence of C. elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Genome: nucleomorph C;Superfamily: heat shock protein C;Keywords: nucleomorph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                heat shock protein 70KD [imported] - Guillardia theta nucleomorph C;Species: nucleomorph Guillardia theta A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 15-Jun-2001 C;Accession: D90093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                       A;Accession: T32879
A;Status: preliminary; translated
                                                                                                                                                                                                                                                                                               A; Description: The sequence A; Reference number: Z21240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AF165818; NID:g13794501; PIDN:AAK39876.1; GSPDB:GN00150 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 410, 1091-1096, 2001
A;Title: The highly reduced genome of an enslaved algal nucleus
A;Reference number: A99082; MUID:11323671; PMID:11323671
                                                                                                                                                                     A;Cross-references: EMBL:AF043692; PIDN:AAB97531.1; GSPDB:GN00019; CESP:C17F3.3 A;Experimental source: strain Bristol N2; clone C17F3
                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_rev:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: hsp70
A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-650 < DOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Nature 410, 1091-1096, 2001
                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: T32879
                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein C17F3.3 - Caenorhabditis elegans
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             Query Match
Best Local Similarity
                                                                                                  Map position:
                                                                                                                            Gene: CESP:C17F3.3
                                                                                                                                                   Genetics:
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Conservative
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                    10.7%;
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Score 91; DB Pred. No. 11; 7; Mismatches
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Pred. No. 29;
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DNA Res. 1, 1-14, 1994
A;Title: Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chrom A;Reference number: S65967; MUID:96051385; PMID:7584024
A;Accession: S66040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Bacillus subtilis
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C;Accession: S66040; I9830; A92275; A92307; B61335; D69612; A23307
R;Ogasawara, N.; Nakai, S.; Yoshikawa, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Stocker, S.; Hiery, M.; Marriott, G.
Mol. Biol. Cell 10, 161-178, 1999
A;Title: Phototactic migration of Dictyostelium cells is A;Reference number: Z20823; MUID:99096692; PMID:9880334
A;Accession: T30330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gelsolin-related protein GRP125 - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
                                        A;Residues: 48-226,'Q',228-443 <RES>
A;Cross-references: GB:M13766; NID:g142816; PIDN:AAA22375.1; PID:g142817
                                                                                                                                            A;Cross-references: EMBL:D26185; NID:9467326; PIDN:BAA05246.1; PID:9467400
A;NOtes: the nucleotide sequence was submitted to the EMBL Data Library, Decer R;Todd, J.A.; Roberts, A.N.; Johnstone, K.; Piggot, P.J.; Winter, G.; Ellar, J. Bacteriol. 167, 257-264, 1986
A;Title: Reduced heat resistance of mutant spores after cloning and mutagene; A;Reference number: 139830, MUID:86250662; PMID:3087956
A;Accession: 139830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           serine-type D-Ala-D-Ala carboxypeptidase (EC: N;Alternate names: penicillin-binding protein
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A; Residues: 1-1087 < STO>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VKEVAKEETKEEIKEEVN-DEATEVKEVNQVEEEVKEEEVKEEVKVEVKEEEVKGEAKEE
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Strominger, J.
255, 3964-3976,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL: U95159; NID: g4100185; PID: g4100186; PIDN: AAD00774.1
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C; Bron, S; Brouillet, S; Bruschi, C.V.; Çaldwell, B.; Capuano, V.; Carter, N.M.; Cho A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Natture 390, 249-255, 1997

A,Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koethers: Lauber, J.; Lazarevic, V.; Lee, S.M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Fevine, A.; Liu, H.; Masuda, S.; Maueelly, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Reference number: A69580; MUID:98044033; PMID:9384377

A, Recession: D69612
                                                                               ORF MSV230 hypothetical protein - Melanoplus sanguinipes entomopoxvirus C;Species: Melanoplus sanguinipes entomopoxvirus C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
                          R; Afonso,
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A;Mesidues: 55-68 <YOC>
A;Residues: 55-68 <YOC>
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ben
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
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A; Accession: B61335
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A;Title: Mechanism of penicillin action: penicillin and
A;Reference number: A61335; MUID:79223865; PMID:111240
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R;Waxman, D.J.; Strominger, J.L.
J. Biol. Chem. 256, 2067-2077, 1981
A;Title: Primary structure of the COOH-terminal membranous segment A;Reference number: A92307; MUID:81117303; PMID:6780559
A;Accession: A92307
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A;Accession: A92275
                                                       C; Accession: T28391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Start codon:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Yocum, R.R.; Waxman, D.J.; Rasmussen, Proc. Natl. Acad. Sci. U.S.A. 76, 2730-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-443 <KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: GB:Z99104; GB:AL009126; NID:g2632267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                             C.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILNKDTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FSMKEIYAEGDQVKGHK-TISVDKGKEKEVGIVTNKAFSLPVKNGE-EKNYKAK-----
Tulman, E.R.; Lu,
33-552, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                     415
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                             Z.;
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Pred. No. 22;
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                             Oma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J.R.;
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                             Kutish, G.F.; Rock,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
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A;Title: The genome of Melanoplus sanguinipes entomopoxvirus. A;Reference number: Z20484; MUID:99102612; PMID:9847359 A;Accession: T28391 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-835 <AND>
A;Cross-references: EMBL:Z35950; MIPS:YBR081c
A;Cross-references: EMBL:Z35950; MIPS:YBR081c
R;Haynes, S.R.; Dollard, C.; Winston, F.; Beck, S.; Trowsdale, J.; Dawid, Nucleic Acids Res. 20, 2603, 1992
A;Title: The bromodomain: a conserved sequence found in human, Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-1332 <STE>
A;Cross-references: EMBL:Z35950; NID:g536341; PIDN:CAA85026.1; PID:g536342; MIPS:YBR081c
A;Cnoss-references: EMBL:Z35950; NID:g536341; PIDN:CAA85026.1; PID:g536342; MIPS:YBR081c
R;Andre, B.; Cziepluch, C.; Hein, C.; Jauniaux, J.C.; Urrestarazu, A.; Vissers, S.
submitted to the Protein Sequence Database, August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 28-Jan-1994 #sequence revision 09-Sep-1994 #text_change 20-Sep-1999 (C;Accession: S41552; S45946; S45948; S40800; S45478; S54985; S59716 R;Gansheroff, L.; Dollard, C.; Tan, P.; Winston, F. submitted to the EMBL Data Library, July 1993 A;Reference number: S41552
  A; Molecule type: DNA
A; Residues: 1-624, 'L
                                                                                                         A; Title: Sequence analysis of a 31 kb DNA
A; Reference number: S45462; MUID:95076715;
                                                                                                                                                          R; van der Aart, Q.J.M.;
Yeast 10, 959-964, 1994
                                                                                                                                                                                         A;Cross-references: EMBL:M87651; NID:g172683; PIFR;van der Aart, Q.J.M.; Barthe, C.; Doignon, F.;
                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 463-523 <HAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-835 <A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the Protein Sequence A; Reference number: S45893
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A; Residues: 1-1332 <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Steensma, H.Y.; van der Aart, Q.J.M.
submitted to the Protein Sequence Database, August 1994
A;Reference number: S45932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:L22537; NID:g349189; PIDN:AAC37424.1; PID:g349190 R;Steensma, H.Y.; van der Aart, Q.J.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-1332 <GAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable transcription factor SPT7 - yeast (Saccharomyces cerevisiae) N; Alternate names: protein YBR0739; protein YBR081c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-670 < AFO>
                                                                                A; Accession: S45478
                                                                                                                                                                                                                                                                                                                                  A, Accession: S40800
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                                                   Status: nucleic acid sequence not shown; translation not
                                                                                                                                                                                                                                                                                                      Status: nucleic acid sequence
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Species: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: S45948
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1-624, 'LRGKKRKI',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEDLOREEHSOKSDSTKDVTATVLDKNNISSKSTTNNPNK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSDSDSGVNIDESQNSDSKVNINKLENESQNSDSKVNIDESQNSDS-KVNINKLENESQN 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VNFEEKKQIISTLLKFNNFDKTEMCGVSVEKFVQLINNKSASEKYSDVDSSIDESQNSDS
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                                                                                                                                                                                                                                                                                                                                                               conserved sequence found in MUID:92285152; PMID:1350857
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Pred. No. 35;
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                                                                                                               fragment from the right arm PMID:7985423
                                                                                                                                                                                         PIDN:AAA35087.1; PID:g172684
F.; Aigle, M.; Crouzet, M.; S
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                                                                                                                                         of Saccharomyces
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26 TIQNGKEMSSTI---

--VSEEDFILPVYKGELEKGY---QFDGWEISGFEGKKDA 72

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A; Molecule type: DNA
A; Residues: 1-2401 <SIN>
A; Cross-references: EMBL: U36927; NID: g1041784; PID: g1041785;
A; Cross-references: EMBL: U36927; NID: g1041784; PID: g1041785;
A; Cross-references: EMBL: U36927; NID: g1041784; PID: g1041785;
A; Cross-references: EMBL: U36927; NID: g1041784; PID: g1041784; PID: g1041784; PID: g1041784; PID: g1041784; PID: g1041784; PID: g1041784; PID: g1041784; PID: g1041784; PID: g1041784; PID: g1041784; PID: g1041784; PID: g1041784; PID: g1041784; PID: g1041784; PID: g1041784; PID: g1041784; PID: g1041784; PID: g1041784; PID: g1041784; PID: g1041784; PID: g1041784; PID: g1041784; PID: g1041784; PID: g1041784; PID: g1041784; PID: g1041784; PID: g1041784; PID: g1041785; PID: g1041784; PID: g1041785; PID: g1041784; PID: g1041784; PID: g1041785; PID: g1041785; PID: g1041784; PID: g1041785; PID: g1041784; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785; PID: g1041785
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R;Sinha, K.A.; Keen, J.K.; Ogun, S.A.; Holder, A.A.
Mol. Biochem. Parasitol. 76, 329-332, 1996
A;Title: Comparison of two members of a multigene family
A;Reference number: Z20507; MUID:97077455; PMID:8920022
A;Accession: T28676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Plasmodium yoelii
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
C;Accession: T28676; A45521
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A;Molecule type: DNA
A;Residues: 1-1332 <VAM>
A;Residues: 1-1332 <VAM>
A;Cross-references: EMBL:X76294; NID:g974203; PIDN:CAA53940.1;
A;Cross-references: Extrain S288C
                                                                                                                                          A;Molecule type: DNA
A;Residues: 2260-2401 <KEE>
A;Cross-references: GB:M34281
                                                                                                                                                                                                                                                                     A;Reference number: A45521; MUID:91101660; PMID:2270106
A;Accession: A45521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Gansheroff, L.J.; Dollard, C.; Tan, P.; W
Genetics 139, S23-536, 1995
A;Title: The Saccharomyces cerevisiae SPT7
A;Reference number: S54985; MUID:95229044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-132 <GAW>
A;Residues: 1-132 <GAW>
A;Cross-references: EMBL:L22537; NID:g349189; PIDN:AAC37424.1;
R;van der Aart, Q.J.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Species: Plasmodium yoelii
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A;Map position: 2R
                                                                                                                                                                                                                                              A;Status: preliminary
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                                 Local Similarity
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ALIGNMENTS

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C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence revision 03-Aug-2001 #text_change 03-Aug-2001
C;Accession: F95074
R;Tettelin, H; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heinon, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
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A;Molecule type: DNA
A;Residues: 1-2140 <KUR>
A;Cross-references: GB:AE005672; PIDN:AAK74791.1; PID:g14972117; GSPDB:GN00164; TIGR:SP4
A;Experimental source: strain TIGR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: F95074
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Similarity 100.0%;
74; Conservative 0
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Pred. No. 6.9e-57;
0; Mismatches 0;
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                                             R.H.; Jaskunas, S.R.;
                                                                                                    S.; DeHoff, B, P.; McAhren,
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A;Accession: A97942
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2144 <KUR>
A;Cross-references: GB:AE007317; PIDN:AAK9:C;Genetics:
A;Gene: prtA
C;Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: PC4334
A;Molecule type: protein
A;Residues: 79-83;299-412;485-502 <BUR2>
A;Residues: 79-83;299-412;485-502 <BUR2>
A;Experimental source: brain
C;Comment: This protein inhibits neural cell adhesion and neurite outgrowth
C;Keywords: chondroitin sulfate proteoglycan; glycoprotein; keratan sulfate
E;267-270;Aegion: cell attachment (R-G-D) motif
E;112,213,490/Binding site: carbohydrate (Asn) (covalent) #status predicted
E;152,249,440,793,820/Binding site: chondroitin sulfate (Ser) (covalent) #st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NyAlternate names: keratan sulfate proteoglycan
(;Species: Gallus gallus (chicken)
C;Date: 07-Jul-1997 #sequence revision 12-Sep-1997 #text_change 21-Jul-2000
C;Accession: JC5497; PC4334; S37561
R;Burg, M.A.; Cole, G.J.
J. Neurobiol. 25, 1-22, 1994
A;Title: Claustrin, an antiadhesive neural keratan sulfate proteoglycan, is
A;Reference number: JC5497; MUID:94157526; PMID:7906711
A;Accession: JC5497
A;Molecule type: mRNA
A;Residues: 1-1038 <BURL:
A;Cooss-references: EMBL:X67778; NID:g406318; PIDN:CAA47988.1; PID:g406319
A;Cooss-references: EMBL:X67778; NID:g406318; PIDN:CAA47988.1; PID:g406319
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9; Mismatches
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Pred. No. 1.1e-56;
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C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C;Accession: B71609
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O. Science 282, 1126-1132, 1998
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submitted to the EMBL Data Library,
A;Reference number: Z18937
A;Accession: T18467
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A:Experimental source: clone 3D7
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A; Residues: 1-665 < GAR>
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TFD----VSKKKDNPQVNHSQLNESHRKEDLQR-EEHSQKSDSTKDVTATVLDKNNISSK 166
                                                    KGKQ----DISNSNAENKKD-
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                                                                                                                KDDNNNNNGTKQIEEKNKINKSDL--HRQNELNLQSGK-----NEQDI-----NKNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KINK
                                                                                  KGYQFDGWEI--SGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKE---
                                                                                                                                              KDFARNTTVKEFILNKDTGEVSELKPHRVT-VTIQNGKEMSSTIVSEEDFILPVYKGELE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EHNINNVNLKKEKEYTDIQRDKRKHKRSLSQKSDSYKKRPFNKRKTSIER-SLSNKRYDE
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                                                                                                                                                                                               12.2%;
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                                                                                                                                                                                32;
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                                                                                                                                                                                                                                                                                             GB:AE001362; NID:g3845245; PIDN:AAC71925.1; PID:g384524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENKPTFDVSK-KKDNPQVNHSQLNE-----SHRK 135
                                                                                                                                                                                               Score 109;
Pred. No. 1
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Pred. No. 1.3;
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November 1998
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                                                                                                                                                                                               .9;
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                                                    -VKEGVKELEEKKKEEKISDDHKVEENKK
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                                                                                                                                                                                                            Length 665
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                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                              Aravind, L.; Koonin, R.; White, O.; Smith,
                                                                                                                                                                                 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-Jan-2002
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                                                                                   EENKP 111
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203

SDDHKVEENKKSDDHKVEENKKSDDHKI EEVKKVEEHEEDEEE-----DKKEKKSE

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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, S.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: D86432

A;Accession: D86432
                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein G5 - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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                       S
                                                                                                                                                                                                                                                                                           A;Reference number: Z14684; MUID:98198836; A;Accession: T18283
                                                                                                                                                                                                                                                                                                                                                          R;Rieben Jr., W.K.; Gonzales, C.M.; Gonzales, Genetics 148, 1117-1125, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-325 < RIE>
                                                                                                                                                                                                                                                          A:Status: preliminary; translated from GB/EMBL/DDB:
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                                                                                                                                                             A; Introns: 85/1
                                                                                                                                                                                                                                                                                                                                     A; Title: Dictyostelium discoideum nuclear plasmid Ddp5 is a chimera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE005172; NID:g4587525; PIDN:AAD25756.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues:
                                                                                                                                                                                                       Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                          Similarity
HRVTVTIQNGKEMSSTIVSEEDFILPVYK-GEL--EKGYQFDGWEISGFEGK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -ALSDLKSKLEEAIVDN----TLLKTKKKESSPMKEKKEEVVKPEAEVEKKKE--EAAEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WEISGFEGKKDAGYVINLSKDTFIKPVFKK----IEEKKEEENKPTFDVSKKKDNPQVNHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTVKA-VVEETKVEEDESKP-----EGVEKSASFKEESDFFADLKESEKK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVEEEKKSEAVVTEEAPKAETVEAVVTEEIIPKEEVTT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTVKEFILNKDTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDG
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                                                                                                                                                                                                     EMBL:U00796; NID:g2702254; PID:g2702258; PIDN:AAC18634.1
                                                                                        11.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28;
                                                                   Score 103.5; I
Pred. No. 2.1;
25; Mismatches
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                                                                                                                                                                                                                                                                                                                  PMID: 9539429
                                                                                                                                                                                                                                                                                                                                                                              S.T.; Pilkington, K.J.; Kiyosawa,
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                                                                     Indels
                                                                                                               Length
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                                                                     63;
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                                                                     Gaps
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RESULT 9
A90570
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submitted to the EMBL Data Library,
...paference number: Z19271
                                                                                                                                                                            lipoprotein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change
C;Accession: A90570
                                                                                        A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma A;Reference number: A99512; MUID:21267165; PMID:11353084 A;Accession: A90570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein E02A10.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 15-Oct.1999 C;Accession: T20410
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 A;Cross-references: GB:AL445566; PID:g14089879; PIDN:CAC13638.1; GSPDB:GN00153 A;Experimental source: strain UAB CTIP
                                    A; Molecule type: DNA
A; Residues: 1-622 < KUR>
                                                                                                                                               Nucleic Acids Res. 29,
                                                                                                                                                                   R;Chambaud,
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A; Introns: 32/1; 72/1;
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A; Residues: 1-385 <WIL>
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A; Experimental source:
                                                                       A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                             -KKEEEKKEEEQKE--EVEKKEË----EEKKDEEPKKEEEEKKEDEVEEKSEKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NHIKDSGYYATNEEIEIFLESCTLCKEITAQTKRNSYKKRNIINKLPEEEEEEEEEEE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---KDAGYV-----INLSKDTFIKPV-----FKK-----
                                                                                                                                                                                                                                                                                                                                      EEK 373
                                                                                                                                                                                                                                                                                                                                                                        LDK 160
                                                                                                                                                                                                                                                                                                                                                                                                                                               FKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATV
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                                                                                                                                               Heilig, R.; Ferris,
es. 29, 2145-2153, 2
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Pred. No. 3;
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                                                                                                                                                                 S.; Barbe,
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                                                                                                                                                                   Galisson, F.;
                                                                                                                                                                                                     03-Aug-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----EP-
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                                                                                                                                                                     Moszer,
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RESULT 10
G81339
           hypothetical protein CO2H7.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #t.C;Accession: T37189 R;Leimbac, D.; Minx, M.
                                                                               RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypelarence number: A81250; MUID:20150912; PMID:10688204
A;Accession: G81339
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: G81339
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, C.W.; Ouall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, Nature 403, 665-668, 2000
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A;Genetic code: SO
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Matches 46
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                                                                                                                                                                  NNPN 173
                                                                                                                                                                                             KKANEIKNIQTKTQIQTKSNQATTQTKQEKKELTNSIEKIQKTETKIQKPLIIEKKLDVK 176
                                                                                                                                                                                                                     KKDNP----QVNHSQLNESHRKEDLQREEHSQKSDSTKDV--TATVLDKNNISSK--STT
                                                                                                                                                                                                                                                EEYESKHTKKSNIYLKED---LINVKLEEKQSLAKKIFSKMKERRKEENKKTKKNFLFSR 118
                                                                                                                                                                                                                                                                   KGYQFDGWEISGFEGKKDAGYVINL---SKDTFIKPVFKKIEEKKEEENKPT---FDVSK 117
                                                                                                                                                                                                                                                                                                                                EFILNKDTGEVSELKPHRVTVTIQNGKEMSSTI----VSEEDFILPVYK------GELE
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                                                                                                                                       NOPN
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Data Library,
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Pred. No. 5.
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Pred. No. 2.8;
 February 1996
                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                       03-Dec-1999 #text_change 18-Feb-2000
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probable membrane protein YDL074c - yeast (Saccharomyces N;Alternate names: hypothetical protein D2483 C;Species: Saccharomyces cerevisiae C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_C;Accession: S67610 R;Wambutt, R.; Wedler, H.; Wedler, E.; Scharfe, M. submitted to the Protein Sequence Database, July 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
S67610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: T37189
A;Status: preliminary; translated
A;Molecule type: DNA
A;Residues: 1-535 <LEI>
A;Cross-references: EMBL:U49945; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Description: The sequence of A;Reference number: Z20523
                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 4L
C;Keywords: transmembrane protein
F;69-85/Domain: transmembrane #status predicted <TVM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-700 <WAND
A;Cross-references: EMBL:Z74122; NID:g1431087; PID:e253213; PID:g1431088; GSPDB:GN00004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Experimental source: strain S288CC;Genetics:
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A; Accession: S67610
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A;Introns: 47/3; 100/3; 149/3; 304/2; 347/3; 458/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: SGD: S0002232
                                                                                                                                                                                                                                                                                               Matches
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Experimental source: strain Bristol N2; clone C02H7
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                                                                                                                                                                                                                                                                                                                     Similarity
EHSQKSDSTKDVTATVLDKNNISSK 166
                                     AAMRSKDSILIEIKTLSKSLSKSNEL-----ILQLKDSDRLLQQKIGNLHKQLDLSQN 541
                                                                              INL-SKDTF---IKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQRE 141
                                                                                                                        ----QDALIKEIQ-DLEKGFR----ELSDLTHKKYSEIINHESVISKLTVEKTKADQKYF
                                                                                                                                                                                                            KDVVRIRTARDDLLSKIAILEAEKSKTEVLSDLQ-HAIDILKEQWTKIDQRSNDTKSSST
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                                                                                                                                                                                                                                                     KDFARNTTVKEFILNK------DTGEVSELKPHRVTVTIQ------
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Pred. No. 5.2;
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Pred. No. 7
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                                                                                                                                                                                                                                                     -NGKEMSST
                                                                                                                                                                                                                                                                                               Gaps
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myosin-like protein MLP1 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YKR415
C;Species: Saccharomyces cerevisiae
C;Date: 03-May-1994. #sequence revision 03-May-1994 #text_change
C;Accession: S38173; S40647; S31207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
S38173
                                              A;Molecule type: DNA
A;Residues: 1-1875 <BOU>
A;Residues: 1-1875 <BOU>
A;Cross-references: EMBL:X73541; NID:g450550; PIDN:CAA51948.1;
A;Experimental source: strain S288C
A;Experimental source: strain S288C
R;Koelling, R.; Nguyen, T.; Chen, E.Y.; Botstein, D.
Mol. Gen. Genet. 237, 359-36, 1993
A;Title: A new yeast gene with a myosin-like heptad repeat stru A;Reference number: S31207; MUID:93247549; PMID:8483450
A;Accession: S31207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: S38173; S40647; S3120/
R;Baladron, V.; Ballesta, J.P.G.; Bou, G.; submitted to the Protein Sequence Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ঠ
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A;Cross-references: GB:AE001771; GB:AE000512; NID:g4981678; PIDN:AAD36218.1;
A;Experimental source: strain MSB8
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                    A;Experimental source: strain S288C
R;Bou, G.; Esteban, P.F.; Baladron, V.; Gonzalez, G.A.; Cantalejo, J.G.; Remacha, Yeast 9, 1349-1354, 1993
Yeast 9, 1349-1354, 1993
A;Title: The complete sequence of a 15 820 bp segment of Saccharomyces cerevisiae A;Reference number: S40644, MUID:94205265; PMID:8154186
A;Accession: S40647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: A72200;
A;Accession: B72291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Ri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Nelson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-1875 <BAL>
A;Residues: 1-1875 <BAL>
A;Cross-references: EMBL:228320; NID:9486586; PID:9486587; MIPS:YKR095w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: S38158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Evidence for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 399, 323-329, 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S38173
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1-300, 'A', 302-1875 < KOE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPFVGEPLIIEIF-KEDADFVLEKDENAVKVDTVPNEVRRDRIYVTDSPDVAKTLQEK 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NPQVNHSQLNESHRKED----LQREEHSQKSDS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FAGFGVRGTPTFFFFKGKEGLGYLPGYVDKDNFIK-ILKYVAQELKED----FQTYLKKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NLFKKEVFPKEDFQEI--LIPNFVFVELYATDEKTTLFAKE-----VLGEESVSYRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NTTVKEFILNKDTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NERRLIDSSKTETLKIIDLNNTSTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lateral gene transfer between Archaea
72200; MUID:99287316; PMID:10360571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEGKKDAGYVIN-LSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   del Rey, F.
, March 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F.; Esteban,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 219;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---TKDVTATVLDK 160
                                                                                                       structure
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                                                                                                                                                                                                          PID:g450554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153
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                                                                                                                                                                                                                                                                                                                                                                                              M.; Ji
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                                              submitted to the EMBL Data A; Reference number: Z17031 A; Accession: T10466
A; Molecule type: DNA
                                                                                                                                   R; Cheesman, S.J.
                                                                                                                                                      C;Date: 16-Jul-1999 #sequence_revision C;Accession: T10466
                                                                                                                                                                                                             DNA topoisomerase (ATP-hydrolyzing)
C;Species: Plasmodium falciparum
                                                                                                                                                                                                                                                                                         RESULT 16
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A; Status: preliminary; translated

from GB/EMBL/DDBJ

Library,

September 1995

16-Jul-1999

#text_change

20-Jun-2000

(EC 5.99.1.3) II - malaria parasite (Plasmodium

falc

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                                                                                                                                                                                                                                                                                                                                                                                             R;Maggi, L.; Le, T.
submitted to the EMBL Data Library, February 1997
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C;Genetics:
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                                                                                                                                                                                                              A; Introns: 30/2; 200/3
                                                                                                                                                                                                                                               A; Gene: CESP: T23B3.5
                                                                                                                                                                                                                                                                                   A; Experimental source:
                                                                                                                                                                                                                                                                                                    A; Cross-references:
                                                                                                                                                                                                                                                                                                                    A; Residues: 1-211 < MAG>
                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A; Accession: T25911
                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical
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A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /pothetical protein T23B3.5 - Ca
Species: Caenorhabditis elegans
                                                                                                                                          Matches
                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                              position:
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 129
                               133 HRKEDLOREEHSOKSDSTKDVTATVLDKNNISSKSTTNNPNK 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          760 VHLEKNIKQEINK----ISPEKDSIRIMVTQIQTIQKEREDLIEETRKSCOKKIDELEDA 815
                                                                                                        77
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                                                                                                                                        l Similarity
30; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 VKDFARNTTVKEFILNKDTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDF-----ILPVY
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50; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KAENDQLRKRFDY----LQNTILKQDSKTHETLNEYVSCKSKLSIVETELLNLKEEQKLR 759
EKKODKKOEKKOEKKOEKKEKSKKSKKSKKSKKSKKSK 170
                                                                                                        EGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNH----SQLNES 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TA----TVLDKNNISSKSTTNNPN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KGE---LEKGYQFDGWEISGFEGKKDA-----GYVINLSKDTFIKPVFKKIEEK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISQITRESTENMSLLNK---EIQDLYDSKSDISIKLGKEKSSRILAEERFKLLSNTLDLT 703
                                                                   EGEKKDGEKKSEKKDGDKKEEEKKDEEKKDGDKKEDDKKDEKKDEDKKDEKKDADEKKDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----KEEENKPTFDVSKKKDNPQVNHSQLNESHR-KEDL---QREEHSQKSDSTKDV 153
                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                   EMBL:U88309; PIDN:AAB42334.1; GSPDB:GN00019; ce: strain Bristol N2; clone T23B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGD:S0001803; MIPS:YKR095w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.18;
                                                                                                                                                           11.0%;
29.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans
                                                                                                                                          17;
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                                                                                                                                                           Score 99; DB Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 100; D
Pred. No. 28;
                                                                                                                                            Mismatches
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                                                                                                                                                                           DB 2;
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                                                                                                                                          51;
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                                                                                                                                                                             Length 211;
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                                                                                                                                          Gaps
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A;Residues: 1-1397 <CHE>
A;Cross-references: EMBL:X79345
C;Genetics:
A;Gene: TopoII
A;Map position: 14
C;Superfamily: eukaryotic type
C;Keywords: ATP; DNA binding; i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: A84152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-614 <STO>
A;Cross-references: GB:AP001520; GB:BA0000004; NID:g10176401; PIDN:BAB07736.1; GSPDB:GN00
A;Experimental source: strain C-125
C;Genetics:
                   C;Accession: S46817
R;Favello, T.
                                                  hypothetical protein YHR080c - yeast (Saccharomyces cerevisiae) C;Species: Saccharomyces cerevisiae C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change
                                                                                                              RESULT 18
S46817
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C;Date: 01-Dec-2000
C;Accession: A84152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
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 submitted to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein BH4017 [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Bacillus halodurans
Date: 01-Dec-2000 #sequence_revision
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Best Local (
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                                                                                                                                                                                        483
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                     FEGKKDAGYVINLSKDTFIKPVFKKIEEKK--EEENKPTFDVSKKK----DNPQVNHSQL
                                                                                                                                                                                                                                                                                                                                                             SELKPHRYTYTIONGKEMSSTIVSE-----EDFILPVYKGELEKGYQFDGW----EISG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TVLDKWNISSKSTTNNPN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----KKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQ----KSDSTKDVTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DYLLSMPIFSLTLEK---VEDLLTQLKEKERELEILRNITVETMMLKDIEKVEEAIEFQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DFIL--PVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KVLVEELYRKGYDPYKDINKIKKEEIFEQELLDAAD-NPE-----DNEEIIAGITVKDY 1144
                                                                                                                                                                                        GKVIGIVDLGRKYHKGKEDLERRLSKSQIE 512
                                                                                                                                                                                                                             NESHRKEDLQREEHSQKSDSTKDVTATVLD 159
                                                                                                                                                                                                                                                                                                                                                                                                               10.9%; Score 97.5; ilarity 27.3%; Pred. No. 12 Conservative 26; Mismatche
 EMBL
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Data Library, June 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                -GKIEEEKLQDKYNNYTFDFFKKEVVNVQSPIKSTSAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --GPSSMKKKKKKKKKLSSDEESEGGDTSDSSEFLVN 1254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-Dec-2000 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus halodurans (strain C-125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length .1397, 24;
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                                                      #text_change 19-Apr-2002
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A;Description: The sequence of S. cerevisiae cosmid 9205.
A;Reference number: S46795
A;Accession: S46817
A;Accession: S46817
A;Molecule type: DNA
A;Residues: 1-1345 <FAV>
A;Cross-references: EMBL:U10556; NID:g500825; PIDN:AAB68895.1; PID:g500838; MIPS:YHR080c
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein T209.90 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000 C;Accession: T47835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: SGD:S0001122
A;Map position: 8R
C;Keywords: transmembrane protei
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A; Introns: 158/2; 329/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
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Best Local Similarity
Matches 43; Conserv
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Best Local
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                                                                                                         111 PTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDS----TKDVTATVLDKNNISSK 166
                                                                                                                                                                                                                           476 SRRTSKEIAVVAKOTKTGRAKUNIKKQTDTKTESSDDDDDEKEENSKTEKKTVADKKKSV 535
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                                                                                                                                                   536 ADFLKRIKKNSPQKGK----
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                                                                                                                                                                                      52 -DFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEENK 110
                                                                                                                                                                                                                                                                8 ARNTTVKEFILNKD--TGEV-SELKPHRVTVT---
                                                                        KKSDGNVKKENSKVKPRELRSSTGKKKVEVENNNSKSSSKRKQTKETAEVATGKRGRESG
                                     STINNPNK 174
KUDKQPRK
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                                                                                                                                                                                                                                                                                                    10.8%; Score 97; DB 22.9%; Pred. No. 14; tive 29; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Columbia; BAC clone T209
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Pred. No. 29;
                                                                                                                                                    -ETTSKNQKKNDGNV
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                                                                                                                                                                                                                                                                                                         72;
                                                                                                                                                                                                                                                                                                                                         Length 644
                                                                                                                                                                                                                                                                  ---IQNGKEMSSTIVSEE---
                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33;
                                                                                                                                                                                                                                                                                                         44;

    KKENDHQ

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hypothetical protein T28D5.30 - C; Species: Arabidopsis thaliana

Arabidopsis thaliana (mouse-ear cress)

RESULT

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C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-C;Accession: T14188
R;Bevan, M; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; submitted to the Protein Sequence Database, August 1999
A;Reference number: Z17931
A;Accession: T14188
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R;Bevan, M.; Wedler, H.; Wedler, E.; Wambutt submitted to the Protein Sequence Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein F9D16.270 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999 C;Accession: T05612
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A;Introns: 162/3; 201/3; 416/3; 438/3; 460/3; 482/3; 504/3; 519/3; C;Superfamily: Arabidopsis thaliana hypothetical protein T21C14.40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-988 <BEV>
A;Cross-references: EMBL:AL109819
   hypothetical protein Y53C12B.3a - C;Species: Caenorhabditis elegans
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A; Introns: 110/3;
A; Note: F9D16.270
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A;Experimental source: cultivar Columbia; BAC clone
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A; Residues: 1-456 < BEV>
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A; Accession: T05612
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                                                       RESULT 22
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                                                                                                                                             DLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNN--PNK 174
                                                                                                                                                                                KKKAPYEKVAKKNKETYLQ-AMEEYKRTKEEE---
                                                                                                                                                                                                                KKDAGY--VINLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKE
                                                                                                                                                                                                                                                     KNKKEKDPLKPKHPVSAFLVYANERRAALREENKSVVEVAK-----ITGEEWKNLSD
                                                                                                                                                                                                                                                                                      KDTGEVSELKP-HRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IKPVFKKIEEKKE------EENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGRQRNSNVQSSVDEILSYYTDKVPSGVGLNVSERDIVELVEDDVRSAGGLSPNVQRDN-
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                                                                                                         ALOMLKKKEKTON-----LIKKEKATKKKKNENVDPNK 378
                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               247/2; 282/3; 304/3; 361/3; 390/2; 418/3
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22.1%; Pred. No.
                                                                                                                                                                                                                                                                                                                                         10.8%; Score 96.5;
25.0%; Pred. No. 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E.; Wambutt, R.; Hoheisel,
e Database, February 1999
                    Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                         60;
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                                                                                                                                                                                                                                                                                                                                                          456;
                                                                                                                                                                                EEELLKLHKQE
                                                                                                                                                                                                                                                                                                                         31;
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RESULT 24
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hypothetical
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T27136
R;Kershaw, J.; Lennard, N. submitted to the EMBL Data Library, September 1997
A;Reference number: Z20316
A;Accession: T27136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Kershaw, J.; Lennard, N. submitted to the EMBL Data A; Reference number: Z20316 A; Accession: T27135
                                                                                                                                                                                                                                                                                                                                                                     A; Map position: 2
A; Introns: 100/3; 177/3; 218/1; 423/3; 717/2; 867/3
                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: CESP:Y53Cl2B.3b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:299278; PIDN:CAB16492.1; GSPDB:GN00020; CESP:Y53C12B.3bA;Experimental source: clone Y53C12B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-871 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein Y53C12B.3b - Caenorhabditis elegans C;Species: Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: CESP:Y53C12B.3a
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A; Residues: 1-867 <WIL>
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  751
                                                                                                                                                                                          654 KKTPKKDFKVDQEASIEATKTEISEENPK--TDDIQSKDDVTS------KSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100/3; 177/3; 218/1; 423/3; 714/2; 864/3
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45; Conserv
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                                                                                              HCYRCEHYOLPASEVSSHNIRKDNG----
                                                                                                                                 E----KGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIE----EKKEEENKPTFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKTPKKDFKVDQEASIEATKTEISEENPK--TDDIQSKDDVTS------KSEL
CPKKKEEERVAKSR--ESSQKPIDPQEISDDQDDTVPDVPDQIVEQDNQSHKSRHNSENR
                                               VSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 174
                                                                                                                                                                                                                                      RNTTVKEFILNKDTG-----EVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVYKGEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E----KGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIE----EKKEEENKPTFD
                                                                                                                                                                                                                                                                                   10.8%; Score 96.5; I larity 25.0%; Pred. No. 21; Conservative 33; Mismatches
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25.0%; Pred. No. 21;
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                                                                                                --DLWCEHM-KKIKCGHCEATGEQGHHPLI 750
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                                                                                                                                                                                                                                                                                                                                     Length 871;
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protein CAC2985 [imported]

Clostridium acetobutylicum

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R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; I.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: C97267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: C97267
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Mol. Biochem. Parasitol. 94, 185-196, 1998
A;Title: A Plasmodium chabbaudi protein contains a repetitive.
A;Reference number: Z18922; MUID:98418765; PMID:9747969
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C;Accession: T18372
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C;Species: Plasmodium chabaudi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-491 < KUR>
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A; Residues: 1-1939 <WER>
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                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local (
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                                                                                                                                         396 KLIKEKETELNEIHKKYNLEIETIKNELNEKEEELEKNKKAHTVEVINLTKE--IKLLEK
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                                                                                                                                                                             56 PVYK-----GELEKGYQFDGWEISGFEGKKDAGY-----
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                                                                                                                                                                                                                                                        1 KIVVKDFARNTTVKE----FILNKDTGEVSELKPHRVTVTIQNGKEMSSTIV-SEEDFIL 55
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DIKTLNDLI---NNLKNEINTSDNKMNK 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKEEENKPTFD-----VSKKKDN-PQVNHSQLNE----SHRKEDLQREEHSQKSD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KINIDEYGRSEISREF--
                                STKDVTATVLDKNNISSKSTT--NNPNK 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEEKKETEVVKEKIEVKKKEETKEESR 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELEKGYQFDGWEISG-----FEGKKDAGYVINLSKDTFIKPV---FKKIE-----E 103
                                                                      KTEDAKEGHKNELNELNNQLSKLNKEKDNIKNENTELNDKISSLNSEVNILNKDKQTLGN
                                                                                                         KIEEKKE-----EENKPTFDVSKKKDNPQVNHSQLNES----HRKEDLQREEHSQKSD
                                                                                                                                                                                                                       KLEIKDLSQSLVEKEREIFEIKNEYDDKINNMKEKLSSI - - - NDKGIDNTVLHSEEEKIN 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -STKDVTATVLDKNNISSKSTTNNPNK 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KKENLNRNIFDKYEEKIEKEKKNIEEKNNHEIEEKKEVNTKKEDPKLEKEETNVDKKEPR
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                                                                                                                                                                                                                                                                                            46; Mismatches
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Pred.
                                                                                                                                                                                                                                                                                                             Score 96;
Pred. No.
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. 12;
                                                                                                                                                                                                                                                                                                               DB 2;
57;
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                                                                                                                                                                                                                                                                                                                                 Length 1939;
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R;Gardner, M.J.; Tettelin, H.
; Pertea, M.; Salzberg, S.;
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Lawson, D.; Bowman, S.; Barrell, I submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein C0335c - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-2500 <GAR>
A;Cross-references: GB:AE001408;
A;Experimental source: clone 3D7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;A:LLE: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A;Reference number: A71600; MUID:99021743; PMID:9804551 A;Accession: G71609
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C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C;Accession: G71609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Date: 15-Oct-1999
C; Accession: T18427
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C;Species: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                          C;Genetics:
A;Introns: 307/1; 1545/2
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A; Residues: 1-3724 <LAW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A; Accession: T18427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:Z98547; NID:e1325376; PID:e1325379; PIDN:CAB11104.1
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                                                                                                                                                                                                                                                   1 KIVVKDFARNTTVKEFILNKDTGEVSELK---
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                                            NLSKDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNH-SQLNESHRKEDLQREEHSQ 145
                                                                                                                                             ---PHRVTVTIQNGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVI 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----SKOTFIKPVFKKIESKKBESNKPTFDVSKKKONPQVNHSQLNE----SHRKED 137
                                                                                                                                                                                                 KILNKDMKKNKEQEFFKTDETFGSLQSHKIKKYNKGEEKHDKNNEEEKNILYDENQVYSV 1041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Z18935
                                                                                                                                                                                                                                                                                                                         10.6%; Score 95.5; DB 2;
19.1%; Pred. No. 1.3e+02;
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26.1%; Pred. No.
MENKNDMEKKN--DMEKKNDIEKKNDMEKKNDMEKKNDME 1136
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Vugt, B White

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RESULT 29
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C;Date: 12-Aug-1996 #sequence revision 12-Aug-1996 #text_change 21-Jul-2000
C;Accession: I37271; SS2774
R;Hess, H.; Heid, H.; Zimbelmann, R.; Franke, W.W.
Exp. Cell Res. 218, 174-182, 1995
Exp. Cell Res. 218, 174-182, 1995
A;Title: The protein complexity of the cytoskeleton of bovine and human spen A;Reference number: I37271; MUID:95255491; PMID:7737358
A;Accession: I37271
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C;Superfamily: Ascolobus probable DNA-directed DNA polymerase C;Superfamily: Ascolobus probable DNA-directed DNA polymerase C;Keywords: DNA binding; mitochondrion; nucleotidyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable DNA-directed DNA polymerase (EC 2.7.7.7) - fungus (Ascobolus immer C;Species: mitochondrion Ascobolus immersus C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
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A; Residues: 1-1202 < KEM>
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Mol. Gen. Genet. 218, 523-530, 1989
A;Title: In organello replication and viral affinity of linear, extrachromosomal DNA
A;Reference number: S05362; MUID:90066356; PMID:2573821
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Best Local
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SKWPNLKLNKDKTSGEIRMTIKNKNNQSYDI--IGHMIINDGENVITFNRAVDNSIIKIF
                                       NK-PTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNI----
                                                                              DIDESKFPKGSLSFDFKPLKTIEGTKYANYTFPIKKDIVVKDINKKINFNGLDLPKTMDL
                                                                                                                 ELEK-----GYOFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIE-----EKKEEE
                                                                                                                                                           NFTQPFFVVNAKIKFPTGNVRSIGFGNVT-TLTDKETLIKTLAIFLEREDIHTVMSYDEG
                                                                                                                                                                                                NTTVKEFILNK----DTGEVSELKPHRVTVTIQNGKEMSSTI----VSEEDF--ILPVYKG
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Pred. No.
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Pred. No.
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T28391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-277 < KLE>
A; Cross-references: GB: AE000790; NID: g2690224;
A; Cross-references: strain B31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete,
A;Reference number: A70100; MUID:98065943; PMID:9403685
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                                                                                                                                                                                                                                                                                                                                                         R;Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; J. Virol. 73, 533-552, 1999
A;Title: The genome of Melanoplus sanguinipes entomopoxvirus. A;Reference number: Z20484; MUID:99102612; PMID:9847359
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORF MSV230 hypothetical protein - Melanoplus sanguinipes entomopoxvirus C;Species: Melanoplus sanguinipes entomopoxvirus C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                            A; Cross-references: EMBL: AF063866;
                                                                                                                                                                                                                                                                             A;Status: preliminary;
A;Molecule type: DNA
A;Residues: 1-670 <AFO:
                                                                                                                                                                                                                                                                                                                                         A; Accession: T28391
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Best Local :
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                                                                                                                                        Local Similarity
es 42; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226 IDYNKVTIŠEKTIELDLLPHEQVFQMNKNFTKILDTITDLNNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 VNHSQLNESHRKEDLQREEHSQKSDSTKDVTA---TVLDKNNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 LKNFKEIKNIENFFQNQDLLFVLTLKDKNNNNTINIMLNPPNDIQKPKDYILKDLKDTIK 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64
                  50 EEDFILPVYKGELEKGY---
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                                                                                                 3 VVKDFARNTTVKEFILNKDTGEVSELKPHRVTVTIQNGKEMSSTI-----
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                                                                                                                                                                                                                                                                             -670 <AFO>
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                                                              ILLDKVINMKIEKFI----
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                                                                                                                                      39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 94.5; DB
Pred. No. 7.8;
28; Mismatches
                                                                                                                                                           Score 94.5;
Pred. No. 22;
---QFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIE-E 103
                                                                                                                                                                                                                                                                                                                      from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                          NID: 94049647; PIDN: AAC97713.1;
                                                              -KLLKYKYDNVNFEEKKQIISTLLKFNNFDKTEMCGVS
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                                                                                                                                        82;
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                                                                                                                                                                                                                                                              PID:g4049753
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A;Experimental source: (C;Genetics: A;Gene: CESP:T22B11.4
A;Map position: 4
A;Introns: 16/2; 121/1;
                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Caenorhabditis (C;Date: 20-Sep-1999 #sequer C;Accession: T15094 R;Rohlfing, T.; Wohldmann,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein E03H12.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C;Accession: T28771 R;Nelson, J.; Wohldmann, P.; Sansone, J.
                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-553 < ROH>
                                                                                                                                                                                                                                                                                                                                                                        A; Description: The sequence
                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 'A; Introns: 30/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:AF000299; PIDN:AAC47980.1; GSPDB:GN00022; A;Experimental source: strain Bristol N2; clone E03H12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, June 1997
A;Description: The sequence of C. elegans cosmid E03H12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein T22B11.4 - Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                              Species: Caenorhabditis elegans;Date: 20-Sep-1999 #sequence_revision;Accession: T15094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                   Cross-references: EMBL:AF039040; NID:g2736374; PID:g2736378; PIDN:AAB94184.1; GSPDB:GN Experimental source: strain Bristol N2; clone T22B11
                                                                                                                                                                                                                                                                                                           Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                               Reference number: Z18292
Accession: T15094
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Best Local (
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                                                                             Matches
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                                                                           43;
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                                                                                             Similarity
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VKDAEETATVVQ--VDKDEGDVSEETGGTNFFEEEEKKEEGETKKEESS---EEEDGVLK 361
                        VKDFARNTTVKEFILNKDTGEVSE------LKPHRVTVTIQNGKEMSSTIVSEEDFILP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKKODKKDEKKDEKKDEKKEKSKKSKKSKKSKKSKKSK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGKKDAGYVINLSKOTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISSKSTTNNPNK 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKEEENKPTFDVSKKKDNPQVNHSQL-NESHRKEDLQREEHSQKSDSTKDVTATVLDKNN
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                                                                                                                                                    121/1; 167/3; 215/3; 520/3
                                                                           Conservative
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                                                                                     10.5%;
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                                                                           26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18; Mismatches
                                                                       Score 94; DB
Pred. No. 19;
26; Mismatches
                                                                                                                                                                                                                                                                                                               from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 94; DB 2; Pred. No. 6.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-Sep-1999 #text_change 20-Sep-1999
                                                                                                               2;
                                                                                                                                                                                                                                                                                                                                                                          T22B11
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                                                                                                               Length 553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: ODC
C;Function:
            C;Accession: T03045
R;Bahr, U.; Tidona, C.A.; Darai, G.
Virus Genes 15, 235-245, 1997
A;Title: The DNA sequence of Chilo iridescent virus between the ge.
A;Reference number: Z14834; MUID:98141693; PMID:9482589
A;Accession: T03045
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-456 < BAH-
A;Residues: 1-456 < BAH-
A;Cross-references: EMBL:AF003534; NID:g2738385; PIDN:AAB94419.1;
C;Superfamily: Chilo iridescent virus hypothetical protein 009R
                                                                                                                                                                                                                               hypothetical protein 009R - Chilo iridescent virus C;Species: Chilo iridescent virus C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999
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T03045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
T03795
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A; Cross-references:
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Plasmodium raiciparum
C;Date: 23-Apr-1999 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Description: catalyzes the decarboxylation of ornithine to C;Keywords: carbon-carbon lyase; carboxy-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ornithine decarboxylase (EC 4.1.1.17) - malaria parasite C_7Species: Plasmodium falciparum
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Pred. No.
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C;Accession: E89883
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 36
E89883
                  dhak-type molecular chaperone hsp70 - Pyrenomonas salina nucleomorph N;Alternate names: heat shock protein 70 C;Species: nucleomorph Pyrenomonas salina A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endos: C;Date: 13-Jan-1995 #sequence revision 27-Jan-1995 #text_change 20-Si C;Accession: S42488; 345576 C;Accession: S42488; 345576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
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                                                                                                                                                           RESULT 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conserved hypothetical protein SA0976 [imported] - Staphylococcus aureus (strain C;Species: Staphylococcus aureus
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Hofmann, C.J.B.
che EMBL Data Library, March 1993
                                                                                                                                                                                                               DNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT---PTK 543
                                                                                                                                                                                                                                              EDLQ----REEHSQKSDSTKDVT-ATVLDKNNISSKSTTNNPNK 174
                                                                                                                                                                                                                                                                                  GQYHVRIVDKEAFTKANTDKSNKKEQQDNSAKKEATPATPSKPTPSPVEKESQKQDSQKD
                                                                                                                                                                                                                                                                                                                   AGYVINL-SKDTFIKPVFKKIEEKKEEENKPTFDV----SKKKDNPQVNHSQLNESHRK 135
                                                                                                                                                                                                                                                                                                                                                     MVMETTNDDYWKDFMVEGQRVRTISKDAKNNTRTIIFPYVEGKTLYDAIVKVHVKTIDYD
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Pred. No. 16;
39; Mismatches
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Pred. No. 24;
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                                                                                                                                                                                             A;Residues: 1-629 <STO>
                                                                                                                                                                                                            A; Molecule type: DNA
                                                                                                                                            Gene: F17J6.14
                                                                                      Query Match
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Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khayi C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mait C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; S.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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A;Title: The smallest known eukaryotic genomes A;Reference number: S45576; MUID:94268506; PMII A;Accession: S45576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule 'type: DNA A; Molecule 'type: DNA A; Residues: 1-24, 'Q', 26-91, 'H', 93-578 <HOF> A; Cross-references: EMBL: X72621; NID: 9461335 A; Note: the sequence is revised in GenBank entry
                                                                                                                                                                                                                                                                                                     A; Reference number: A86141; A; Accession: G96542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein F17J6.14 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Keywords: ATP; molecular chaperone; nucleomorph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Description: involved in protein folding and assembling/disassembling C; Superfamily: heat shock protein 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Description: Smallest known eukaryotic genomes encode a protein gene: towards understa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Theologis, A.; Ecker, J.R.; Palm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -- VLEFIETNEDLEKEEYEEKEKELKNFANPIISK 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDK 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --LDKKLEAKNSLENYAYNIRNTVRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGFEGKKDA-----GYVINLS---KDTFIKPVFKKIEEKKEEENKPTFDVSKKKDNPQVN 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILNKDTGEVSELKPHRVTVTIQNG---KEMSSTIVSEEDFILPVYKGELEKGYQFDGWEI 73
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     Conservative
                                                                                                                                                                                           GB:AE005173;
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10.4%; Score 93; DB
19.6%; Pred. No. 26;
ive 39; Mismatches
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                                                                                                                                                                                              NID:g11054631;
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Pred. No. 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.J.; Federspiel, N.A.; Conway, A.B.; Conway, A.B.;
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     73;
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                                                      Length
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  Indels
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Mueller, S.B.;
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     52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S.; White, reasy, T.H.;
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Maiti, R.; Marziali
     Gaps
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; Dewar, K.;
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A;Molecule type: mRNA
A;Residues: 1-2464 «NOB»
A;Residues: 1-2464 «NOB»
A;Cross-references: EMBL:X51396; NID:952999; PIDN:CAA35761.1;
A;Cross-references: EMBL:X51396; NID:952999; PIDN:CAA35761.1;
A;Sanchez, C.; Padilla, R.; Paciucci, R.; Zabala, J.C.; Avila
Arch. Biochem. Biophys. 310, 428-432; 1994
A;Title: Binding of heat-shock protein 70 (hsp70) to tubulin.
A;Reference number: S44387; MUID:94234720; PMID:8179328
A;Accession: S44387; MUID:94234720; PMID:8179328
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serine-type D-Ala-D-Ala carboxypeptidase (EC 3.4.16.4) N;Alternate names: penicillin-binding protein 5 C;Species: Bacillus subtilis C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #tex C;Accession: S66040; I39830; A92275; A92307; B61335; D6 R;Ogasawara, N.; Nakai, S.; Yoshikawa, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: protein
A;Residues: 653-663,'IC' <SAN>
C;Superfamily: microtubule-assc
C;Keywords: microtubule bindin
F;589-786/Domain: microtubule le
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J. Cell Biol. 109, 3367-3376, 1989
A;Title: The microtubule binding domain of microtubule-associated protein M;A;Reference number: A33645; MUID:90094539; PMID:2480963
A;Accession: S07549
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Best Local S
Matches 49
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,1861-2064/Region: 17-residue repeats
,1861-2064/Region: 17-residue repeats
,91,116,351,888,1124,1153,1168,1208,1662,1877,1918,2003,2030,2054,2083/Binding
,91,116,351,888,1124,1153,1702,1708,1990,2057,2063,2419/Binding site: phosphate (
,147,969,1336,1562,1563,1702,1708,1990,2057,2063,2419/Binding site: phosphate (
,147,969,1336,1562,1563,1702,1708,1990,2057)
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589-786/Domain: microtubule binding #status experimental 
589-592,639-642,649-652,655-658,660-663,668-671,674-677,679-682,683-686,687-690,
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                                                                                                                                                                                                                                                                                  PRKEEVKKEIKKEIKKEERKELKKEVKKETPLKDAKKEVKKEEKKEVKKEEKEPKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 93; DB 1;
Pred. No. 1.2e+02;
4; Mismatches 57
                                                                                                                                                                                                                                                                                                                                      EHSQKSDSTKDVTATVLDKNNISSKSTTNNPNK 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIDN:CAA35761.1;
bala, J.C.; Avila,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -AMNPIVEKAMSQIVEAEDAAINQAVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57;
                               #text_change 20-Jun-2000
5; D69612; A23307
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                                                                                                                                         Bacillus subtilis
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A; McCesleur, Type: protein
A; McCesleur, Type: protein
A; Residues: 55-68 < YOC>
R; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Broulllet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
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A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
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Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueell
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portecelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R., Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
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Riccital School of the Gram-positive bacterium subtilis.
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J. Biol. Chem. 255, 3964-3976, 1980
A;Title: Sequence of active site peptides from the penicillin-sensitive D-alanine A;Reference number: A92275; MUID:80182289; PMID:6768745
A;Accession: A92275
A;Accession: A92275
A;Molecule type: protein
A;Residues: 32-95, 'X', 97-98, 'XQX', 102 <WAX>
A;Residues: 32-95, 'X', 97-98, 'XQX', 102 <WAX>
R;Waxman, D.J.; Strominger, J.L.
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A;Title: Primary structure of the COOH-terminal membranous segment of a penicillin A;Reference number: A92307; MUID:81117303; PMID:6780559
A;Accession: A92307
                                                                                                                         C;Superfamily: penicillin-binding protein 5 C;Keywords: cell wall synthesis; hydrolase; F;67/Active site: Ser #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Yocum, R.R.; Waxman, D.J.; Rasmussen, J.R.; Strominger, Proc. Natl. Acad. Sci. U.S.A. 76, 2730-2734, 1979
A;Title: Mechanism of penicillin action: penicillin and su A;Reference number: A61335; MUID:79223865; PMID:111240
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Decer R;Todd, J.A.; Roberts, A.N.; Johnstone, K.; Piggot, P.J.; Winter, G.; Ellar, J. Bacteriol. 167, 257-264, 1986
A;Title: Reduced heat resistance of mutant spores after cloning and mutageneral R;Reference number: 139830; MUID:86250602; PMID:3087956
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A;Residues: 48-226,'Q',228-443 <RES>
A;Cross-references: GB:M13766; NID:g142816; PIDN:AAA22375.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein A; Residues: 414-443 < WA2:
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A;Status: preliminary; translated from
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                                                                                                                                                                                                                                  A;Start codon:
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                                                                                                                                                                                                                                                                                                                              A;Experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type:
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                                 Similarity
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                                                                                                                                                                                                                                                                                                                                 GB:Z99104;
ce: strain 1
                                 10.3%;
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168
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   26;
                                 Score 92.5;
Pred. No. 19;
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   49;
                                                            2:
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   Indels
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   33;
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M. Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,

B Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,

Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,

Cronin A., Davies R., Davis P., Dear P., Dearden R., Doggett J.,

Peltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,

A Harper D., Hauser H., Hornoby T., Holroyd S., Horrocks P.,

A Humphray S., Jagels K., James K.D., Johnson D., Kethornou A.,

Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,

Knights A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,

A Knights A., Maddison M., Mclean J., Wooney P., Moule S., Murphy L.,

A Cliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch E.,

A Chilling S., Smith R., Squares R., Squares M., Simmonds M.,

Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,

A Taylor K., Tivey A., Unwin L., Whitehead S., Moodward J.,

"Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
                                                                   Query Match
Best Local S
Matches 44
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Hall N.,
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SEQUENCE 49
                                                                                                                                                                                                      Nature 419:527-531(2002).
EMBL; AL929354; CAD51629.1; -
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N., Bowman S., C
ted (SEP-2002)
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36963
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Churcher C., Quail M., Barrell B.;
) to the EMBL/GenBank/DDBJ databases
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01-MAY-1997
01-MAR-2003
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Hypothetical protein.
SEQUENCE 211 AA; 23955 MW;
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STRAIN=Bristol N2;
MEDLINE=99069613;
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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STRAIN-Bristol N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted
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Science 282:2012-2018(1998).
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Copyright (c) 1993 - 2004 Compugen Ltd.
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TIGR01167; LPXTG	Pfam; PF00082; Peptidase_S8; PRINTS: PR00723: SUBTILISIN.	5; PA; 1.	PF00746; Gram_pos_anchor;	IPR001680; WD40.	IPR000209; Peptidase			IPR001899; Gram p	064;	P00782; 2SBT.	AF291699; AAK19159.1;	AN AMIDE BOND (BY SIMILARITY).	SUBCELLULAR LOCATION: ATTACHED	n. 69:1593-1598	otection agains	ole Genome Appr	Langermann S., Johnson S., Koenig S.;	Brewah Y.A., Walsh W., Barren P.,	Barash S.C., Rosen C.A., Masure H.R.,	T.M., Heinrichs J.H., Adamou J.E.,	MEDLINE=21116976; PubMed=11179332;		M N.A.		313;	· .		Streptococcus pneumoniae.		(Fragmer		•	(TrEMBLrel. 17,		PRELIMINARY;	
LPXIG anchor; 1.	ν.	•	hor; 1.		ase_S8.		ı	Gram pos anchor.				ARITY).	TTACHED TO	(2001).	t Streptoco	oach To Ide	Koenig S.;	h W., Barre	en C.A., Ma	H., Adamou	179332;						Lactobacillales;					Last sequence	Created)		PRT; 21	
													THE CELL WALL PEPTIDOGLYCAN BY	Infect. Immun. 69:1593-1598(2001).	ccus pneumoniae Infection.";	a Whole Genome Approach To Identify Vaccine Molecules		Lathigra R.,	H.R., Tuomanen E.,	J.E., Erwin A.L., Kunsch C.,			•				Streptococcaceae;					nce update)			2119 AA.	

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                TIGRFAMS; TIGRO1167; LPXTG_anchor; 1.
PROSITE; PS50847; GRAM POS_ANCHORING;
PROSITE; PS50840; PA; 1.
PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00138; SUBTILASE SER; 1.
PROSITE; PS00138; SUBTILASE SER; 1.
PROSITE; PS00678; WD REPEATS 1; 1.
PROSITE; PS00678; WD REPEATS 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.; "Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                                                                                   InterPro; IPR001899; Gram pos ancl
InterPro; IPR006192; LPXTG.
InterPro; IPR003137; PA.
InterPro; IPR000209; Peptidase S8.
InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pneumoniae.";
Science 293:498-506(2001).
EMBL; AE007373; AAK74791.1;
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01-MAR-2003
                                                                                                                                                                                Pfam; PF00082; Peptidase S8; 2. PRINTS; PR00723; SUBTILISIN.
                                                                                                                                                                                                                                Pfam; PF00746; Gram pos_anchor; Pfam; PF02225; PA; 1.
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PS00138; SUBTILASE_SER; 1.
PS00678; WD_REPEATS_1; 1.
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Best Local Sim
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Best Local S
Matches 174
Q9S4M8;
Q9S4M8;
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01-MAY-2000
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EMBL; AE008434; AAK99365.1; -.
Hydrolase; Complete proteome.
SEQUENCE 2144 AA: 2000.
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Q8DQP7;
Q1-MAR-2003
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Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett & DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringes DeHoff B.S., Estrem S.T., Khoja H., Kraft A.R., Lagace R.E., Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E., LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P., LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P., McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I., Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P., Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G., Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud i
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Bacteria; Firmicutes;
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"Genome of the bacterium
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(TrEMBLrel.
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                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pneumoniae (strain ATCC BAA-255 / R6).
nicutes; Lactobacillales; Streptococcaceae;
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Last annotation updat
proteinase PrtA (EC 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 894; DB 16;
Pred. No. 1.3e-53;
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Pred. No. 7.8e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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(EC 3.4.21.-).
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sequence update)

01-MAR-2003 (TrEMBLrel. 23,

Last annotation update)

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Best Local Similarity
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InterPro; | PR001680; WD40.
Pfam; PF00746; Gram_pos_anchor; 1.
Pfam; PF00225; PA; 1.
Pfam; PF00225; PA; 1.
Pfam; PF00225; PA; 1.
Pfam; PF00223; SUBTILISIN.
TIGRPAMs; TIGR01167; LPXTG anchor; 1.
PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
PROSITE; PS50840; PA; 1.
PROSITE; PS50840; PA; 1.
PROSITE; PS50840; PA; 1.
PROSITE; PS00138; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE_SER; 1.
PROSITE; PS00138; SUBTILASE_SER; 1.
PROSITE; PS00678; WD_REPEATS_IR; 1.
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                        Q8CPK8
STRAIN=ATCC
Zhang Y., Re
                                                             SEQUENCE FROM N.A.
                                                                                                                                                     Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacil
                                                                                                                                                                                                                                                Penicillin-binding
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InterPro; IPR006192; LPXTG.
InterPro; IPR003137; PA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-1- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bethe G., ten Thoren E.,
"Cloning and seguencing o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=3.B
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NCBI_TaxID=1313;
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                                                                                                                    NCBI_TaxID=1282;
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Ren S., Li
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Pred. No. 1.5e-53;
2; Mismatches 0
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Best Local Similarity
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Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE016746; AA004453.1; -.
Complete proteome.
SEQUENCE 775 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q90784;
01-NOV-1996
01-NOV-1996
                                                                                                                                                                                                                                     structurally related to MAP1B.", J. Neurobiol. 25:1-22(1994). EMBL; X67778; CAA47988.1; -.
                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                  MEDLINE=94157526;
Burg M.A., Cole G
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                                                                                                                                                                                                                                                                                                                                                                                                           Gallus.
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Archosauria; Aves; 1
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                                                                                                                                                                                                                                                                                                                                                     Cole G.J.
                                                                                                                                                                                                                                                                                                                                                               TISSUE=Brain;
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                                                                                        LEKPQKLESKEKTPVKKEKAVKPETKTIVAEKDV
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                                                                                                                                                                                                                           1038 AA;
                                                                                                                                                                               Conservative
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                     EHSQKSDSTKDV 153
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                                                                                                                                                                                                                                                                                                                                                                                                                      Neognathae;
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Neognathae; Galliformes; Phasianidae; Phasiani
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Pred. No. 5.7;
29; Mismatches
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Last annotation update)
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Pred. No. 2;
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                                             -KKEEKPKKEDI
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Abuckee C.O., Burrows C., Cherevach I., Chillingworth C.,
Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
A Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
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A Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
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A Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
Line A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,
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A Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
A Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
Seguence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
"Seguence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
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Okenu D.M.N., Thomas A.W., Conway D.J.;
Okenu D.M.N., Thomas A.W., Conway D.J.;
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NCBI_TaxID=36329;
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Mol. Biochem. Parasitol. 109:185-188 (2000).
EMBL; AJZ52286; CAB65754.1; -.
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NON TER 346 346
SEQUENCE 346 AA; 39127 MW; A804B96BDFAFA010 CR
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MCCOll D.J., Silva A., Foley M., Kun J.F., I
Thompson J.K., Marshall W.M., Coppel R.L., I
"Molecular variation in a novel polymorphic
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Mol. Biochem. Parasitol. 68:53-67(1994).
                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                        Plasmodium falciparum merozoite surface protein-3 (MSP-3).";
MO1. Biochem. Parasitol. 90:21-31(1997).
EMBL; L28825; AAC09377.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=NF54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum (isolate NF54).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antigen.
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01-OCT-2002
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                                                                                                                                                                                                                                                                                                                McColl D.J., Anders R.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=5843;
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                                                                                                                                                                                                                                                                                                                               MEDLINE=98156743; PubMed=9497029;
                                                                                                                                                                                                                                                                                                  Conservation of structural motifs and antigenic diversity
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
169
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TNN 171
                                                                                                                                     STKTKEYAEKAKNAYEKAKNAYQKANQAVLKAKEASS----YDYIL-----
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                          EETESEISEDEEEEEEEEKEEENDKKKEQEKEQSNENNDQKKDMEA----
                                                   NKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISSKST 168
                                                                                                        DGWEISGF--EGKKDAG-----KVINLSKDTFIKPVFKKIEEKKEE-----E
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                                                                                                                                                                                                                                               40119 MW;
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Pred. No. 2.
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annotation update)
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Kemp D.J., An
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antigen associated with
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RESULT 11
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Best Local Similarity
                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Merozoite surface protein 3 (Fragment).
Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI TaxID=5833;
                                                                                                                                                                                                                                                                                                           Q95PI5;
Q95PI5;
01-DEC-2001
Monkeys.";
Submitted
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                                                                  STRAIN=FVO;
Hisaeda H., Saul A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 419:498-511(2002).
EMBL; AE014834; AAN35542.1;
SEQUENCE 354 AA; 40119 M
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Eukaryota; Alveolata; Apicomplexa; H
MCBI_TaxID=36329;
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                                              "Merozoite Surface
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                                              Protein
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                                                                  Long C.A.,
the
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Pred. No. 2.5;
35; Mismatches
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EMBL/GenBank/DDBJ databases
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                                                                     Miller L.H.,
                                              Protection
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                                          Against Malaria
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                                                                     Stowers
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RESULT 13
Q815F3
Q815F
AC Q815F
AC 01-MA
DT 01-MA
DT 01-MA
DT 01-MA
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Q9U6C9
ID Q9U6C
AC Q9U6C
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AC Q9U6C
DT 01-MA
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DE POlym
GN MSP-3
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OC EUKAR
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Best Local S
Matches 43
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Matches
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        Q815F3;
Q815F3;
01-MAR-2003
01-MAR-2003
01-MAR-2003
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Q9U6C4;
01-MAY-2000
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum.
Eukaryota; Alveolata;
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13,
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           Last sequence up
                                 Created)
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Last annotation update)
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         update)
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Hypothetical

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Matches 41
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Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.
Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Valdya A.B.,
Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
Fraser C.M., Barrell B.,
"Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum.
Eukaryota; Alveolata;
NCBI_TaxID=5833;
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NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                           MEDLINE=98156743; PubMed=9497029;
MCCOll D.J., Anders R.F.;
"Conservation of structural motifs and antigenic of the conservation of structural motifs and antigenic of the conservation of structural motifs and antigenic of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the conservation of the 
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Plasmodium falciparum
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3L; U08852; AAC47832.1; -.
QUENCE 379 AA; 43302 MW; ABF9D54E1
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MEDLINE=95198774; PubMed=7891748;

MCCOll D.J., Silva A., Foley M., Kun J.F., F
Thompson J.K., Marshall V.M., Coppel R.L., K
"Molecular variation in a novel polymorphic
Plasmodium falciparum merozoites.";
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MA Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,

Da Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,

Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,

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A Cronin A., Davies R., Davies P., Dearden F., Doggett I.,

Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,

A Harper D., Hauser H., Horneby T., Holroyd S., Horrocks P.,

A Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,

A Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,

A Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,

A Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,

A Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,

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"Conservation of structural motifs and antigenic diversity in Plasmodium falciparum merozoite surface protein-3 (MSP-3).";
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Best Local S
Matches 52
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                                                                                                                             Gardner M.J., Hail N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K. Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Wartin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Venter C.M., Barrell B.,
                                                                                                                                                                                                                                                                                                                                 MEDLINE=99021743; PubMed=9804551;
Gardner M.J., Tettelin H., Carucci D.J., Cummings L.M.,
Koonin E.V., Shallom S., Mason T., Yu K., Fujii C., Pedt
Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Pert
Salzberg S., Zhou L., Sutton G.G., Clayton R., White O.,
Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.;
"Chromosome" 2 sequence of the human malaria parasite Pla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AL929351; CAD51431.1;
Hypothetical protein.
SEQUENCE 3008 AA; 356023
                                                                              Nature 419:498-511(2002).
EMBL; AE001410; AAC71925.2;
                                                                                                                                                                                                                                                                       STRAIN=3D7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical
                                                                                                                     Genome sequence of
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                                                                                                                                                                                                                                                                                                            282:1126-1132(1998).
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951 AA; 1
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             12.2%;
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Last annotation updat
 Score 109; DE
Pred. No. 12;
32; Mismatches
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Pred. No. 39;
                                                    AC8D889358A84F4F
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                                                                                                                        Plasmodium
                           Length 951;
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49;

Indels

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Gaps

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01-OCT-2000 (Trembirel 15, L
01-OCT-2002 (Trembirel 22, La
Hypothetical 71.7 kDa protein.
PEC0465C, MAL3P4.20.
Plasmodium falci-
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Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T.,
Churcher C.M., Craig A., Davies R.M., Harris D., Holroyd S., Hornsby
Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Hornsby
Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S.,
Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,
Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,
Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,
Whitehead S., Woodward J.R., Newbold C., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical
SEQUENCE 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Falciparum .";
Falciparum - 400:532-538(1999).
Nature 400:532-538(1999).
EMBL; AL0088970; CAAL5610.2; --
InterPro; IPR002483; PWI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01480; PWI; 1.
SMART; SM00311; PWI; 1.
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Eukaryota; Alveolata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KDDNNNNNGTKQIEEKNKINKSDL--HRQNELNLQSGK-----NEQDI-----NKNE
                                                                                                                                                              NPNK 174
                                                                                                                                                                                                                                                                                                                             LELLINEEKKEEHIADTLNENK-TNDIKKVKNENENINENVYNENKDISNKDKEHVSHQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IVSEEDFILPVY-----KGELEKGYOFDGWEISGFEGKK----DAGYVINLSKDTFIKPV
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                                                                                                                                                                                                                                                                                                                                                                            FKKI--EEKKEE-----ENKPTFDVSK-KKUNPQVNHSQLNE-----SHRK 135
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600 AA; 71663 MW; 57EAB42565CAD64C CRC64;
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Last annotation updat
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Pred. No. 8.3;
22; Mismatches
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01-MAR-2001
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Pfam; PF00278; Orn_DAP_Arg_deC; 1.
PRINTS; PR01179; ODADCRBXLASE.
                                                                                                                                                                                                                                                                                                                                                                                                             Birkholtz L., Joubert F., Neitz A.W.H., Louw P. "Molecular characterisation of Plasmodium falc decarboxylase cDNA obtained by RACE."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Alveolata;
NCBI_TaxID=5833;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eyermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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HSSP; P07805; 1F3T.
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Pred. No. 7.5;
32; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical SEQUENCE 3
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EMBL; AE014818; AAN36777.1;
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Fraser C.M., Barrell B.,
"Genome sequence of the human malaria parasite Plasmodium
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Gardner M.J., Hall N., Fung E., Wh
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01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 25, 01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TremBrel. 23, 01-OCT-2002 (TremBrel. 23, 01-OCT-2002 (TremBrel. 23, 01-OCT)
                                        DNA Res.
EMBL; APC
                                                                                                      Nakamura Y.;
"Structural analysis of Arabidopsis
Sequence features of the regions of
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01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-OCT-2002 (TrEMBLrel. 22, Last annotation
Genomic DNA, chromosome 3, BAC clone: T19N8.
Arabidopsis thaliana (Mouse-ear cress).
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBI_TaxID=57266;
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"Allelic lineages of the merozoite surface protoplasmodium reichenowi and Plasmodium falciparum Mol. Biochem. Parasitol. 109:185-188(2000).
EMBL; AJ252287; CAB85901.1; -.
   SEQUENCE
                                                                                                                                                                                                                                                                                  STRAIN=Columbia;
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Submitted (MAY-2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3702;
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Res. 7:217-221(2000)
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                                                                                                                                                                                                                                                                                                                                                                                         Sato S., Nakamura Y., Asamizu E., To the EMBL/GenBank/DDBJ databases
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NCBI_TaxID=36329;
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01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Harris B., Lennard N., Clark L., Line A., Barron A., Corton C., Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                   Putative phosphatidyl-inositol-transfer protein. T5I8.14.
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1; Mismatches
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Pred. No. 84;
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Matches 40
SEQUENCE FROM N.A. Chang C.H. Yamada K., Chan M.M., Chang C.H. Quach H.L., Tang C.C., Toriumi M Yu G., Yuan S., Chen H., Cheuk R Palm C.J., Shinn P., Southwick A Ecker J.R., Theologis A.;
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                                                                                                                                              STRAIN-cv. Columbia;
Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C.,
Vysotskaia V.S., Schwartz J.R., Ngan I., Gonzalez A., All
Li J., Kremenetskaia I., Luros J., Ngan I., Gonzalez A., All
Araujo R., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N
Huizar L., Kim C., Palm C., Rowley D., Shinn P., Walker M.,
Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
"Arabidopsis thaliana chromosome 1 BAC T518 sequence.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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OSSA84

OSSA84;

O1-MAY-2000 (TrEMBLrel. 13, Created)

O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)

O1-MAR-2003 (TrEMBLrel. 23, Last amnotation update)

T5I8.14 protein (Hypothetical protein).

T5I8.14 OR ATIG30690.
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InterPro; IPR001071; RetBind/tocTrans.
Pfam; PF00650; CRAL TRIO; 1.
Pfam; PF03765; CRAL_TRIO; 1.
PRINTS; PR00180; CRATINIALDHBP.
SMART; SM00516; SEC14; 1.
PROSITE; PS50191; CRAL_TRIO; 1.
                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core en
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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PS50191; CRAL_TK10, ...
F40 AA; 61166 MW;
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               Chang C.H., Da
, Toriumi M., W
H., Cheuk R., (
Southwick A.,
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165 161

Lenz C., Liu ez A., Altafi

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N.

Davis Nguyen M., Davis R.W.,

с., Lee

æ . J.М., Wu н.С., eudicots;

Rosidae;

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Best Local Similarity
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EMBL; BT000959; AAN41359.1; -.
InterPro; IPR001251; CRAL TRIO.
InterPro; IPR001071; RetBind/tocTrans.
Pfam; PF00650; CRAL_TRIO; 1.
Pfam; PF03765; CRAL_TRIO, 1.
PRINTS; PR00180; CRETINALDHBP.
SMART; SM00516; SEC14; 1.
                                                                                                                                                                                                                                           EMBL; U00796; AAC18634.1; -. SPOTTENCE 325 AA; 38448 MW;
                                                                                                                                                                                                                                                                  MEDLINE=98198836; PubMed=9539429; Rieben W.K. Jr., Gonzales C.M., Gonzales S. Kiyosawa H., Hughes J.E., Welker D.L.; "Dictyostelium discoideum nuclear plasmid the Ddpl and Ddp2 plasmid families,"; Genetics 148:1117-1125(1998).
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Eukaryota; Mycetozoa; Dic
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                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50191; CRAL_TRIO; 1.
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233
                     152
                                               173
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                     D 152
o.
                                                                    --IEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKE-----DLQREEHSQKSDSTK 151
                                                                                             NHIKDSGYYATNEEIEIFLESCTLCKEITAQTKRNSYKKRNIINKLPEEEEEEEEEEEE
                                                                                                                                                                    HRVTVTIQNGKEMSSTIVSEEDFILPVYK-GEL--EKGYQFDGWEISGFEGK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KVEEEKKSEAVVTEEAPKAETVEAVVTEEIIPKEEVTT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QLNESHRKEDLQREEHSQKSDSTKDVTATVLDKNNISS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -ALSDLKSKLEEAIVDN----TLLKTKKKESSPMKEKKEEVVKPEAEVEKKKE--EAAEE 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WEISGFEGKKDAGYVINLSKDTFIKPVFKK---IEEKKEEENKPTFDVSKKKDNPQVNHS
                                             EBEBEGEEEVEKPTISEBEEBETPAVSBEBKEBBEBEBETPAVSBEBKEBEGGEBDKEK
                                                                                                                        ---KDAGYV-----
                                                                                                                                             HRTITSIKN--RFSVKKIGDEEKLFRISKNGELIVLNELEFDNFHIK--EGKHLRKSKMF 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTVKA-VVEETKVEEDESKP-----EGVEKSASFKEESDFFADLKESEKK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61189 MW;
                                                                                                                                                                                                        11.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.6%;
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                                                                                                                                                                                                                                                                                                                                                                                            eum (Slime mold).
Dictyosteliida; Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                 22,66
                                                                                                                      -INLSKDTFIKPV-----FKK---
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                                                                                                                                                                                              25;
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                        Score 103.5; | Pred. No. 9.5;
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Pred. No. 15;
                                                                                                                                                                                                                                             69A43D0C632058A6 CRC64;
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                                                                                                                                                                                              Mismatches
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RESULT 30
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Best Local S
Matches 52
                                           093424
(093424; P90801;
(093424; P90801;
(01-JAN-1999 (TrEMBLrel. 09, Created)
(01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
(01-JAN-1999 (TrEMBLrel. 23, Last annotation update)
(11-MAR-2003 (TrEMBLrel. 23, Last annotation update)
(12-MAR-2003 (TrEMBLrel. 23, Last annotation E02A10.2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q812Z6
Q812Z6;
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C., Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J., Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z., Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P., Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A., Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N., Line A., Maddison M., Melean J., Mooney P., Moule S., Murphy L., Oliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch E., Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M., Reeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K., Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J., Sulston J.E., Craig A., Newbold C., Barrell B.G; "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
             Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical SEQUENCE 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDILING SALES CO., MEDILING SALES C., MEDILING SALES C., MEDILING SALES C., CHARLES C., MARCHER S., Barron A., Brooks K., Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K., Mungall K., Bowman S., Atkin R., Chillingworth C., Burrows C., Cherevach I., Chillingworth C., Corton C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Alveolata;
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein. PFI0765W.
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01-MAR-2003
                                        Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIQIRKEKTTTSQNQL---KEKEKTQETKKHD-----ENNKSNNNVVNSSENF-MKIYKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 AA;
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             Nematoda; Chromadorea; cinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.5%;
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Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 103; DB Pred. No. 7.4; 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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                              Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Length
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Best Local S
Matches 48
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01-MAR-2003
01-MAR-2003
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SEQUENCE FROM N.1
STRAIN=BRISTOL NI
                            MEDLINE=22255705; PubMed=12368864;
Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.
Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Valdya A.B.,
Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
Fraser C.M., Barrell B.,
"Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thomas K.;
Submitted
                                                                                                                                                                                   Plasmodium falciparum Eukaryota; Alveolata; NCBI_TaxID=36329;
                                                                                                                                                                                                                                 01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
Hypothetical protein.
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                                                                                                                                                       SEQUENCE FI
STRAIN=3D7
            Nature
                     falciparum."
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SIGNAL
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PRINTS; PR01228; EGGSHELL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WormPep; E02A10.2; CE09116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUN-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=BRISTOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REVISIONS
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P10968; 2CWG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KIVVKDFARNT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48;
 419:498-511(2002).
1E014842; AAN35996.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                 FROM N.A.
                                                                                                                                                                                                                                                                                                                                               EEK 371
                                                                                                                                                                                                                                                                                                                                                                     LDK 160
                                                                                                                                                                                                                                                                                                                                                                                                     FKKIEEKKEEENKPTFDVSKKKDNPQVNHSQLNESHRKEDLQREEHSQKSDSTKDVTATV
                                                                                                                                                                                                                                                                                                                                                                                                                                     INHKEVAEK--NEEDKKEEEPKKEEEKKEEVEKKE---EDEKKDE
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                                                                                                                                                                                                                                                                                                                                                                                         -KKEEEKKEEEQKE--EVEKKEE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                         -NGKEMSSTIVSEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPV
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N2;
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36963
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26.2%;
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Apicomplexa;
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                                                                                                                                                                                                                                                                   Created)
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POTENTIAL.
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Pred. No. 13
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RESULT
Q98QA1
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Best Local S
Matches 48
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Best Local
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=UAB CTIP;
MEDLINE=21267165; PubMed=11353084;
Chambaud I., Heilig R., Ferris S., B.
Chambaud I., Dybvig K., Wroblewski H.,
Moszer I., Dybvig K., Wroblewski H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein. SEQUENCE 449 AA; 5
                                                                                                                                                                                                                        MypuList; MYPU_4650; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q98QA1
                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                         Mycoplasma pulmonis
Nucleic Acids Res. !
                                                                                                                                                                                                                                                                                         Moszer I., Dy
Blanchard A.;
                                                                                                                                                                                                                                                                                                                                                                                                   MYPU 4650
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q98QA1;
                                                                                                                                                                                                                                               EMBL; AL445564;
                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=2107;
                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                       Mycoplasma pulmonis.
                                                                                                                                                                                                                                                                                                                                                                                                             LIPOPROTEIN.
                                                                                                                                                                                                                                                                             "The complete genome sequence of the murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32
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189
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                                                                                                                                                 9
                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KIVVKDFARNTTVKE---FILNKDTGEVSELKPHRVTVTIQNGKEMSSTIVSEEDFILPVY
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NDSKEKNDENTNK
                  NISSKSTTNNPNK
                                                     NKPTFDVSKKKD----NPQVNHSQLNES--HRKEDLQREEHSQKSDSTKDVTATVLDKN-
                                                                                  SEDNIIFSLLNIENNAKFQLDEF-
                                                                                                      SEEDFILPVYKGELEKGYQFDGWEISGFEGKKDAGYVINLSKDTFIKPVFKKIEEKKEEE
                                                                                                                            KNDSAKNFVLKSSDLISISEKFQFKFKNNLDKNQKIIEGVITFINSETKEIVKKETILNL
                                                                                                                                               RNTTVKEFIL-NKDTGEVSEL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSVRKDVADFLNVEESYFSENKEK-
                                         - KITDNISSKEDEKNKNPKDNENSNNNSSDQKNDELQKNNSDKLNDNVQDEKANKENSNS
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                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                              CAC13638.1;
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                                                                                                                                                                                                                73762 MW;
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201
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22,
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0; Mismatches
                                                                                                                                                                                Score 102;
Pred. No.
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Pred. No. 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85B62272D6257C68 CRC64;
                                                                                                                                                                                                                 42BD88930861960D CRC64;
                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                               Barbe V.,
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Rocha E.F
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                                                                                                                                                                                                                                                                              respiratory pathogen
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                                                                                   VSKDEKFKIKFQEINFSQTEQ
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                                                                                                                                                                                                                                                                                                               Galisson
                                                                                                                                                                                             622;
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                                                                                                                                                                        Gaps
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H
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RESULT 33

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RESULT 34
Q81FN0
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Best Local S
Matches 52
Query Match
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InterPro; IPR001985; SAM_decarbox.
Pfam; PF02784; Orn_Arg_deC_N; 1.
Pfam; PF00278; Orn_DAP_Arg_deC; 1.
Pfam; PF01536; SAM_decarbox; 1.
PRINTS; PR01179; ODADCRBXLASE.
ProDom; PD002379; SAM_decarbox; 1.
                                               SEQUENCE FROM N.A.

Hamlin N., Pain A., Berriman B., Hall N., Bown
Harris B., Harris D., Lawson D., Quail M., Ba:
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ
EMBL; AL035477; CAD49270.1; -.
                        Hypothetical SEQUENCE 16
                                                                                                                                       Eukaryota;
                                                                                                                                                              Hypothetical protein. PFD1115C.
                                                                                                                                                                                        01-MAR-2003
                                                                                                                                                                                                    01-MAR-2003
                                                                                                                                                                                                                 01-MAR-2003
                                                                                                                                                                                                                          QBIFNO;
                                                                                                                                                                                                                                          Q8IFN0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-WAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2000 (TrEMBLrel. 22, Last annotation update)
S-adenosylmethionine decarboxylase-ornithine decarboxylase.
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01-MAY-2000
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                                                                                                                                                 Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Biol. Chem. 275:8097-8102(2000)
EMBL; AF094833; AAF00073.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthesized by a Bifunctional Ornithine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mueller S., Da'dara A., Lu
Madhubala R., Walter R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=20179918; PubMed=10713131;
MEDLINE=20179918; PubMed=10713131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=5833;
                                                                                                                        NCBI_TaxID=36329;
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                                                                                                                                                                                                                                                                                                      GQGNIMNDLIITSTNDSTSKKNDHSSSQVIQNVSCTIRDKEGDNIKINTHTINNPN
                                                                                                                                                                                                                                                                                                                                                                                                         KTKYGYYSFEKISLAINMSIDHY----FSHMKDNLRVICEPGRYMVAASSTLAVKIIGKR
                                                                                                                                                                                                                                                                                                                                                                                                                                  LPVY-----KGELEKGYQFDGWEISGFEGKKD-----AGYVINLSKDTFIKPVFKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VKDFARNTTVKEFILNKDTGEVSEL------KPHRVTVTIQNGKEMSSTIVSEEDFI
                                                                                                                                                                                                                                                                                                                                                      RPTFQGIMLKELKDHYDPLNFAQQENKKQDETKINHNNDNNDNNDNNDNNINNNNNQKG
                                                                                                                                                                                                                                                                                                                                                                             -----IEEKKEEENKPTF--DVSKKKDNPQVNH---SQLNESHRKEDLQREEHSQK- 146
                                                                                                                                       Alveolata;
                        il protein.
1612 AA;
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                                                                                                                                                                                                                                         PRELIMINARY;
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                        190946 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1_decarbox; 1.
166441 MW; 8842B97C05056E6E CRC64;
11.4%;
                                                                                                                                                                                                                                                                                                                               --SDST-----
                                                                                                                                     Apicomplexa; Haemosporida;
                                                                                                                                                  (isolate 3D7)
                                                                                                                                                                                       23,
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                                                                                                                                                                                       Last sequence update)
Last annotation update
                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
Score 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 102;
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                       F00A408EB4521D07 CRC64;
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DB
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Barrell B
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                                                             databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1419;
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Length 1612;
                                                                                                                                    Plasmodium
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                                                                                     Churcher
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RESULT 35
Q9PPL5
ID Q9PPI
  AC QOUTO
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Matches 47; Conserv
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Best Local Similarity
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Q9V7J0 I
Q9V7J0; Q9GQ8
01-MAY-2000
01-OCT-2002
01-OCT-2002
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Q9PPL5;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDILINE EXCLUSIVE, EMPIRED E. W., Mungall K., Ketley J.M., Churcher C., Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C., Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W., Ouail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
Campylobacteraceae; Campyl
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01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 403:665-668(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervariable sequences.";
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  ; Q9GQ81;
-2000 (TrEMBLrel. 1
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-2002 (TrEMBLrel. 2
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312 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KGYQFDGWEISGFEGKKDAGYVINL---SKDTFIKPVFKKIEEKKEEENKPT---FDVSK 117
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                                                                                               PRELIMINARY;
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B.W., Mungall K.,
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9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 101.5;
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RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Hardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Henderson S.N.,
RA Hardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Defeiffer B.D.,
RA Hardon R.C., Rogers Y.-H.C., Miklos G.L.G.,
RA Hardon R.C., Rogers J.-H.C., An H.-J., Andrews-Pfannkoch C.R., Miklos G.L.G.,
RA Hardon M.R., Basun A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basun A. Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies S.M.,
RA Coler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Cholos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dudbin K.J. Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Ghabart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Hasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pelleb J.M.,
RA Melson D.R., Welson K.A., Nixon K., Nusskern D.R., Pelleb J.M.,
RA Rainert K., Renington K., Standers R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiansos I., Simpson M., Skupski M.P., Smith T.,
RA Spier B., Spradling A.C., Standers R.D.C., Scheeler F., Shen H.,
RA Glibs R.A., Waess T., Zhong W., Zhan M., Zhang G., Zhao Q.A.,
RA Glebs R.A., Myers E.M., Zhong W., Zhan S., Zhu X., Smith H.O.,
RA Jeng X.H., Zhong F.N., Zhong W., Zhan S., Zhu X., Smith H.O.,
RA Jeng X.H., Sheng L., Shenghila melanogaster.*;
                                                                                                                                                                                                                                                              A Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
A Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
A Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
A Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
A Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
A Phouanenavong S., Pittman G.S., Pari V., Richards S., Scheeler F.,
A Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
A Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,
T. "Sequencing of Drosophila melanogaster genome.",
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D. Andams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R. Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Henderson George R.A., Lewis S.E., Richards S., Ashburner M., Henderson Sutten G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutten G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
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Ephydroidea; Drosophilidae; Drosophila.
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Drosophila melanogaster (Fruit
         Tupy J.L., Bergman Clamp M., Drysdale
                                                                                          Hradecky P.,
                                                                                                                                                                                          SEQUENCE FROM
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Matthews B.B., Bayraktaroglu L., Campbell
Kaminker J.S., Prochnik S.E., Smith C.D.,
Berman B., Carlson J.W., Celniker S.E.,
Emmert D., Frise E., de Grey A., Harris N.
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R.C., Rogers Y.,
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Matches 34
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Q17595;
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O'Neil K.T., Focht
Friedman P.A.;
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SEQUENCE FROM N.A.
MEDLINE=20564328; PubMed=10956665;
Dinchuk J.E., Henderson N.L., Burn T.C
                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
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SEQUENCE FROM
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STRAIN=Bristol
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Science 282:2012-2018(1998).
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e EMBL/GenBank/DDBJ
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S., Hollis J.M.,
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   RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Bandari D., Bolshakov S.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., McPherson D.L.,
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Eukaryota; Metazoa; Arthropoda; Harabycera; Brachycera;
Neoptera; Endopterygora; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
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A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese
A Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
A Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
A Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang J.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.,
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T "The genome sequence of Drosophila melanogaster.";
I Science 287:2185-2195(2000).
                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hradecky P., Lusuy M.A., Matthews B.B., Bayraktaroglu L., Campbell K. Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Krommiller B., Marshall B., Milburn G., Richter J., Russo S., Searle S.M.J., Smith B., Shu S., Smutrniak F., Mhitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/nnpr 3-1."
                                                                                                                                                                                                                                                                           EMBL; AE003808; AAF58064.2; FlyBase; FBgn0034075; Asph. SEQUENCE 556 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M., Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D., Ferriera S., Frise E., Galle R.F., Gary N.S., George R.A., Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., WILINGSH T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J., Paceleb J., Paragas V., Park S., Patel S., Pfeiffer B., Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M., "Sequencing of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Banzon J., An H., Baldwin
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                                                                                                                                                                                                                                                                                                                                                                                                                          Gibbs
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                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                        ibbs R.A., Rubin G.M., Venter C.J.;
EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                             Score 101.5;
Pred. No. 23;
212
                                168
                                                                                                                                                                                                                                                                                B420980CBD6C357A CRC64;
                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bayraktaroglu L., Campbell K., Prochnik S.E., Smith C.D., lson J.W., Celniker S.E.,
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                                                                                                                                                                                                                                              DB 5;
                                                                                                                                                                                                             51;
                                                                                                                                                                                                               Indels
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X., Smith H.O.,
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                                                                                                                                                                                                           Gaps
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                                                                     193
                                                                                                                                         135
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RESULT 39 Q9GQ82 ID Q9GQ8

Q9GQ82

PRELIMINARY;

PRT;

785

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RC STRAINB-Erkeley; PubMed=10731132;
RX MEDLINB=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barlew R.M., Bayeard A., An H.-J., Andrews Pfannkoch C.R., Miklos G.L.G.,
RA Barlew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beseon K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Grablos B., Delcher A., Domes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Ghant P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Mostreila N.V., Mobarry C., Morris J., Moshreti A.,
RA Lisko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lisko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lisko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lisko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lisko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshreti A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshreti A.,
RA Rainert K., Reningron K., Saunders R., D.C., Scheeler F., Shen H.,
RA Rainert K., Reningron K., Stapleton M., Strong R., Sun E.,
RA Wang Z.-Y., Wassaman D.A., Weinstock G.M., Weissenbach J.,
RA Mary S., Shen H., P., Saith T.,
RA Shen B.
SEQUENCE FACTOR OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERT
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Aspartyl beta-fydroxylase variant 1 (CG8421-PA)
ASPH OR CG8421 OR CG18658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20564328; PubMed=10956665; Dinchuk J.E., Henderson N.L., Burn T.O'Neil K.T., Focht R.J., Scully M.S.,
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Catalytic
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S., Hollis J.
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Hollis G.
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Jietz S.
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                                                                                                                                                                                                                                            D.A.,
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REPRESENTATION OF THE PROPERTY

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Best Local S
Matches 34
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Q815S6;
01-MAR-2003
Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Eisen J.A., Rutherford K., Saberg S.L., Craig A., Kyes S., Chan M.-S., Nene V., Shallom S.J., Sh.B., Peterson J., Angiuoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
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e EMBL/GenBank/DDBJ
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McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Veneer J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B.; "Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                          DB 5; Length 1377;
                                                               falciparum.";
Nature 419:498-511(2002).
EMBL; AE014846; AAN36214.1; -.
Initiation factor.
SEQUENCE 1377 AA; 166059 MW; 587CF2E3F2C8FBE9 CRC64;
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